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OM protein - protein search, using sw model

Run On: September 13, 2000, 02:22:07 ; Search time 17.65 Seconds  
(without alignments)  
18.788 Million cell updates/sec

Title: US-09-155-076-1

Perfect score: 14  
Sequence: 1 AEFHRWSSYVHWK 14

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0  
Searched: 188963 seqs, 23686106 residues

Word size: 0

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0  
Maximum DB seq length: 1000000

Post-processing: Listing first 45 summaries

Database: A\_Geneseq\_36.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	100.0	14	1 W35340	Human acetylcholin
2	14	100.0	39	1 R77010	Alternative human
3	14	100.0	45	1 W48800	C-terminal fragmen
4	14	100.0	45	1 W68144	Human AChE splice
5	14	100.0	45	1 W74586	Amino acid sequenc
6	14	100.0	500	1 R06990	Human foetal acety
7	14	100.0	613	1 R06989	Human acetylcholin
8	14	100.0	614	1 R80726	Human acetylcholin
9	64.3	575	1	1 W39078	Torpedo californic
10	9	64.3	575	1 W39079	Peptide fragment o
11	5	35.7	12	1 R63398	Streptococcus pneu
12	5	35.7	111	1 W61227	Human secreted pro
13	5	35.7	136	1 W74955	Product of ORF 1 f
14	5	35.7	256	1 P70559	Polyhydroxyalkanoa
15	5	35.7	261	1 R63805	Hepatitis C virus
16	5	35.7	319	1 R63349	Human acetylcholin
17	4	28.6	4	1 W35341	Human acetylcholin
18	4	28.6	4	1 W35342	Human acetylcholin
19	4	28.6	4	1 W35343	ICAM-1 inhibiting
20	4	28.6	8	1 R25957	Human platelet gly
21	4	28.6	10	1 W32750	LM609 grafted anti
22	4	28.6	12	1 W76015	LACI K1 derivative
23	4	28.6	12	1 R78593	Hepatitis C virus
24	4	28.6	12	1 R78598	Hepatitis C virus
25	4	28.6	12	1 R96443	Clot-inducing pept
26	4	28.6	12	1 R96444	Prorenin derived s
27	4	28.6	13	1 R67073	Prorenin derived s
28	4	28.6	14	1 W21535	Retro-peptide. New
29	4	28.6	14	1 W21536	Snake venom lopus
30	4	28.6	15	1 R26578	Snake venom lopus
31	4	28.6	15	1 W50991	Snake venom lopus
32	4	28.6	15	1 W50990	Snake venom lopus
33	4	28.6	15	1 W50992	Snake venom lopus

Peptide which bind  
Snake venom derive  
Vasopressin type 2  
Amino acid sequenc  
N-terminal sequenc  
H. horridum extendi  
Human B-type natri  
N-terminal sequenc  
Snake venom derive  
Human 5' EST secre  
UGT1BP Exon 1 prod  
Transcriptional si

## ALIGNMENTS

RESULT 1  
W35340  
ID W35340 standard; peptide; 14 AA.  
AC W35340;  
DC 17-APR-1998 (first entry)  
DE Human acetylcholinesterase 14-mer peptide.  
KW Acetylcholinesterase; AChE; neuronal degeneration;  
KW Parkinson's disease; Alzheimer's disease; stroke; cancer;  
KW calcium channel modulator; antibody; inhibitor.  
OS Homo sapiens.  
PN W09735962-AL.  
PD 02-OCT-1997; G00796.  
PF 21-MAR-1997; G00796.  
PR 22-MAR-1996; GB-006040.  
PA (ISIS-) ISIS INNOVATION LTD.  
PI Greenfield SA, Vaux DU;  
DR WPI: 97-489626/45.  
PT Peptide(s) from acetylcholine esterase which open calcium channels -  
PT used for treating disorders of the central nervous system, cancer  
PT and stroke  
PS Claim 1; Page 20; 27pp; English.  
CC This 14-mer peptide corresponds to residues 535-548 of the  
CC Acetylcholinesterase mature protein. This peptide is known to  
CC act alone or in synergism with a fragment of beta-amyloid to  
CC contribute to neuronal degeneration. Compounds that inhibit the  
CC biological activity of the novel peptides, and antibodies, can be  
CC used to control cytoplasmic calcium ion currents in vivo, and are  
CC useful for treating disorders of the central nervous system  
CC (e.g. Parkinson's and Alzheimer's diseases), stroke and cancer.  
SQ Sequence 14 AA;

Query Match 100.0%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 4.6e-11;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14  
DB 1 AEFHRWSSYVHWK 14

## RESULT 2

R77010  
ID R77010 standard; Protein; 39 AA.  
AC R77010;  
DC 31-MAR-1996 (first entry)  
DE Alternative human acetylcholinesterase (ACHE) protein.  
KW Acetylcholinesterase; Acetyl cholinesterase; EC-3.1.1.7;  
KW Chromosome-12q22; acetylcholine-hydrolyzing enzyme.  
OS Homo sapiens.  
PN W09523158-AL.  
PD 31-AUG-1995.  
PF 28-FEB-1995; U02806.  
PR 28-FEB-1994; US-202755.  
PR 09-JUN-1993; US-370156.  
PA (KOHN/) KOHN K I.

RPEP

PA (YISS ) YISSUM RES & DEV CO.  
 PI Shani M, Soreq H, Zakut H;  
 DR WPI: 95-311499/40.  
 PT Alternative forms of human acetyl cholinesterase (ChE) gene -  
 PT expressed in transgenic animal assay system for evaluating anti-ChE  
 PT activity of organo:phosphate(s), etc. Or as model of ChE imbalance  
 PS Disclosure; Fig.6; 55pp; English.  
 CC Human acetylcholinesterase (EC-3.1.1.7) is accumulated at  
 CC neuromuscular junctions where it serves a vital function in  
 CC modulating cholinergic neurotransmission. This alternatively  
 CC spliced form of human AChE may be expressed in transgenic animals  
 CC which are used in an assay system for determining the anti-ChE  
 CC activity of organophosphates, carbamates, anti-ChE drugs, plant  
 CC glycoalkaloids and snake venoms.  
 SQ Sequence 39 AA;

Query Match 100.0%; Score 14; DB 1; Length 39;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-10;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSVMVHWK 14  
 DB 11 AEFHRWSSVMVHWK 24

RESULT 3

ID W48800 standard; protein; 45 AA.

AC W48800;  
 DT 07-OCT-1998 (first entry)  
 DE C-terminal fragment of human acetylcholine esterase variant El-4.6.  
 KW Human acetylcholine esterase-14 readthrough splice variant; AChE-14; CNS;  
 KW blood/brain barrier; BBB; 14 peptide; antibiotic; brain tumour; glioma;  
 KW chemotherapeutic drug; central nervous system.  
 OS Homo sapiens.

FT Key Location/Qualifiers  
 FT Region 1..5  
 FT /note= "This region is encoded by the 3' end of  
 FT AChE exon 4"

FT Region 5..45  
 FT /note= "Residues encoded by AChE exon 6"

FN W09822132-A2.

PD 28-MAY-1998.

PF 20-NOV-1997; U21696.

PR 21-JUL-1997; US-053200.

PR 20-NOV-1996; US-031194.

PR 12-DEC-1996; US-035266.

PA (KOHN/) KOHN K I.

PA (YISS ) YISSUM RES & DEV CO.

PI Friedman A, Kaufman S, Soreq H;

DR WPI: 98-312172/27.

PT Increasing the permeability of the blood/brain barrier - using e.g.  
 PT adrenaline, atropine or acetylcholine esterase 14 splice variant  
 PT peptide, useful for imaging and/or treatment of central nervous  
 PT system disorders

PS Disclosure; Fig 2; 71pp; English.

CC The present sequence represents a C-terminal fragment of the human  
 CC acetylcholine esterase splice variant El-4.6. The AChE El-4.6 variant  
 CC comprises of residues encoded by exons 1-4 of AChE linked to residues  
 CC encoded by the alternatively spliced AChE exon 6. The invention claims  
 CC for the human acetylcholine esterase-14 (AChE-14) readthrough splice  
 CC variant (W48797). The invention provides a pharmaceutical composition,  
 CC for facilitating passage of compounds through the blood/brain barrier.  
 CC (BBB), comprising of AChE-14, 14 peptide (see W48797) or AChE-14,  
 CC analogues (such as the AChE El-4.6 variant) together with a  
 CC pharmaceutically acceptable carrier. The pharmaceutical composition  
 CC is claimed to facilitate a reversible disruption of the BBB allowing  
 CC transport of compounds through the BBB. The compounds, e.g. imaging  
 CC agents, antibiotics or chemotherapeutic drugs, are claimed to be useful  
 CC for the diagnosis and treatment of diseases or disorders of the CNS such  
 CC as infections, neurochemical disorders, brain tumours, gliomas, etc.  
 SQ Sequence 45 AA;

Query Match 100.0%; Score 14; DB 1; Length 45;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-10;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSVMVHWK 14  
 DB 17 AEFHRWSSVMVHWK 30

RESULT 4

ID W68144 standard; protein; 45 AA.

AC W68144;  
 DT 05-OCT-1998 (first entry)

DE Human AChE splice variant El-4. 6.

KW Nuclease resistant; acetylcholinesterase; human; myasthenia gravis;  
 KW AChE; Parkinson's disease; Alzheimer's disease; central nervous system;  
 KW neuromuscular junction; cholinergic signalling; brain.

OS Homo sapiens.

PN W09826062-A2.

PD 18-JUN-1998.

PF 12-DEC-1997; U23598.

PR 21-JUL-1997; US-053334.

PR 12-DEC-1996; US-035266.

PR 13-FEB-1997; US-037777.

PR 02-MAY-1997; US-850347.

PA (KOHN/) KOHN K I.

PA (YISS ) YISSUM RES & DEV CO.

PI Eckstein F, Friedman A, Kaufman S, Soreq H;

DR WPI: 98-348522/30.

PT Synthetic nuclease resistant antisense oligodeoxynucleotides -  
 PT directed against acetylcholinesterase, useful for treating  
 PT Parkinson's and Alzheimer's diseases and myasthenia gravis

PS Disclosure; Fig 12; 89pp; English.

CC This represents the amino acid sequence of a human acetylcholinesterase  
 CC (AChE) splice variant. The invention provides sequences shown in V41278  
 CC to V41285 that represent synthetic nuclease resistant antisense  
 CC oligodeoxynucleotides which are capable of selectively modulating human  
 CC acetylcholinesterase (AChE) production. These oligonucleotides are  
 CC targeted to a splice junction in a splice variant of AChE mRNA and are  
 CC capable of selectively modulating human AChE production in the central  
 CC nervous system and neuromuscular junction. The invention also provides a  
 CC method for determining the efficacy of these human AChE specific  
 CC antisense oligonucleotides. These antisense oligonucleotides can be used  
 CC to restore balanced cholinergic signalling in the brain, particularly  
 CC related to learning and memory as well as stress disorders, Parkinson's  
 CC and Alzheimer's disease. They can also be used to reduce production and  
 CC therefore deposition of AChE in the neuromuscular junctions of patients  
 CC with e.g. myasthenia gravis. The oligonucleotides work effectively at low  
 CC doses while avoiding many of the side effects associated with Tacrine and  
 CC related cholinergic drugs for Alzheimer's disease and pyridostigmine and  
 CC related drugs for myasthenia gravis.

SQ Sequence 45 AA;

Query Match 100.0%; Score 14; DB 1; Length 45;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-10;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSVMVHWK 14  
 DB 17 AEFHRWSSVMVHWK 30

RESULT 5

ID W74586 standard; protein; 45 AA.

AC W74586;  
 DT 21-DEC-1998 (first entry)

DE Amino acid sequence of the human AChE variant 1.  
 DE Nuclease resistance; inhibition; human; acetylcholinesterase; AChE;

KW Nuclease resistance; inhibition; human; acetylcholinesterase; AChE;

SQ Sequence 45 AA;

RESULT 7

R06989 R06989 standard; protein; 613 AA.

AC R06989;

DT 16-JAN-1991 (first entry)

DE Human acetylcholinesterase (hAChE) primary transcript.

KW Organophosphorous poisoning; OP; cancer; leukaemia;

KW megakaryocytopoiesis; ovarian cancer.

OS Homo sapiens.

PN EP-388906-A.

PD 26-SEP-1990.

PF 20-MAR-1990; 105274.

PR 21-MAR-1989; IL-089703.

PA (YISS ) YISSUM RES DEV CO.

PI Soreq H, Zakut H.

WPI; 90-291865/39.

DR N-PSDB; Q05998.

PT Human acetylcholinesterase DNA and prodn. of recombinant hAChE -

PT for treatment of organo-phosphorous poisoning and diagnosis of haemo-

PT cytopoietic disorders and ovarian carcinomas.

PS Claim 5; Page 25; 47pp; English.

CC Gene product is useful as an active pharmacological component for the

CC prophylaxis and treatment of organophosphorous poisoning, and post-

CC surgical apnea due to succinylcholine administration.

CC cDNA probe to the sequence may be used in diagnosis of various

CC leukaemias, abnormal megakaryocytopoiesis and ovarian carcinomas.

CC Sequence 613 AA;

QY 1 AEFHRWSSYVHWK 14

DB 585 AEFHRWSSYVHWK 598

Query Match 100.0%; Score 14; DB 1; Length 613;

Best Local Similarity 100.0%; Pred. No. 1.1e-09; Mismatches 0; Indels 0; Gaps 0;

Matches 14; Conservative 0;

QY 1 AEFHRWSSYVHWK 14

DB 585 AEFHRWSSYVHWK 598

RESULT 8

R0726 R0726 standard; Protein; 614 AA.

ID R0726;

AC R0726; 1996 (first entry)

DT 31-MAR-1996 (first entry)

DE Human acetylcholinesterase (AChE) protein.

KW Acetylcholinesterase; acetyl cholinesterase; EC-3.1.1.7;

KW chromosome-7q22; acetylcholine-hydrolyzing enzyme.

OS Homo sapiens.

PN WO9523158-A1.

PD 31-AUG-1995.

PF 28-FEB-1995; 002806.

PR 28-FEB-1994; US-202755.

PR 09-JAN-1995; US-370156.

PA (KOHN/) KOHN K I.

PA (YISS ) YISSUM RES & DEV CO.

PI Shani M, Soreq H, Zakut H;

WPI; 95-31499/40.

DR N-PSDB; Q99002.

PT Alternative forms of human acetyl cholinesterase (ChE) gene -

PT expressed in transgenic animal assay system for evaluating anti-ChE

PT activity of organo-phosphate(s), etc. or as model of ChE imbalance

PS Claim 3; Fig.18; 55pp; English.

CC Human acetylcholinesterase (EC-3.1.1.7) is accumulated at

CC neuromuscular junctions where it serves a vital function in

CC modulating cholinergic neurotransmission. Alternatively spliced

CC forms of human AChE may be expressed in transgenic animals which

CC are used in an assay system for determining the anti-ChE activity

CC of organophosphates, carbamates, anti-ChE drugs, plant glycoalkaloids

CC and snake venoms.

CC Sequence 614 AA;

QY 1 AEFHRWSSYVHWK 14

DB 585 AEFHRWSSYVHWK 598

Query Match 100.0%; Score 14; DB 1; Length 614;

Best Local Similarity 100.0%; Pred. No. 1.1e-09; Mismatches 0; Indels 0; Gaps 0;

Matches 14; Conservative 0;

Central nervous system; CNS.

OS Homo sapiens.

PN WO9839486-A1.

PD 11-SEP-1998.

PR 06-MAR-1998; 004503.

PR 06-MAR-1997; US-040203.

PA (KOHN/) KOHN K I.

PA (YISS ) YISSUM RES & DEV CO.

PI Seidman S, Shohami E, Soreq H;

WPI; 98-506377/43.

PT Treatment of injury to central nervous system - by administration of

PT inhibitor of acetylcholinesterase production

PS Disclosure; Page 61; 88pp; English.

CC This is the amino acid sequence of a human acetylcholinesterase

CC (AChE) variant used in the method of the invention, where inhibitors

CC of AChE are used to treat injury to the central nervous system (CNS).

CC The AChE inhibitor can also be used to facilitate transplantation of

CC neuronal cells to the CNS of a patient. The inhibitor can also be

CC used to improve hippocampal neuron survival following injury to the

CC CNS. The CNS injuries that can be treated with the method include

CC epilepsy, stroke, Huntington's disease, head injury, spinal injury,

CC pain, Parkinson's disease, myelin deficiencies, neuromuscular

CC disorders, neurological pain, amyotrophic lateral sclerosis,

CC Alzheimer's disease, and affective disorders of the brain.

CC Sequence 45 AA;

QY 1 AEFHRWSSYVHWK 14

DB 17 AEFHRWSSYVHWK 30

Query Match 100.0%; Score 14; DB 1; Length 45;

Best Local Similarity 100.0%; Pred. No. 1.2e-10; Mismatches 0; Indels 0; Gaps 0;

Matches 14; Conservative 0;

QY 1 AEFHRWSSYVHWK 14

DB 17 AEFHRWSSYVHWK 30

RESULT 6

R06990 R06990 standard; protein; 500 AA.

AC R06990;

DT 16-JAN-1991 (first entry)

DE Human foetal acetylcholinesterase (hAChE) primary transcript.

KW Organophosphorous poisoning; OP; cancer; leukaemia;

KW megakaryocytopoiesis; ovarian cancer.

OS Homo sapiens.

PN EP-388906-A.

PD 26-SEP-1990.

PR 20-MAR-1990; 105274.

PR 21-MAR-1989; IL-089703.

PA (YISS ) YISSUM RES DEV CO.

PI Soreq H, Zakut H;

WPI; 90-291865/39.

DR N-PSDB; Q05999.

PT Human acetylcholinesterase DNA and prodn. of recombinant hAChE -

PT for treatment of organo-phosphorous poisoning and diagnosis of haemo-

PT cytopoietic disorders and ovarian carcinomas.

PS Disclosure; Fig 1c; 47pp; English.

CC Gene product is useful as an active pharmacological component for the

CC prophylaxis and treatment of organophosphorous poisoning, and post-

CC surgical apnea due to succinylcholine administration.

CC cDNA probe to the sequence may be used in diagnosis of various

CC leukaemias, abnormal megakaryocytopoiesis and ovarian carcinomas.

CC Sequence 500 AA;

QY 1 AEFHRWSSYVHWK 14

DB 472 AEFHRWSSYVHWK 485

Query Match 100.0%; Score 14; DB 1; Length 500;

Best Local Similarity 100.0%; Pred. No. 9.4e-10; Mismatches 0; Indels 0; Gaps 0;

Matches 14; Conservative 0;

Best Local Similarity 100.0%; Pred. NO. 1.1e-09;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSVMVHWK 14  
DB 586 AEFHRWSSVMVHWK 599

## RESULT 9

W39078 ID W39078 standard; protein; 575 AA.  
AC W39078;

DT 08-APR-1998 (first entry)  
DE Torpedo californica acetylcholinesterase AChE.  
KW Acetylcholinesterase; AChE; organophosphate; detoxification; oxime;  
OS ray: chemical agent; treatment; prevention; aging; mutant.

Key Location/Qualifiers

FT Region 67..94  
FT /note= "region as indicated in specification."  
FT Modified\_site 59..61  
FT /note= "site as indicated in specification"  
FT Region 254..265  
FT /note= "region as indicated in specification"  
FT Region 402..521  
FT /note= "region as indicated in specification"  
FT Modified\_site 416..418  
FT /note= "site as indicated in specification"  
FT Modified\_site 457..459  
FT /note= "site as indicated in specification"  
FT Modified\_site 569..571  
FT /note= "site as indicated in specification"

US5695750-A.

PD 09-DEC-1997.

PF 25-NOV-1994; 348920.

PR 25-NOV-1994; US-348920.

PI (USSA ) US SEC OF ARMY.

PI Doctor BP, Maxwell D, Radic Z, Saxena A, Taylor P;

DR WPI; 98-041233/04.

PT Mutant Torpedo acetylcholinesterase - useful for detoxifying

PT organo-phosphate compounds

PS Disclosure; Fig 1; 12pp; English.

CC This sequence represents an acetylcholinesterase (AChE) from Torpedo californica which is used to create enzymes capable of detoxifying organophosphates. Mutant versions of this AChE are useful when combined with an oxime for detoxifying chemical warfare agents such as sarin or as a means of treating or preventing the deleterious effects of organophosphate exposure in organisms. Such variants can also destroy organophosphates in an environmentally friendly manner and be more resistant to aging than wild-type enzymes.

CC Sequence 575 AA;

SQ

Query Match 64.3%; Score 9; DB 1; Length 575;  
Best Local Similarity 100.0%; Pred. No. 0.001;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EFRWSSVM 10

DB 548 EFRWSSVM 556

## RESULT 10

W39079 ID W39079 standard; protein; 575 AA.  
AC W39079;

DT 08-APR-1998 (first entry)  
DE Torpedo californica acetylcholinesterase AChE mutant E1990.  
KW Acetylcholinesterase; AChE; organophosphate; detoxification; oxime;  
OS ray: chemical agent; treatment; prevention; aging; mutant.  
OS Torpedo californica.  
OS Synthetic.

Key Location/Qualifiers

FT Modified\_site 59..61  
FT /note= "site as indicated in specification"  
FT Region 67..94  
FT /note= "region as indicated in specification"  
FT Modified\_site 199  
FT /label= E1990  
FT /note= "wild-type Glu is replaced by Gln"  
FT Region 254..265  
FT /note= "region as given in specification"  
FT Region 402..521  
FT /note= "region as given in specification"  
FT Modified\_site 416..418  
FT /note= "site as given in specification"  
FT Modified\_site 457..459  
FT /note= "site as given in specification"  
FT Modified\_site 533..535  
FT /note= "site as given in specification"

US5695750-A.

PD 09-DEC-1997.

PF 25-NOV-1994; 348920.

PR 25-NOV-1994; US-348920.

PI (USSA ) US SEC OF ARMY.

PI Doctor BP, Maxwell D, Radic Z, Saxena A, Taylor P;

DR WPI; 98-041233/04.

PT Mutant Torpedo acetylcholinesterase - useful for detoxifying

PT organo-phosphate compounds

PS Claim 1; Fig 2; 12pp; English.

CC This sequence represents a variant of the enzyme acetylcholinesterase (AChE) from Torpedo californica which is capable of detoxifying organophosphates. This E1990 mutant has greater resistance to aging than the wild-type AChE and can destroy organophosphates in an environmentally friendly manner. When combined with an oxime, this mutant's ability to detoxify several organophosphates is amplified and is predicted to have applications for the detoxification of chemical warfare agents such as sarin or as a means of treating or preventing the deleterious effects of organophosphate exposure in organisms.

CC Sequence 575 AA;

SQ

Query Match 64.3%; Score 9; DB 1; Length 575;

Best Local Similarity 100.0%; Pred. No. 0.001;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EFRWSSVM 10

DB 548 EFRWSSVM 556

## RESULT 11

R63398

ID R63398 standard; Protein; 12 AA.

AC R63398;

DT 09-AUG-1995 (first entry)

DE Peptide fragment of V1 region of hepatitis C virus.

KW Hepatitis C virus; HCV; primer; probe; detection; diagnosis;

KW classification; immunisation; prophylaxis; serotyping.

OS Hepatitis C virus.

PN WO9425601-A.

PD 10-NOV-1994.

PF 27-APR-1994; E01323.

PR 27-APR-1993; EP-401099.

PR 05-AUG-1993; EP-402019.

PA (INNO-) INNOGENETICS NV SA.

PI Maertens G, Stuyver L;

DR WPI; 94-358277/44.

PT New polynucleotide sequences from hepatitis C virus - and related vectors, polypeptide(s) and antibodies, useful for immunisation, treatment, diagnosis and typing of HCV isolates

PS Claim 15; Page 277; 404pp; English

CC Compositions comprising at least 5, and pref. 8 or more contiguous nucleotides selected from an HCV type 3 genomic sequence, more particularly (i) the region spanning positions 417-957 of the Core/E1 region of HCV subtype 3a; (ii) the region spanning positions



CC 4664-4730 of the NS3 region of HCV type 3; (iii) the region spanning  
 CC positions 4892-5292 of the NS3/4 region of HCV type 3; (iv) the  
 CC region spanning positions 8023-8235 of the NS5 region of the BR36  
 CC subgroup of HCV subtype 3a; or (v) an HCV subtype 3c genomic  
 CC sequence, or, from a subtype 2d genomic sequence, a type 4 genomic  
 CC sequence; or the coding region of subtype 5a, may be used as primers  
 CC to amplify nucleic acid from an isolate belonging to a specific  
 CC genotype, or as a probe for specific detection/classification of  
 CC nucleic acid. Polypeptides encoded by the nucleotides in such  
 CC compositions may be used for immunisation against HCV, for the  
 CC detection of antibodies directed against HCV and for serotyping.  
 CC This polypeptide corresponds to positions 192-203 of the VI region  
 CC of HCV.  
 SQ Sequence 12 AA;

Query Match 35.7%; Score 5; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 2.3;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SSVNV 11

Db 8 SSVNV 12

## RESULT 12

W61227  
 ID W61227 standard; Protein; 111 AA.  
 AC W61227;  
 DT 02-OCT-1998 (first entry)  
 DE Streptococcus pneumoniae Sp102 protein.  
 KW Streptococcus pneumoniae; antigen; vaccine; infection; diagnosis;  
 KW detection; pneumonia; otitis media; meningitis.  
 OS Streptococcus pneumoniae.  
 PN W61227-1998.  
 PD 07-MAY-1998.  
 PF 30-OCT-1997; U19422.  
 PR 31-OCT-1996; US-029960.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PI Choi GH, Hromockyj A, Johnson LS, Kunsch CA;  
 DR WPI: 98-272224/24.  
 DR N-PSDB; V27413.  
 DT Nucleic acid encoding antigenic peptide(s) from Streptococcus  
 PT pneumoniae - or their epitope-containing fragments, useful in  
 PT protective or therapeutic vaccines, and for diagnosis  
 PS Claim 11, Page 85; 118pp; English.  
 CC The present sequence represents a protein from Streptococcus pneumoniae.  
 CC The nucleic acid sequence encoding the Streptococcus pneumoniae protein  
 CC can be useful in vaccines for inducing protective antibodies against  
 CC Streptococcus pneumoniae, for treatment or prevention of infection e.g.  
 CC pneumonia, otitis media or meningitis. Probes based on the nucleic acid  
 CC are used to detect Streptococcus infection (by usual hybridisation or  
 CC amplification methods), also for isolating Streptococcus genes or their  
 CC allelic variants. The protein can be used similarly to detect specific  
 CC antibodies in standard immunoassays, especially for diagnosing or  
 CC monitoring infections. Antibodies which bind the protein are used to  
 CC detect corresponding antigens, to purify the protein and for passive  
 CC immunisation (optionally coupled to a toxin). Vaccines are administered,  
 CC e.g. by injection, orally or through the skin, typically at 0.01-1000  
 CC (especially 10-300) mu g/ml per dose.  
 SQ Sequence 111 AA;

Query Match 35.7%; Score 5; DB 1;  
 Best Local Similarity 100.0%; Pred. No. 15;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHR 5

Db 37 AEFHR 41

## RESULT 13

W74955  
 ID W74955 standard; Protein; 136 AA.  
 AC W74955;  
 DT 25-JAN-1999 (first entry)  
 DE Human secreted protein encoded by gene 77 clone HOEAS24.  
 KW Human; secreted protein; testis; tumour; foetal brain tissue;  
 KW fusion protein; cancer; central nervous system; seizure;  
 KW diagnosis; neurodegenerative disease.  
 OS Homo sapiens.  
 PN Key Location/Qualifiers  
 FT Misc-difference 136 /label= unknown  
 FT W09839448-A2.  
 PN 11-SEP-1998.  
 PD 06-MAR-1998; U04493.  
 PR 02-OCT-1997; US-061060.  
 PR 07-MAR-1997; US-038621.  
 PR 07-MAR-1997; US-040161.  
 PR 07-MAR-1997; US-040162.  
 PR 07-MAR-1997; US-040163.  
 PR 07-MAR-1997; US-040333.  
 PR 07-MAR-1997; US-040334.  
 PR 07-MAR-1997; US-040336.  
 PR 07-MAR-1997; US-040626.  
 PR 11-APR-1997; US-043311.  
 PR 11-APR-1997; US-043312.  
 PR 11-APR-1997; US-043313.  
 PR 11-APR-1997; US-043314.  
 PR 11-APR-1997; US-043568.  
 PR 11-APR-1997; US-043569.  
 PR 11-APR-1997; US-043576.  
 PR 11-APR-1997; US-043578.  
 PR 11-APR-1997; US-043580.  
 PR 11-APR-1997; US-043669.  
 PR 11-APR-1997; US-043670.  
 PR 11-APR-1997; US-043671.  
 PR 11-APR-1997; US-043672.  
 PR 11-APR-1997; US-043674.  
 PR 23-MAY-1997; US-047492.  
 PR 23-MAY-1997; US-047500.  
 PR 23-MAY-1997; US-047501.  
 PR 23-MAY-1997; US-047502.  
 PR 23-MAY-1997; US-047503.  
 PR 23-MAY-1997; US-047581.  
 PR 23-MAY-1997; US-047582.  
 PR 23-MAY-1997; US-047583.  
 PR 23-MAY-1997; US-047584.  
 PR 23-MAY-1997; US-047585.  
 PR 23-MAY-1997; US-047586.  
 PR 23-MAY-1997; US-047587.  
 PR 23-MAY-1997; US-047588.  
 PR 23-MAY-1997; US-047589.  
 PR 23-MAY-1997; US-047590.  
 PR 23-MAY-1997; US-047592.  
 PR 23-MAY-1997; US-047593.  
 PR 23-MAY-1997; US-047594.  
 PR 23-MAY-1997; US-047595.  
 PR 23-MAY-1997; US-047596.  
 PR 23-MAY-1997; US-047597.  
 PR 23-MAY-1997; US-047598.  
 PR 23-MAY-1997; US-047599.  
 PR 23-MAY-1997; US-047600.  
 PR 23-MAY-1997; US-047601.  
 PR 23-MAY-1997; US-047612.  
 PR 23-MAY-1997; US-047613.  
 PR 23-MAY-1997; US-047614.  
 PR 23-MAY-1997; US-047615.  
 PR 23-MAY-1997; US-047617.  
 PR 23-MAY-1997; US-047618.  
 PR 23-MAY-1997; US-047632.  
 PR 23-MAY-1997; US-047633.  
 PR 06-JUN-1997; US-048964.  
 PR 06-JUN-1997; US-048974.

PR 13-JUN-1997; US-049610.  
 PR 08-JUL-1997; US-051926.  
 PR 16-JUL-1997; US-052874.  
 PR 18-AUG-1997; US-055724.  
 PR 22-AUG-1997; US-056630.  
 PR 22-AUG-1997; US-056631.  
 PR 22-AUG-1997; US-056632.  
 PR 22-AUG-1997; US-056636.  
 PR 22-AUG-1997; US-056637.  
 PR 22-AUG-1997; US-056662.  
 PR 22-AUG-1997; US-056664.  
 PR 22-AUG-1997; US-056845.  
 PR 22-AUG-1997; US-056862.  
 PR 22-AUG-1997; US-056864.  
 PR 22-AUG-1997; US-056872.  
 PR 22-AUG-1997; US-056874.  
 PR 22-AUG-1997; US-056875.  
 PR 22-AUG-1997; US-056876.  
 PR 22-AUG-1997; US-056877.  
 PR 22-AUG-1997; US-056878.  
 PR 22-AUG-1997; US-056879.  
 PR 22-AUG-1997; US-056880.  
 PR 22-AUG-1997; US-056881.  
 PR 22-AUG-1997; US-056882.  
 PR 22-AUG-1997; US-056884.  
 PR 22-AUG-1997; US-056886.  
 PR 22-AUG-1997; US-056887.  
 PR 22-AUG-1997; US-056888.  
 PR 22-AUG-1997; US-056889.  
 PR 22-AUG-1997; US-056892.  
 PR 22-AUG-1997; US-056893.  
 PR 22-AUG-1997; US-056894.  
 PR 22-AUG-1997; US-056903.  
 PR 22-AUG-1997; US-056908.  
 PR 22-AUG-1997; US-056909.  
 PR 22-AUG-1997; US-056910.  
 PR 22-AUG-1997; US-056911.  
 PR 05-SEP-1997; US-057650.  
 PR 05-SEP-1997; US-057669.  
 PR 05-SEP-1997; US-057761.  
 PR 12-SEP-1997; US-058785.  
 PA (HUMA-) HUMAN GENOME SCI INC.

PI Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA,  
 PI Feng P, Ferrie AM, Fischer CL, Florence KA, Greene JM, Hu JS,  
 PI Kyaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA,  
 PI Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;  
 DR WPI: 98-506364/43.  
 DR N-PSDB: V59740.  
 PT New isolated human genes and the secreted polypeptide(s) they encode  
 PT - useful for diagnosis and treatment of e.g. cancers, neurological  
 PT disorders, immune diseases, inflammation or blood disorders  
 PS Claim 1; Page 672; 721pp; English.  
 CC This sequence represents a secreted human protein encoded by the nucleic  
 CC acid molecule designated Gene 77 from the human cDNA clone HOEAS24  
 CC (deposited as clone ATCC 97900 and ATCC 209046).  
 CC The gene can be used to generate fusion proteins by linking to the gene  
 CC to a human immunoglobulin Fc portion (e.g. V59502) for increasing the  
 CC stability of the fused protein as compared to the human protein only.  
 CC The invention relates to 186 novel genes and their fragments (nucleic  
 CC acid sequences: V59511-V59812; amino acid sequences W74731-W75026) which  
 CC are useful for preventing, treating or ameliorating medical conditions  
 CC e.g. by protein or gene therapy. Also, pathological conditions can be  
 CC diagnosed by determining the amount of the new polypeptides in a sample  
 CC or by determining the presence of mutations in the new polynucleotides.  
 CC Specific uses are described for each of the 186 polynucleotides, based on  
 CC which tissues they are most highly expressed in (see V59511 for described  
 CC uses).  
 SQ Sequence 136 AA;

Query Match 35.7%; Score 5; DB 1; Length 136;  
 Best Local Similarity 100.0%; Pred. No. 18;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SSYMV 11  
 |||||  
 Db 33 SSYMV 37

## RESULT 14

P70559  
 ID P70559 standard; Protein; 256 AA.  
 AC P70559;  
 DT 30-APR-1991 (first entry)  
 DE Product of ORF 1 from MiMV strand (a).  
 KW Geminivirus.  
 OS Mungbean yellow mosaic virus.  
 PN J62126982-A.  
 PD 09-JUN-1987; 266080.  
 PF 28-NOV-1985; JP-266080.  
 PR WPI: 87-196308/28.  
 PA (TEIJ ) TEIJIN KK.  
 DR N-PSDB: N70892.  
 PT Novel DNA and hybrid DNA useful - as vector for recombinant work  
 PT of plant gene.  
 PS Disclosure; Fig 5; 21pp; Japanese.  
 CC The sequence is encoded by ORF 1 which occurs on the positive  
 CC strand of the (a) molecule of the geminivirus.  
 CC See also P70560-P70567  
 SQ Sequence 256 AA;

Query Match 35.7%; Score 5; DB 1; Length 256;  
 Best Local Similarity 100.0%; Pred. No. 31;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HRWSS 8  
 |||||  
 Db 19 HRWSS 23

## RESULT 15

R63805  
 ID R63805 standard; Protein; 261 AA.  
 AC R63805;  
 DT 07-DEC-1994 (first entry)  
 DE Polyhydroxyalkanoate decomposing activity polypeptide.  
 KW Polyhydroxyalkanoate decomposing enzyme; PHA.  
 OS Zoogloea ramigera.  
 PN J06086681-A.  
 PD 29-MAR-1994.  
 PF 07-SEP-1992; 279099.  
 PR 07-SEP-1992; JP-279099.  
 PA (ELED ) DENKI KAGAKU KOGYO KK.  
 PA (UYKA-) GH KANAGAWA DAIGAKU.  
 PA (CHIK-) ZH CHIKYU KANKYO SANGYO GIJITSU KENKYU.  
 DR WPI: 94-140539/17.  
 DR N-PSDB: Q63879.  
 PT DNA encoding poly-hydroxy-alkanoate decomposing enzyme - useful  
 PT for preparing poly-hydroxy-alkanoate in large quantities  
 PS Claim 3; Page 13-14; 15pp; Japanese.  
 CC R63805 is encoded by ORF 2 of Q63789, which produces a polypeptide  
 CC which shows polyhydroxyalkanoate decomposing activity. The method  
 CC used allows the polypeptide to be prepared in large quantities.  
 SQ Sequence 261 AA;

Query Match 35.7%; Score 5; DB 1; Length 261;  
 Best Local Similarity 100.0%; Pred. No. 32;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHR 5  
 |||||  
 Db 84 AEFHR 88

Wed Sep 13 08:11:25 2000

us-09-155-076-1.rag

Page 7

Search completed: September 13, 2000, 02:25:00  
Job time: 173 sec



Wed Sep 13 08:11:29 2000

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 13, 2000, 02:24:38 ; Search time 22.46 Seconds  
(without alignments)  
43.218 Million cell updates/sec

Title: US-09-155-076-1  
Perfect score: 14  
Sequence: 1 AEFHRWSSVMVHWK 14

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 225878 seqs, 69334122 residues

Word size : 0

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0  
Maximum DB seq length: 1000000

Post-processing: Listing first 45 summaries

Database : SPTREMBL.12.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	100.0	611	6	O62763 felis silve
2	10	71.4	633	13	O42275 electrophor
3	9	64.3	95	13	Q9W6Y8 torpedo cal
4	6	42.9	469	2	P73738 synchocyst
5	5	35.7	149	12	Q81753 hepatitis c
6	5	35.7	193	12	Q81558 hepatitis c
7	5	35.7	219	8	Q9XQU7 Q9xqu7 heterocapsa
8	5	35.7	235	13	Q9W7Q8 P88361 paralicthty
9	5	35.7	244	12	P88361 human immun
10	5	35.7	251	12	P88358 human immun
11	5	35.7	255	5	Q22117 caenorhabdi
12	5	35.7	262	12	O10441 mouse adeno
13	5	35.7	263	6	O97972 oryctolagus
14	5	35.7	285	2	Q52970 rhizobium m
15	5	35.7	294	8	Q9XMG3 Q9xmg3 epichloe ty
16	5	35.7	318	12	Q68691 hepatitis c
17	5	35.7	319	12	Q81557 hepatitis c
18	5	35.7	335	1	O29464 archaeoglob
19	5	35.7	339	2	O32123 bacillus su

Q9ZVP5 arabidopsis  
O16472 caenorhabdi  
O83906 treponema p  
O24322 phaseolus v  
Q9ZVU5 arabidopsis  
O15679 leishmania  
O18710 leishmania  
O18713 leishmania  
O77439 leishmania  
O23853 brassica ca  
O80346 raphanus sa  
O23033 arabidopsis  
O23852 brassica ca  
Q93795 caenorhabdi  
O15322 homo sapien  
O9zak2 anabaena va  
O13601 schizosacch  
O68307 nostoc pec7  
O44216 anabaena sp  
O61745 caenorhabdi  
Q95779 synchocyst  
Q9XSB8 canis famill  
O18097 caenorhabdi  
O18044 drosophila  
Q956P3 chlamydia p  
O13858 schizosacch

## ALIGNMENTS

RESULT 1  
O62763 PRELIMINARY; PRT; 611 AA.  
AC O62763;  
DT 01-AUG-1998 (TREMREL. 07, Created)  
DT 01-AUG-1998 (TREMREL. 07, Last sequence update)  
DE 01-NOV-1999 (TREMREL. 12, Last annotation update)  
DE ACETYLCHOLINESTERASE COLLAGEN-TAILED OR GLOBULAR FORM PRECURSOR.  
GN ACHE.  
OS Felis silvestris catus (Cat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA BARTELS C.F., XIE W.-H., MILLER-LINDHOLM A.K., LOCKRIDGE O.;  
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF053485; AAC08995.1; -  
DR HSSP; P22303; 2CLJ.  
DR PROSITE; PS00122; CARBOXYLESTERASE\_B\_1; 1.  
DR PROSITE; PS00941; CARBOXYLESTERASE\_B\_2; 1.  
DR PFAM; PF00135; Coesterase; 1.  
DR PRINTS; PR00878; CHOLNESTRASE.  
SQ SEQUENCE 611 AA; 67298 MW; 172DEB16 CRC32;

Query Match 100.0%; Score 14; DB 6; Length 611;  
Best Local Similarity 100.0%; Pred. No. 3.5e-11;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSVMVHWK 14  
DB 583 AEFHRWSSVMVHWK 596

RESULT 2  
O42275 PRELIMINARY; PRT; 633 AA.  
ID O42275;  
AC O42275;  
DT 01-JAN-1998 (TREMREL. 05, Created)  
DT 01-JAN-1998 (TREMREL. 05, Last sequence update)  
DT 01-NOV-1999 (TREMREL. 12, Last annotation update)  
DE ACETYLCHOLINESTERASE CATALYTIC SUBUNIT PRECURSOR (EC 3.1.1.7).

OS Electrophorus electricus (Electric eel).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;  
 OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Gymnotiformes;  
 RN Gymnotidae; Electrophoridae; Electrophorus.  
 RP SEQUENCE FROM N.A.  
 RA SIMON S., MASSOULIE J.;  
 RL J. Biol. Chem. 0:0-0(1997).  
 DR EMBL; AF030422; AAB86606.1; -.  
 DR HSP; P04058; 1ACL.  
 DR PROSITE; PS00122; CARBOXYLSTERASE\_B\_1; 1.  
 DR PROSITE; PS00941; CARBOXYLSTERASE\_B\_2; 1.  
 DR PFAM; PF00135; Coesterase; 2.  
 DR PRINTS; PR00878; CHOLINESTERASE.  
 KW Signal; Hydrolase.  
 FT SIGNAL 1 23 POTENTIAL.  
 FT CHAIN 24 633 POTENTIAL.  
 SQ SEQUENCE 633 AA; 71814 MW; 6050AB05 CRC32;

Query Match 71.4%; Score 10; DB 13; Length 633;  
 Best Local Similarity 100.0%; Pred. No. 8e-06;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AEFHRSSYM 10  
 Db 605 AEFHRSSYM 614  
 |||||

RESULT 3  
 Q9W6Y8 PRELIMINARY; PRT; 95 AA.  
 AC Q9W6Y8;  
 DT 01-NOV-1999 (TRENBLrel. 12, Created)  
 DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)  
 DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)  
 DE ACETYLCOLINESTERASE (FRAGMENT).  
 OS Torpedo californica (Pacific electric ray).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
 OC Elasmobranchii; Rajiformes; Torpedinoidei; Torpedinidae; Torpedo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MAULET Y., CAMP S., GIBNEY G., RACHINSKY T.L., EKSTROM T.J.,  
 RA TAYLOR P.;  
 RL Submitted (OCT-1990) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; X56517; CAB37951.1; -.  
 DR EMBL; X56516; CAB37951.1; JOINED.  
 FT NON\_TER 1  
 SQ SEQUENCE 95 AA; 11752 MW; F7387712 CRC32;

Query Match 64.3%; Score 9; DB 13; Length 95;  
 Best Local Similarity 100.0%; Pred. No. 4e-05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 EFRHRSSYM 10  
 Db 68 EFRHRSSYM 76  
 |||||

RESULT 4  
 P73738 PRELIMINARY; PRT; 469 AA.  
 AC P73738;  
 DT 01-FEB-1997 (TRENBLrel. 02, Created)  
 DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)  
 DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)  
 DE HYPOTHETICAL 52.5 KD PROTEIN.  
 OS Synecocystis sp. (strain PCC 6803).  
 OC Bacteria; Cyanobacteria; Chroococcales; Synecocystis.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-PCC6803;

RA TABATA S.;  
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-PCC6803;  
 RX MEDLINE; 97061201.  
 RA KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,  
 RA MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,  
 RA HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K., OKUMURA S.,  
 RA SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,  
 RA TABATA S.;  
 RT "Sequence analysis of the genome of the unicellular cyanobacterium  
 RT Synecocystis sp. strain PCC6803. II. Sequence determination of the  
 RT entire genome and assignment of potential protein-coding regions.";  
 RL DNA Res 3:109-136(1996).  
 DR EMBL; D90909; BAAL7786.1; -.  
 DR PFAM; PF00355; Rieske; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 469 AA; 52544 MW; 0887A65E CRC32;

Query Match 42.9%; Score 6; DB 2; Length 469;  
 Best Local Similarity 100.0%; Pred. No. 1.4;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AEFHRW 6  
 Db 349 AEFHRW 354  
 |||||

RESULT 5  
 Q81753 PRELIMINARY; PRT; 149 AA.  
 AC Q81753;  
 DT 01-NOV-1996 (TRENBLrel. 01, Created)  
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
 DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)  
 DE PRECURSOR PROTEIN (FRAGMENTS).  
 OS Hepatitis C virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 OC Hepatitis C-like viruses.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 95052487.  
 RA VAN DOORN L.J., KLETER B., STUYVER L., MAERTENS G., BROUWER H.,  
 RA SCHALM S., HEIJTINK R., QUINT W.;  
 RT "Analysis of hepatitis C virus genotypes by a line probe assay and  
 RT correlation with antibody profiles.";  
 RL J. Hepatol. 21:122-129(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA VAN DOORN L.J., KLETER B.G.E.M., STUYVER L., MAERTENS G.,  
 RA BROUWER J.T., SCHALM S.W., HEIJTINK R.A., QUINT W.G.V.;  
 RL J. Gen. Virol. 0:0-0(0).  
 DR EMBL; L39294; AAA67817.1; -.  
 DR PFAM; PF01542; HCV\_core; 1.  
 DR PFAM; PF01539; HCV\_env; 1.  
 FT NON\_TER 1  
 FT CHAIN 1 >32 CORE PROTEIN.  
 FT NON\_CONS 32 33  
 FT CHAIN 33 >149 E1 PROTEIN.  
 FT NON\_TER 149 149  
 SQ SEQUENCE 149 AA; 15854 MW; EB9593D2 CRC32;

Query Match 35.7%; Score 5; DB 12; Length 149;  
 Best Local Similarity 100.0%; Pred. No. 13;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 SSYMV 11  
 Db 40 SSYMV 44  
 |||||

```

RESULT 6
Q81558 ID Q81558 PRELIMINARY; PRT; 193 AA.
AC Q81558;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE (NE92) CORE PROTEIN (FRAGMENTS).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepatitis C-like viruses.
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=NE92;
RC MEDLINE; 95023999.
RX STUYVER L., VAN ARNHEM W., WYSEUR A., HERNANDEZ F., DELAPORTE E.,
RA MAERTENS G.;
RT "Classification of hepatitis C viruses based on phylogenetic analysis
of the envelope 1 and nonstructural 5B regions and identification of
five additional subtypes.";
RT Proc. Natl. Acad. Sci. U.S.A. 91:10134-10138(1994).
RL EMBL; L29633; AAA65816.1; -.
DR PFAM; PF01542; HCV_core; 1.
DR PFAM; PF01539; HCV_env; 1.
KW Envelope protein.
FT NON_TER 1
FT CHAIN 1
FT NON_CONS 65
FT CHAIN 66
FT CHAIN 66
FT CHAIN 66
FT NON_TER 193
FT NON_TER 193
SQ SEQUENCE 193 AA; 20460 MW; 9FOAD762 CRC32;

Query Match 35.7%; Score 5; DB 12; Length 193;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SSYMV 11
Db 73 SSYMV 77

RESULT 7
Q9XQ07 ID Q9XQ07 PRELIMINARY; PRT; 219 AA.
AC Q9XQ07;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DE CYTOCHROME B6.
GN PETB.
OS Heterocapsa triquetra.
OG Chloroplast.
OC Eukaryota; Alveolata; Dinophyceae; Peridiniales; Heterocapsaceae;
OC Heterocapsa.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CCMP 449;
RX MEDLINE; 99334925.
RA ZHANG Z., GREEN B.R., CAVALIER-SMITH T.;
RT "Single gene circles in dinoflagellate chloroplast genomes.";
RL Nature 400:155-159(1999).
DR EMBL; AF130037; AD44704.1; -.
KW Chloroplast.
SQ SEQUENCE 219 AA; 24373 MW; 9C1A3172 CRC32;

Query Match 35.7%; Score 5; DB 8; Length 219;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HRWSS 8

RESULT 8
Q9W7Q8 ID Q9W7Q8 PRELIMINARY; PRT; 235 AA.
AC Q9W7Q8;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DE HOXD-4.
GN HOXD-4.
OS Paralicthys olivaceus (Flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
OC Pleuronectiformes; Pleuronectoidae; Bothidae; Paralicthys.
RN [1]
RP SEQUENCE FROM N.A.
RA SUZUKI T., OOHARA I., KUROKAWA T.;
RT "Hoxd-4 expression during pharyngeal arch development in flounder
(Paralicthys olivaceus) embryos and effects of retinoic acid on
expression.";
RT Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 98277852.
RA SUZUKI T., OOHARA I., KUROKAWA T.;
RT "Hoxd-4 expression during pharyngeal arch development in flounder
(Paralicthys olivaceus) embryos and effects of retinoic acid on
expression.";
RL Zool. Sci. 15:57-67(1998).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AB029749; BAA82361.1; -.
DR PROSITE; PS00027; HOMEBOX.1; 1.
KW Homeobox; DNA-binding; Nuclear protein.
SQ SEQUENCE 235 AA; 27101 MW; 57A1C75E CRC32;

Query Match 35.7%; Score 5; DB 13; Length 235;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SSYMV 11
Db 4 SSYMV 8

RESULT 9
P88361 ID P88361 PRELIMINARY; PRT; 244 AA.
AC P88361;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PATIENT H;
RX MEDLINE; 97184515.
RA McDONALD R.A., MAYERS D.L., CHUNG R.C.Y., WAGNER K.F., KIM S.,
RA BIRX D.L., MICHAEL N.L.;
RT "Evolution of human immunodeficiency virus type 1 env sequence
variation in patients with diverse rates of disease progression and T-
cell function.";
RT J. Virol. 71:1871-1879(1996).
DR EMBL; U69437; AAC56748.1; -.
DR PFAM; PF00516; GP120; 1.
KW Envelope protein.
FT NON_TER 1
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FT NON\_TER 244 244  
SQ SEQUENCE 244 AA; 27027 MW; 11A44107 CRC32;

Query Match 35.7%; Score 5; DB 12; Length 244;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SSVW 11  
DB 71 SSVW 75

## RESULT 10

P88358 ID P88358 PRELIMINARY; PRT; 251 AA.  
AC P88358;  
DT 01-MAY-1997 (TRENBLrel. 03, Created)  
DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)  
DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)  
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroviridae; Retroviridae; Lentivirus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-PATIENT H;  
RX MEDLINE: 97184515.  
RA MCDONALD R.A., MAYERS D.L., CHUNG R.C.Y., WAGNER K.F., KIM S.,  
RA BIER D.L., MICHAEL N.L.;  
RT "Evolution of human immunodeficiency virus type 1 env sequence  
variation in patients with diverse rates of disease progression and T-  
cell function."  
RL J. Virol. 71:1871-1879(1996).  
DR EMBL: U69434; AAC56745.1; -;  
DR PFM: PF00516; GP120; 1.  
KW Envelope protein.  
FT NON\_TER 1 1  
FT NON\_TER 251 251  
SQ SEQUENCE 251 AA; 27714 MW; A06370E1 CRC32;

Query Match 35.7%; Score 5; DB 12; Length 251;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SSVW 11  
DB 78 SSVW 82

## RESULT 11

Q22117 ID Q22117 PRELIMINARY; PRT; 255 AA.  
AC Q22117;  
DT 01-NOV-1996 (TRENBLrel. 01, Created)  
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
DT 01-JAN-1999 (TRENBLrel. 09, Last annotation update)  
DE T03F7.5 PROTEIN.  
GN T03F7.5.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;  
OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC MORTIMORE B.;  
RA Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE: 94150718.  
RA WILSON R., AINSOUGH R., ANDERSON K., BAYNES C., BERKS M.,  
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,  
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,  
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,  
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,  
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,  
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,  
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,  
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,  
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
RT elegans."  
RL Nature 368:32-38(1994).  
DR EMBL: Z74041; CAA98520.1; -;  
SQ SEQUENCE 255 AA; 29600 MW; FAC3B217 CRC32;

Query Match 35.7%; Score 5; DB 5; Length 255;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EFHW 6  
DB 208 EFHW 212

## RESULT 12

O10441 ID O10441 PRELIMINARY; PRT; 262 AA.  
AC O10441;  
DT 01-JUL-1997 (TRENBLrel. 04, Created)  
DT 01-JUL-1997 (TRENBLrel. 04, Last sequence update)  
DT 01-AUG-1998 (TRENBLrel. 07, Last annotation update)  
DE PUTATIVE 30 KDA PROTEIN.  
GN L2 COMP. ORF.  
OS Mouse adenovirus type 1 (NAV-1).  
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEISSNER J.D., HIRSCH G.N., LARUE E.A., FULCHER R.A., SPINDLER K.R.;  
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL: U95843; AAB53756.1; -;  
SQ SEQUENCE 262 AA; 30266 MW; 6FE03EED CRC32;

Query Match 35.7%; Score 5; DB 12; Length 262;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RWSS 9  
DB 59 RWSS 63

## RESULT 13

O37972 ID O37972 PRELIMINARY; PRT; 263 AA.  
AC O37972;  
DT 01-MAY-1999 (TRENBLrel. 10, Created)  
DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)  
DT 01-MAY-1999 (TRENBLrel. 10, Last annotation update)  
DE INDOLETHYLAMINE N-METHYLTRANSFERASE.  
GN INMT.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LUNG;  
RX MEDLINE: 99069450.  
RA THOMPSON M.A., WEINSHILBOUM R.M.;  
RT "Rabbit lung indolethylamine N-methyltransferase. cDNA and gene  
cloning and characterization."  
RL J. Biol. Chem. 273:34502-34510(1998).  
DR EMBL: AF077828; AAC97492.1; -;  
DR EMBL: AF077827; AAC97492.1; JOINED.

DR EMBL: AF077826; AAC97491.1; --  
 KW Transferase; Methyltransferase.  
 SQ SEQUENCE 263 AA; 28955 MW; CE43D9F6 CRC32;

Query Match 35.7%; Score 5; DB 6; Length 263;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SSWYV 11  
 Db 202 SSWYV 206  
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RESULT 14  
 Q52970 PRELIMINARY; PRT; 285 AA.  
 AC Q52970;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 DE 01-NOV-1998 (TReMBLrel. 08, Last annotation update)  
 DE MODULATION GENES NODA, NODB AND NODC.  
 OS Rhizobium meliloti.  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 OC Rhizobiaceae; Sinorhizobium.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 85087953.  
 RA TOEROEK I., KONDOROSI E., STEPKOWSKI T., POSFAI J., KONDOROSI A.;  
 RT "Nucleotide sequence of Rhizobium meliloti nodulation genes.";  
 RL Nucleic Acids Res. 12:9509-9524(1984).  
 DR EMBL: X01649; CAA25807.1; --  
 SQ SEQUENCE 285 AA; 32342 MW; 157B9F20 CRC32;

Query Match 35.7%; Score 5; DB 2; Length 285;  
 Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WSSYM 10  
 Db 86 WSSYM 90  
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RESULT 15  
 Q9XMG3 PRELIMINARY; PRT; 294 AA.  
 AC Q9XMG3;  
 DT 01-NOV-1999 (TReMBLrel. 12, Created)  
 DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)  
 DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)  
 DE ET2.OL ORF1 PROTEIN (FRAGMENT).  
 GN ET2.OL ORF1.  
 OS Epichloe typhina.  
 OG Mitochondrion  
 OG Mitochondrial plasmid.  
 OC Eukaryota; Fungi; Ascomycota; Euascomycetes; Pyrenomycetes;  
 OC Hypocreales; Clavicipitaceae; Epichloe.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-PRG: PLASMID-MITOCHONDRIAL PLASMID;  
 RX MEDLINE; 92145777  
 RA MOGEN K.L., SIEGEL M.R., SCHARDL C.L.;  
 RT "Linear DNA plasmids of the perennial ryegrass choke pathogen,  
 Epichloe typhina (Clavicipitaceae).";  
 RL Curr. Genet. 20:519-526(1991).  
 DR EMBL: X57200; CAA40486.2; --  
 KW Mitochondrion.  
 FT NON\_TER 1  
 FT NON\_TER 294  
 SQ SEQUENCE 294 AA; 35780 MW; 90A243F8 CRC32;

Query Match 35.7%; Score 5; DB 8; Length 294;  
 Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EFHRW 6  
 Db 197 EFHRW 201  
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Search completed: September 13, 2000, 02:27:31  
 Job time: 173 sec



OM of: US-09-155-076-1 to: EST:\* out\_format : pfs

Date: Sep 13, 2000 3:34 AM

About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:  
-MODEL=frame.p2n.model -DRV=xlpl  
-Q/cgn2/\_USPTO.spool/US09155076/runat\_29082000\_092538\_16898/app\_query.fasta\_1.144  
-DB=EST -FASTA=fastap -SUFFIX=est -GAPOP=4.500 -GAPEXT=0.050  
-MINMATCH=0.100 -LOOPCL=0.000 -LOPEXT=0.000 -GAPOP=4.500  
-GAPEXT=0.050 -GAPOP=6.000 -GAPEXT=6.000 -GAPOP=6.000  
-GAPEXT=7.000 -GAPOP=6.000 -GAPEXT=6.000 -DELOP=6.000  
-DELEXI=7.000 -START=1 -MATRIX=oligo -TRANS=human4.0.cdi -LIST=45  
-DOALIGN=200 -THR\_SCORE=quality -THR\_MIN=1 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0 -MAXLEN=100000  
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-WAIT -THREADS=1

Search information block:

Query: US-09-155-076-1

Query length: 14

Database: EST\*

Database sequences: 5247842

Database length: -2090053206

Search time (sec): 889.020000

WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPOP=XGAPOP=60.000  
WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=XGAPEXT=60.000

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gb_est25:A1764103	+	14.00	307.01	2.8e-08	362	! A1764103 UI-R-YO-acy-h-04-0-UI
gb_est48:F27586	+	14.00	306.75	2.9e-08	378	! F27586 HSPD15598 HM3 Homo sapie
gb_est44:AA93814	+	14.00	306.72	3.0e-08	380	! AA93814 0184B09.s1 NCI_CGAP_K1
gb_est44:AA612795	+	14.00	306.66	3.0e-08	384	! AA612795 hb33a07.s1 NCI_CGAP_Lu
gb_est44:AA998511	+	14.00	306.52	3.0e-08	393	! AA998511 UI-R-C0-le-h-11-0-UI
gb_est25:A1766812	+	14.00	306.49	3.0e-08	395	! A1766812 w189a12.s1 NCI_CGAP_K1
gb_est26:A1847791	+	14.00	306.49	3.0e-08	395	! A1847791 UI-M-AK1-ave-f-02-0-UI
gb_est19:A1360141	+	14.00	306.26	3.1e-08	410	! A1360141 QY83d10.s1 NCI_CGAP_B1
gb_est24:A1690171	+	14.00	306.25	3.1e-08	413	! A1690171 tx33a02.s1 NCI_CGAP_Lu
gb_est7:AA401251	+	14.00	306.22	3.2e-08	413	! AA401251 zv68801.s1 Soares_tot
gb_est45:AA653940	+	14.00	305.12	3.5e-08	496	! AA653940 102878 MARC_1BOV Bos t
gb_est1:AA030863	+	14.00	305.06	3.7e-08	501	! AA030863 m45c07.r1 Soares_mous
gb_est2:AA118440	+	14.00	304.91	3.7e-08	514	! AA118440 m034a07.r1 Life Tech m
gb_est3:AA141312	+	14.00	304.80	3.7e-08	523	! AA141312 EST291353 Normalized r
gb_est38:AA193377	+	14.00	304.68	3.8e-08	534	! A1325377 m45c07.y1 Soares_mous
gb_est18:A1227851	+	14.00	304.61	3.9e-08	540	! A1227851 EST224546 Normalized r
gb_est19:A1323369	+	14.00	304.51	3.9e-08	549	! A1323369 m45c07.r1 Soares_mous
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gb_est48:F34547	+	11.00	242.35	0.0001	302	! F34547 HSPD29467 HM3 Homo sapie
gb_est26:A1837078	+	10.00	220.06	0.0020	332	! A1837078 UI-M-AK0-adc-b-02-0-UI
gb_est23:A1651494	+	10.00	219.32	0.0022	364	! A1651494 w06d09.s1 NCI_CGAP_GC
gb_est4:AA271549	+	8.00	175.35	0.6142	373	! AA271549 v074f09.r1 Soares_mous
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gb_est47:A1944432	+	7.00	149.59	16.72	709	! A1944432 bs01c12.y1 Drosophila
gb_est11:AA0791533	+	6.00	136.02	95.24	176	! AA0791533 HS_5269_A2_H03_T7A_RPC
gb_est33:AA280727	+	6.00	135.66	99.78	187	! A280727 AV280727 RIKEN full-le
gb_est46:AA736001	+	6.00	134.93	109.48	211	! AA736001 EST331987 KV3 Medicago
gb_est39:AA182192	+	6.00	134.68	113.06	229	! A182192 x71f12.x1 Soares_NFL
gb_est33:AA241723	+	6.00	134.19	120.49	239	! A241723 AV241723 RIKEN full-le
gb_est17:B90397	+	6.00	133.48	131.95	269	! B90397 CIT-HSP-2163A5.TF CIT-HS
gb_est53:T90199	+	6.00	133.35	134.21	275	! T90199 yd39a11.s1 Soares fetal
gb_est51:AA15464	+	6.00	132.99	140.54	232	! A15464 HH161-F Adult heart, Clc
gb_est30:AA049775	+	6.00	132.97	140.91	293	! AA049775 AV049775 Mus musculus
gb_est7:AA048695	+	6.00	132.93	141.65	295	! AA048695 RPK1-11-260520.TV RPK1
gb_est35:AA349284	+	6.00	132.91	142.02	296	! AA349284 AV349284 RIKEN full-le
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gb\_est19:A1361528 - 6.00 132.75 144.96 304 ! A1361528 qy36g04.x1 NCI\_CGAP  
gb\_est5:AA296653 + 6.00 132.59 147.88 312 ! AA296653 EST11192 Uterus Hom  
gb\_est39:AA181786 + 6.00 132.59 147.88 312 ! AA181786 pa08d03.y1 Hawdon A  
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seq\_name: gb\_est50:N90761

seq\_documentation\_block: 248 bp mRNA EST 03-APR-1996  
LOCUS N90761  
DEFINITION zb22e03.s1 Soares\_fetal\_lung\_NbHL19W Homo sapiens cDNA clone  
IMAGE:302812 3' similar to gb:M55040 ACETYLCHOLINESTERASE PRECURSOR  
(HUMAN); mRNA sequence.

ACCESSION N90761  
VERSION N90761.1 GI:1444088

KEYWORDS EST.  
SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 248)

AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,  
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Mafrá,M.,  
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,  
Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and  
Wilson,R.

TITLE The Washu-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT On Dec 30, 1997 this sequence version replaced gi:905921.

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality

Possible reversed clone: polyt not found

Seq primer: ETPPrimer

High quality sequence stop: 1.

FEATURES

Location/Qualifiers  
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/organism="Homo sapiens"  
/db\_xref="GDB:1247744"  
/db\_xref="taxon:9606"  
/clone\_lib="Soares\_fetal\_lung\_NbHL19W"  
/dev\_stage="19 weeks"  
/lab\_host="DH10B (ampicillin resistant)"  
/note="Organ: lung; Vector: pT7T3D (Pharmacia) with a  
modified polylinker; Site: 1: Not I; Site 2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer.  
[5'-TGTTACCACTCACTGAGGCGGCGCAATTTTTTTTTTTT-3']  
double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified pT73 vector  
(Pharmacia). Library went through one round of  
normalization to a Cot = 5. Library constructed by Bento  
Soares and M.Fatima Bonaldo. This library was constructed  
from the same fetus as the fetal heart library, Soares  
fetal heart NbHL19W."

BASE COUNT 47 a 89 c 57 g 47 t 8 others

ORIGIN

alignment\_scores:

Quality: 14.00 Length: 14

Ratio: 1.000 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-155-076-1 x N90761 ..

Align seg 1/1 to: N90761 from: 1 to: 248

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 11 GCCGAGTTCACCGCTGGAGCTCCTACATGGTGCACCTGGAAG 52

seq\_name: gb\_est52:T28280

seq\_documentation\_block: 254 bp mRNA EST 06-SEP-1995  
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 VERSION T28280.1 GI:610378  
 EST.  
 KEYWORDS human.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 254)  
 AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,A.R., Fuldner,R.A.,  
 Buit,C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,  
 White,O., Sutton,G., Blake,J.A., Brandon,R.C., Chiu,M.-W.,  
 Clayton,R.A., Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,  
 FitzGerald,L.M., FitzHugh,W.M., Fritchman,J.L., Geoghagen,N.S.M.,  
 Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkley,J.P.S.,  
 Kelley,J.M., Kline,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M.,  
 Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T.,  
 Pellegrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L.,  
 Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R.,  
 Weidman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A.,  
 Coleman,T.A., Collins,E.-J., Dimke,D., Feng,P., Ferrie,A.,  
 Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,J.M.,  
 Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Ji,H., Li,H.,  
 Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.-F., Wing,J., Xu,C.,  
 Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A.,  
 Haseeltine,W.A., Fields,C., Fraser,C.M., and Venter,J.C.  
 Initial Assessment of Human Gene Diversity and Expression Patterns  
 Based Upon 83 Million Basepairs of cDNA Sequence  
 NATURE 377, 3-174 (1995)  
 JOURNAL 96026280  
 MEDLINE  
 COMMENT On May 10, 1995 this sequence version replaced gi:805490.  
 Other ESTs: THC20776  
 Contact: Venter, JC  
 The Institute for Genomic Research  
 932 Clopper Rd, Gaithersburg, MD 20878  
 Tel: 3018699056  
 Fax: 3018699423  
 Email: tdbinfo@tdb.tigr.org  
 For clone availability, additional sequence and expression  
 information related to this EST, please contact the TIGR Database  
 (tdbinfo@tdb.tigr.org)  
 Insert Length: 1145 Std Error: 0.00  
 Seq primer: M13 Reverse  
 High quality sequence stop: 187.  
 Location/Qualifiers  
 1..254  
 /organism="Homo sapiens"  
 /db\_xref="ATCC (inhost):101797"  
 /db\_xref="taxon:9606"  
 /clone\_lib="Human Embryo"  
 /tissue\_type="embryo"  
 45 a 89 c 78 g 41 t 1 others

# alignment\_scores:

Quality: 14.00 Length: 14  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-155-076-1 x T28280 ..

Align seg 1/1 to: T28280 from: 1 to: 254

1 AlaGluPheHisArgTrpSerTyrMetValHisTrpLys 14  
 |||  
 138 GCCGAGTTCACCGCTGGAGCTCCTACATGGTGCACCTGGAAG 179

seq\_name: gb\_est25:AI764103

seq\_documentation\_block: 362 bp mRNA EST 25-JUN-1999  
 LOCUS AI764103 Rattus norvegicus cDNA clone  
 DEFINITION UI-R-Y0-acy-h-04-0-UI.s1 UI-R-Y0 Rattus norvegicus cDNA clone  
 UI-R-Y0-acy-h-04-0-UI 3', mRNA sequence.  
 ACCESSION AI764103  
 VERSION AI764103.1 GI:5210038  
 EST.  
 KEYWORDS EST.  
 SOURCE Norway rat.  
 ORGANISM Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 REFERENCE 1 (bases 1 to 362)  
 AUTHORS Bonaldo,M.F., Lenon,G. and Soares,M.B.  
 TITLE Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 JOURNAL Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE 97044477  
 COMMENT Contact: Soares, MB  
 Program for Rat Gene Discovery and Mapping  
 University of Iowa  
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: msoares@blue.weeg.uiowa.edu  
 The sequence contained an oligo-dr track that was present in the  
 oligonucleotide that was used to prime the synthesis of first  
 strand cDNA and therefore this may represent a bonafide poly A  
 tail. The sequence tag present in the cDNA between the NotI site  
 and the oligo-dr track served to verify it as a clone from the  
 normalized Eye library cDNA Library Preparation: M.B. Soares Lab  
 Clone distribution: clones will be available through Research  
 Genetics (www.resgen.com) The following repetitive elements were  
 found in this cDNA sequence: 1-30, >POLY\_A#simple\_repeat  
 Seq primer: M13 Forward  
 POLYA=yes.  
 Location/Qualifiers  
 1..362  
 /organism="Rattus norvegicus"  
 /strain="Sprague-Dawley"  
 /db\_xref="taxon:10116"  
 /clone\_lib="UI-R-Y0-acy-h-04-0-UI"  
 /clone\_lib="UI-R-Y0"  
 /dev\_stage="adult"  
 /lab\_host="DH10B (Life Technologies)"  
 /note="vector: pMT30-Pac (Pharmacia) with a modified  
 polylinker; Site\_1: Not I; Site\_2: Eco RI; The UI-R-Y0  
 library is a subtracted library derived from an  
 individually-tagged normalized whole-eye (minus the lens)  
 library. The driver for the subtraction consisted of a  
 pool of all previous libraries (UI-R-A0, UI-R-A1, UI-R-E0,  
 UI-R-E1, UI-R-C0, and UI-R-C1). The tag is a string of  
 3-5 nucleotides present between the Not I site and the  
 oligo-dr track which allows identification of the library  
 of origin of a clone within the mixture. The subtracted  
 library (UI-R-Y0) was constructed as follows: PCR  
 amplified cDNA inserts from previous library clones from  
 which 3' ESTs had been derived were used as a driver in a  
 hybridization with the normalized whole-eye library in  
 the form of single-stranded circles. The remaining  
 single-stranded circles (subtracted library) was purified  
 by hydroxyapatite column chromatography, converted to

double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the U1-R-Y0 library. This procedure has been previously described (Bonaldi, Lennon and Soares, Genome Research 6: 791-806, 1996); TAG\_LIB=U1-R-Y0; TAG\_ISSUE=EYE; TAG\_SEQ=CATTG"

BASE COUNT 71 a 87 c 116 g 88 t  
ORIGIN

alignment\_scores:  
Quality: 14.00 Length: 14  
Ratio: 1.000 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
US-09-155-076-1 x A1764103/rev ..

Align seg 1/1 to reverse of: A1764103 from: 1 to: 362

1 AlagluPheHisArgTyrSerTyrMetValHisTyrLys 14  
340 GCGAGTCCACCGCTGGAGCTCTACATGTCACACTGGAAG 299

seq\_name: gb\_est48:F27586

seq\_documentation\_block:  
LOCUS F27586 378 bp mRNA EST 13-MAY-1999  
DEFINITION HSPD15598 HM3 Homo sapiens cDNA clone s4000002G06, mRNA sequence.

ACCESSION F27586

VERSION F27586.1 GI:4813212

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheraia; Primates; Catarrhini; Homnidae; Homo.

TITLE Lanfranchi, G., Muraro, T., Caldara, F., Pacchioni, B., Pallavicini, A.,

Pandolfi, D., Toppos, S., Trevisan, S., Scarso, S. and Valle, G.

Identification of 4370 expressed sequence tags from a

3'-end-specific cDNA library of human skeletal muscle by DNA

sequencing and filter hybridization

Genome Res. 6 (1), 35-42 (1996)

JOURNAL 96276048

MEDLINE On Jul 7, 1999 this sequence version replaced gi:5410190.

COMMENT Contact: Valle G.

CRIBI Biotechnology Centre

University of Padua

Via Trieste 75, 35121 Padua, Italy

ABI Chromatograms and other information are available on WWW at

http://grup.bio.unipd.it.

Location/Qualifiers

1..378

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="s4000002G06"

/clone\_lib="HM3"

/sex="female"

/tissue\_type="pectoral muscle (after mastectomy)"

/note="Vector: pCDNALL (Invitrogen); Site.1: BstXI;

Site.2: NotI; The library was constructed by G.

Lanfranchi. This library is not subtracted nor normalized.

The first strand cDNA was primed with a biotinylated

oligo-dT-NotI primer

(5'-biotin-AACCGGCTCGAGCGCGCTTTTTTTTTTTTTTTT-3'). The

ds cDNA was sonicated and size-selected in the range

350-550 bp. The 3' specific fragments were selected by

streptavidin coated magnetic beads, ligated to

non-palindromic BstXI adapters, NotI digested and

directionally cloned into BstXI-NotI cut pCDNALL vector."

BASE COUNT 65 a 147 c 102 g 64 t  
ORIGIN

alignment\_scores:  
Quality: 14.00 Length: 14  
Ratio: 1.000 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
US-09-155-076-1 x F27586 ..

Align seg 1/1 to: F27586 from: 1 to: 378

1 AlagluPheHisArgTyrSerTyrMetValHisTyrLys 14  
115 GCGAGTCCACCGCTGGAGCTCTACATGTCACACTGGAAG 156

seq\_name: gb\_est14:AA933814

seq\_documentation\_block:  
LOCUS AA933814 380 bp mRNA EST 26-AUG-1998

DEFINITION O184009.s1 NCI\_CGAP\_Kid5 Homo sapiens cDNA clone IMAGE:1536281 3'

similar to gb:M55040 ACETYLCHOLINESTERASE PRECURSOR (HUMAN);, mRNA

sequence.

ACCESSION AA933814

VERSION AA933814.1 GI:3090082

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheraia; Primates; Catarrhini; Homnidae; Homo.

TITLE NCI\_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

On Feb 11, 1998 this sequence version replaced gi:2873131.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.llnl.gov/bbrp/image/image.html

Insert Length: 437 Std Error: 0.00

Seq primer: -40m13 fwd. ET from Amersham.

Location/Qualifiers

1..380

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:1536281"

/clone\_lib="NCI\_CGAP\_Kid5"

/tissue\_type="2 pooled tumors (clear cell type)"

/lab\_host="DH10B"

/note="Organ: Kidney; Vector: p7T3D-Pac (Pharmacia) with

a modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo(dT) primer [5',

AACTGGAGATTCGCGCCGCAATATTTTATTTTATTTT 3'],

double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified p7T3 vector. Library

went through one round of normalization. Library

constructed by Bento Soares and M. Fatima Bonaldi.

BASE COUNT 65 a 150 c 101 g 64 t

alignment\_scores:  
Quality: 14.00 Length: 14  
Ratio: 1.000 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
US-09-155-076-1 x AA933814

Align seg 1/1 to: AA933814 from: 1 to: 380

1 AlaGluPheHisArgTrpSerSerTyrMetValHisTrpLys 14  
115 GCCGAGTTCACCGCTGGAGCTCTACATGTCACACTGGAG 156

seq\_name: gb\_est44:AW612795

seq\_documentation\_block:  
LOCUS AW612795 384 bp mRNA EST  
DEFINITION hh33a07.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:2956884 3'  
similar to contains PTR5.t3 PTR5 repetitive element ;, mRNA  
sequence.  
ACCESSION AW612795.1 GI:7317981  
VERSION AW612795  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 384)

REFERENCE  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550

Email: Robert\_Strausberg@nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
DNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
image.llnl.gov/image/html/iresources.shtml

Possible reversed clone: polyT not found

Seq primer: -40UP from Gibco.

FEATURES  
source

Location/Qualifiers  
1. 384  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2956884"  
/clone\_lib="NCI CGAP Lu24"  
/tissue\_type="carcinoid"  
/lab\_host="DH10B"  
/note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a  
modified polylinker; Plasmid DNA from the normalized  
library NCI CGAP Lu5 was prepared, and ss circles were  
made in vitro. Following HAP purification, this DNA was  
used as tracer in a subtractive hybridization reaction.  
The driver was PCR-amplified cDNAs from a pool of 5,000  
clones made from the same library (cloneIDs  
1414920-1417991 and 1520904-1522439). Subtraction by Bento  
Soares and M. Fatima Bonaldo."  
BASE COUNT 66 a 154 c 96 g 68 t  
ORIGIN

alignment\_scores:  
Quality: 14.00 Length: 14  
Ratio: 1.000 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-155-076-1 x AW612795

Align seg 1/1 to: AW612795 from: 1 to: 384

1 AlaGluPheHisArgTrpSerSerTyrMetValHisTrpLys 14  
88 GCCGAGTTCACCGCTGGAGCTCTACATGTCACACTGGAG 129

seq\_name: gb\_est14:AA998511

seq\_documentation\_block:  
LOCUS AA998511 393 bp mRNA EST  
DEFINITION UI-R-CO-ie-h-11-0-UI-s1 UI-R-CO Rattus norvegicus cDNA clone  
UI-R-CO-ie-h-11-0-UI 3', mRNA sequence.

ACCESSION AA998511  
VERSION AA998511.1 GI:4290364  
KEYWORDS EST.  
SOURCE Norway rat.  
ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

REFERENCE  
AUTHORS 1 (bases 1 to 393)  
TITLE Bonaldo,M.F., Lennon,G. and Soares,M.B.  
Normalisation and subtraction: two approaches to facilitate gene  
discovery  
JOURNAL Genome Res. 6 (9), 791-806 (1996)  
MEDLINE 97044477

COMMENT On Jun 5, 1998 this sequence version replaced gi:3189162.  
Contact: Soares, MB

Program for Rat Gene Discovery and Mapping

University of Iowa  
451 Eckstein Medical Research Building Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9585

Email: msoares@blue.weeg.uiowa.edu

The sequence tag present in the cDNA between the NotI site and the  
oligo-dr track served to identify it as a clone from the normalized  
adult Brain library. CDNA Library Preparation: M. Fatima Bonaldo,  
Ph.D. Clone distribution: clones will be available through Research  
Genetics. This clone is also available through the I.M.A.G.E.  
Consortium at LLNL (info@image.llnl.gov). IMAGE ID=1774140

Seq primer: M13 Forward  
POLYA-No.

FEATURES  
source

Location/Qualifiers  
1. 393  
/organism="Rattus norvegicus"  
/strain="Sprague-Dawley"  
/db\_xref="taxon:10116"  
/clone="UI-R-CO-ie-h-11-0-UI"  
/clone\_lib="UI-R-CO"  
/dev\_stage="adult"  
/lab\_host="DH10B (Life Technologies)"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker; Site\_1: Not I; Site\_2: Eco RI; The UI-R-CO  
library is a subtracted library derived from the UI-R-Al  
and UI-R-E1 libraries. The UI-R-Al library consisted of a  
mixture of individually tagged normalized libraries  
constructed from rat placenta, adult lung, brain, liver,  
kidney, heart, spleen, ovary, and muscle. The UI-R-E1  
library consisted of a mixture of individually tagged  
normalized libraries constructed from 8, 12 and 18-day  
embryo. The tag is a string of 3-5 nucleotides present  
between the Not I site and the oligo-dr track which  
allows identification of the library of origin of a clone  
within the mixture. The subtracted library (UI-R-CO) was  
constructed as follows: PCR amplified cDNA inserts from a  
pool of UI-R-Al and UI-R-E1 clones from which 3', ESTs had  
been derived was used as a driver in a hybridization with  
the pooled UI-R-Al and UI-R-E1 library in the form of  
single-stranded circles. The remaining single-stranded  
circles (subtracted library) was purified by  
hydroxyapatite column chromatography, converted to  
double-stranded circles and electroporated into DH10B  
bacteria (Life Technologies) to generate the UI-R-CO  
library. This procedure has been previously described  
(Bonaldo, Lennon and Soares, Genome Research 6: 791-806,



wed sep 13 08:11:29 2000

1996" 80 a 92 c 130 g 91 t  
 BASE COUNT  
 ORIGIN  
 alignment\_scores:  
 Quality: 14.00 Length: 14  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
 US-09-155-076-1 x AA998511/rev ..  
 Align seg 1/1 to reverse of: AA998511 from: 1 to: 393

1 AlaGlupPheHisArgTrpSerTyrMetValHisTrpLys 14  
 |||||  
 327 GCCGAGTTCACCGCTGGAGCTCCTACATGGTGCACCTGGAAG 286

seq\_name: gb\_est25:AI766812

seq\_documentation\_block:  
 LOCUS AI766812 395 bp mRNA EST 21-DEC-1999  
 DEFINITION w199a12.x1 NCI\_CGAP\_Kid12 Homo sapiens cDNA clone IMAGE:2400478 3'  
 similar to gb:M55040 ACETYLCHOLINESTERASE PRECURSOR (HUMAN);, mRNA  
 sequence.

ACCESSION AI766812.1 GI:52333321  
 VERSION AI766812  
 KEYWORDS EST.  
 SOURCE human.

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 395)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT On Apr 7, 1998 this sequence version replaced gi:3034669.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA sequencing by: Greg Lennon, Ph.D.

Cloning strategy: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

[www.bio.llnl.gov/bbrp/image/image.html](http://www.bio.llnl.gov/bbrp/image/image.html)

Insert length: 442 Std Error: 0.00

Seq primer: -40UP from Glibco.

Location/Qualifiers

1. .395

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:2400478"

/clone\_lib="NCI-CGAP\_Kid12"

/tissue\_type="2 pooled tumors (clear cell type)"

/lab\_host="DH10B"

/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with

a modified polylinker; Site.1: Not I; Site.2: Eco RI;

Plasmid DNA from the normalized library NCI\_CGAP\_Kid5 was

prepared, and ss circles were made in vitro. Following RAP

purification, this DNA was used as tracer in a subtractive

hybridization reaction. The driver was PCR-amplified cDNAs

from a pool of 5,000 clones made from the same library

(cloneIDs 1323912-1325831, 1471368-1472903 and

1492104-1493255). Subtraction by Bento Soares and M.

Fatima Bonaldo."

64 a 155 c 107 g 69 t

BASE COUNT  
 ORIGIN

alignment\_scores:  
 Quality: 14.00 Length: 14  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
 US-09-155-076-1 x AI766812 ..  
 Align seg 1/1 to: AI766812 from: 1 to: 395

1 AlaGlupPheHisArgTrpSerTyrMetValHisTrpLys 14  
 |||||  
 119 GCCGAGTTCACCGCTGGAGCTCCTACATGGTGCACCTGGAAG 160

seq\_name: gb\_est26:AI847791

seq\_documentation\_block:  
 LOCUS AI847791 395 bp mRNA EST 15-JUL-1999  
 DEFINITION UI-M-AK1-aev-f-02-0-UI-s1 NIH\_BMAP\_MHY\_N Mus musculus cDNA clone  
 UI-M-AK1-aev-f-02-0-UI 3', mRNA sequence.

ACCESSION AI847791  
 VERSION AI847791.1 GI:5491697  
 KEYWORDS EST.  
 SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 395)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene

discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

COMMENT On Apr 7, 1998 this sequence version replaced gi:3035605.

Contact: Chin, H

National Institute of Mental Health

6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD

20892-9643, USA

Tel: 301 443 1706

Fax: 301 443 9890

Email: mEST@mail.nih.gov

The sequence contained an oligo-dT track that was present in the

oligonucleotide that was used to prime the synthesis of first

strand cDNA and therefore this may represent a bonafide poly A

tail. The sequence tag present in the cDNA between the NCI site

and the oligo-dT track served to verify it as a clone from the

normalized hypothalamus library cDNA Library Preparation: M.B.

Soares Lab Clone distribution: NIH BMAP cDNA clones will be made

available by the means that is soon to be determined. When NIH

determines the means for distribution of the BMAP cDNA clones, this

record will be updated accordingly when that means is determined.

Seq primer: M13 Forward

Location/Qualifiers

1. .395

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UI-M-AK1-aev-f-02-0-UI"

/clone\_lib="NIH\_BMAP\_MHY\_N"

/dev\_stage="27-32 days"

/lab\_host="DH10B (Life Technologies)"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified

polylinker; Site.1: Not I; Site.2: Eco RI; The

NIH\_BMAP\_MHY\_N library is a normalized library constructed

from mouse hypothalamus. The tag is a string of 5

nucleotides present between the Not I site and the

oligo-dT track. The library was constructed as described

by Bonaldo, Lennon and Soares, Genome Research 6:  
 791-806, 1996. Tissue provided by Ms. Annie Novakovich,  
 Zivic-Miller Laboratories.; TAG\_LIB=NIH\_BMAP\_MHY\_N;  
 TAG\_TISSUE=hypothalamus; TAG\_SEQ=CGGTA"

```

BASE COUNT      78 a    91 c    137 g    89 t
ORIGIN

alignment_scores:
  Quality: 14.00      Length: 14
  Ratio: 1.000       Gaps: 0
  Percent Similarity: 100.000      Percent Identity: 100.000

alignment_block:
  US-09-155-076-1 x AI360141 ..

Align seg 1/1 to reverse of: AI847791 from: 1 to: 395

1 AlaGluPheHisArgTTPSerSerTyrMetValHisTrpLys 14
|||||
329 GCCGAGTTCACCGCTGAGCTCTACATGTCACATGGAG 288

seq_name: gb_est19:AI360141

seq_documentation_block:
LOCUS      AI360141      410 bp      mRNA      EST      16-FEB-1999
DEFINITION      qy83d10.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2018611 3'
similar to gb:M55040 ACETYLCHOLINESTERASE PRECURSOR
(HUMAN); contains PTR5.b2 TAR1 repetitive element ;, mRNA sequence.
ACCESSION      AI360141
VERSION        AI360141.1 GI:4111762
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 410)
AUTHORS        NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE          National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGAP), Tumor Gene Index
JOURNAL        Unpublished (1998)
COMMENT        On Jun 22, 1998 this sequence version replaced gi:3247207.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 440 Std Error: 0.00
Seq primer: -40UP from Gibco.
Location/Qualifiers
1..410
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2018611"
/clone_lib="NCI_CGAP_Brn25"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH108"
/notes="Organ: brain; Vector: pTT73D-Pac (Pharmacia) with a
modified polylinker; Site:1: Not I; Site:2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTTCACAACTCAAGTCGAGCGCGCATAGTTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pTT73 vector.
Library is normalized, and was constructed by Bento
Soares and M. Fatima Bonaldo."

BASE COUNT      64 a    163 c    113 g    69 t
ORIGIN

alignment_scores:
  Quality: 14.00      Length: 14
  Ratio: 1.000       Gaps: 0
  Percent Similarity: 100.000      Percent Identity: 100.000

alignment_block:
  US-09-155-076-1 x AI360141 ..

Align seg 1/1 to: AI360141 from: 1 to: 410

1 AlaGluPheHisArgTTPSerSerTyrMetValHisTrpLys 14
|||||
119 GCCGAGTTCACCGCTGAGCTCTACATGTCACATGGAG 160

seq_name: gb_est24:AI690171

seq_documentation_block:
LOCUS      AI690171      411 bp      mRNA      EST      16-DEC-1999
DEFINITION      tx33a02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2271338 3'
similar to gb:M55040 ACETYLCHOLINESTERASE PRECURSOR
(HUMAN); contains PTR5.b2 TAR1 repetitive element ;, mRNA sequence.
ACCESSION      AI690171
VERSION        AI690171.1 GI:4901465
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 411)
AUTHORS        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE          National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL        Unpublished (1997)
COMMENT        On Jan 19, 1998 this sequence version replaced gi:2286587.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 458 Std Error: 0.00
Seq primer: -40UP from Gibco.
Location/Qualifiers
1..411
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2271338"
/clone_lib="NCI_CGAP_Lu24"
/tissue_type="carcinoid"
/lab_host="DH108"
/notes="Organ: lung; Vector: pTT73D-Pac (Pharmacia) with a
modified polylinker; Plasmid DNA from the normalized
library NCI_CGAP_Lu5 was prepared, and ss circles were
made in vitro. Following HAP purification, this DNA was
used as tracer in a subtractive hybridization reaction.
The driver was PCR-amplified cDNAs from a pool of 5,000
clones made from the same library (cloneIDs
1414920-1417991 and 1520904-1522439). Subtraction by Bento
Soares and M. Fatima Bonaldo."

BASE COUNT      56 a    162 c    113 g    70 t
ORIGIN

alignment_scores:
  Quality: 14.00      Length: 14
  Ratio: 1.000       Gaps: 0
  Percent Similarity: 100.000      Percent Identity: 100.000

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alignment_block:
US-09-155-076-1 x AI90171 ..
Align seg 1/1 to: AI90171 from: 1 to: 411

1 AlaGlupPheHisArgTrpSerSertYrMetValHisTrpLys 14
|||||
119 GCCAGTTCACCGCTGGAGCTCCTACATGGTGCCTGGAAG 160

seq_name: gb_est7:AA401251
seq_documentation_block:
LOCUS AA401251 413 bp mRNA EST 16-MAY-1997
DEFINITION zv6b01.s1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone
IMAGE:758569 3' similar to gb:M55040 ACETYLCHOLINESTERASE PRECURSOR
(HUMAN); mRNA sequence.
ACCESSION AA401251
VERSION AA401251.1 GI:2055140
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 413)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997
Unpublished (1997)
COMMENT On Jan 17, 1998 this sequence version replaced gi:2044207.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: polyt not found
Seq primer: -41ml3 fwd. ET from Amersham.
Location/Qualifiers
1. .413
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:758569"
/clone_lib="Soares total_fetus_Nb2HF8_9w"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
/notes="vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from pooled 8-9 week
(total) fetus material with a Not I - oligo(dT) primer [5'
TGTACCAATCTCAAGTGGAGCGCGCTTAATTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."
68 a 163 c 111 g 71 t

BASE COUNT 68 a 163 c 111 g 71 t
ORIGIN

alignment_scores:
Quality: 14.00 Length: 14
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-1 x AA401251 ..
Align seg 1/1 to: AI90171 from: 1 to: 411

1 AlaGlupPheHisArgTrpSerSertYrMetValHisTrpLys 14
|||||
119 GCCAGTTCACCGCTGGAGCTCCTACATGGTGCCTGGAAG 160

seq_name: gb_est7:AA401251
seq_documentation_block:
LOCUS AA401251 413 bp mRNA EST 16-MAY-1997
DEFINITION zv6b01.s1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone
IMAGE:758569 3' similar to gb:M55040 ACETYLCHOLINESTERASE PRECURSOR
(HUMAN); mRNA sequence.
ACCESSION AA401251
VERSION AA401251.1 GI:2055140
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 413)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997
Unpublished (1997)
COMMENT On Jan 17, 1998 this sequence version replaced gi:2044207.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: polyt not found
Seq primer: -41ml3 fwd. ET from Amersham.
Location/Qualifiers
1. .413
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:758569"
/clone_lib="Soares total_fetus_Nb2HF8_9w"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
/notes="vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from pooled 8-9 week
(total) fetus material with a Not I - oligo(dT) primer [5'
TGTACCAATCTCAAGTGGAGCGCGCTTAATTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."
68 a 163 c 111 g 71 t

BASE COUNT 68 a 163 c 111 g 71 t
ORIGIN

alignment_scores:
Quality: 14.00 Length: 14
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-1 x AA401251 ..
Align seg 1/1 to: AI90171 from: 1 to: 411

1 AlaGlupPheHisArgTrpSerSertYrMetValHisTrpLys 14
|||||
119 GCCAGTTCACCGCTGGAGCTCCTACATGGTGCCTGGAAG 160

seq_name: gb_est7:AA401251
seq_documentation_block:
LOCUS AA401251 413 bp mRNA EST 16-MAY-1997
DEFINITION zv6b01.s1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone
IMAGE:758569 3' similar to gb:M55040 ACETYLCHOLINESTERASE PRECURSOR
(HUMAN); mRNA sequence.
ACCESSION AA401251
VERSION AA401251.1 GI:2055140
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 413)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997
Unpublished (1997)
COMMENT On Jan 17, 1998 this sequence version replaced gi:2044207.
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: polyt not found
Seq primer: -41ml3 fwd. ET from Amersham.
Location/Qualifiers
1. .413
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:758569"
/clone_lib="Soares total_fetus_Nb2HF8_9w"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
/notes="vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from pooled 8-9 week
(total) fetus material with a Not I - oligo(dT) primer [5'
TGTACCAATCTCAAGTGGAGCGCGCTTAATTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."
68 a 163 c 111 g 71 t

BASE COUNT 68 a 163 c 111 g 71 t
ORIGIN

alignment_scores:
Quality: 14.00 Length: 14
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-1 x AA401251 ..
Align seg 1/1 to: AI90171 from: 1 to: 411

1 AlaGlupPheHisArgTrpSerSertYrMetValHisTrpLys 14
|||||
119 GCCAGTTCACCGCTGGAGCTCCTACATGGTGCCTGGAAG 160

seq_name: gb_est7:AA401251
seq_documentation_block:
LOCUS AA401251 413 bp mRNA EST 16-MAY-1997
DEFINITION zv6b01.s1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone
IMAGE:758569 3' similar to gb:M55040 ACETYLCHOLINESTERASE PRECURSOR
(HUMAN); mRNA sequence.
ACCESSION AA401251
VERSION AA401251.1 GI:2055140
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 413)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997
Unpublished (1997)
COMMENT On Jan 17, 1998 this sequence version replaced gi:2044207.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: polyt not found
Seq primer: -41ml3 fwd. ET from Amersham.
Location/Qualifiers
1. .413
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:758569"
/clone_lib="Soares total_fetus_Nb2HF8_9w"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
/notes="vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from pooled 8-9 week
(total) fetus material with a Not I - oligo(dT) primer [5'
TGTACCAATCTCAAGTGGAGCGCGCTTAATTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."
68 a 163 c 111 g 71 t

BASE COUNT 68 a 163 c 111 g 71 t
ORIGIN

alignment_scores:
Quality: 14.00 Length: 14
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-1 x AA401251 ..
Align seg 1/1 to: AI90171 from: 1 to: 411

1 AlaGlupPheHisArgTrpSerSertYrMetValHisTrpLys 14
|||||
119 GCCAGTTCACCGCTGGAGCTCCTACATGGTGCCTGGAAG 160

seq_name: gb_est7:AA401251
seq_documentation_block:
LOCUS AA401251 413 bp mRNA EST 16-MAY-1997
DEFINITION zv6b01.s1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone
IMAGE:758569 3' similar to gb:M5504
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PRECURSOR (HUMAN); gb:X56518 Mouse mRNA for acetylcholinesterase (MOUSE);, mRNA sequence.  
 AA030863  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Mus musculus  
 house mouse.  
 EST.  
 GI:1500851  
 REFERENCE  
 1 (bases 1 to 501)  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 AUTHORS  
 Marra,M., Hallier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wyllie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.  
 TITLE  
 The WashU-HMI Mouse EST Project  
 JOURNAL  
 COMMENT  
 Unpublished (1996)  
 Contact: Marra M/Mouse EST Project  
 WashU-HMI Mouse EST Project  
 Washington University School  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@wustl.edu  
 This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
 MGI:280292  
 Seq primer: -28M13 rev2 from Amersham  
 High quality sequence stop: 168.  
 Location/Qualifiers  
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 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:466476"  
 /clone\_lib="Soares mouse embryo NDBE13.5 14.5"  
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 /tissue\_type="embryo"  
 /dev\_stage="13.5-14.5dpc total fetus"  
 /lab\_host="DH10B"  
 /note="Vector: p7T73D-Pac (Pharmacia) with a modified polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGGTACCAATCTGAAGTGGAGCGCCGCGAATTTTTTTTTTTTTTTTTTTT T 3'], on equal amounts of mRNA from 2 13.5dpc and 2 14.5dpc embryos (total RNA provided by Minoru Ko, Wayne State Univ., from 2 ]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7R3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."

# FEATURES Source

1..514  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:555444"  
 /clone\_lib="Life Tech mouse embryo 13 5dpc 10666014"  
 /tissue\_type="embryo"  
 /dev\_stage="13.5dpc embryos"  
 /lab\_host="DH10B"  
 /note="Organ: whole embryo; Vector: pCMV-SPORT2; Site\_1: SalI; Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT. 13.5dpc embryos. pCMV-SPORT2 vector."

## BASE COUNT ORIGIN

89 a 180 c 130 g 115 t  
 alignment\_scores:  
 Quality: 14.00 Length: 14  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
 US-09-155-076-1 x AA118440 ..  
 Align seg 1/1 to: AA118440 from: 1 to: 514

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 202 GCGGAGTTCACCGCTGGAGCTCCTACATGTGCTGCTGGAAG 243

seq\_name: gb\_est2:AA118440  
 seq\_documentation\_block:

LOCUS  
 DEFINITION  
 AA118440 514 bp mRNA EST 19-NOV-1996  
 mo3407.r1 Life Tech mouse embryo 13 5dpc 10666014 Mus musculus  
 cDNA clone IMAGE:555444 5' similar to gb:M55040  
 ACETYLCHOLINESTERASE PRECURSOR (HUMAN); gb:X56518 Mouse mRNA for  
 acetylcholinesterase (MOUSE);, mRNA sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Mus musculus  
 house mouse.  
 EST.  
 GI:15076072

REFERENCE  
 1 (bases 1 to 514)  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 AUTHORS  
 Marra,M., Hallier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wyllie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.  
 TITLE  
 The WashU-HMI Mouse EST Project  
 JOURNAL  
 COMMENT  
 Unpublished (1996)  
 Contact: Marra M/Mouse EST Project  
 WashU-HMI Mouse EST Project  
 Washington University School  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@wustl.edu  
 This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
 MGI:336236  
 Seq primer: -28M13 rev1 from Amersham  
 High quality sequence stop: 234.  
 Location/Qualifiers  
 1..514  
 /organism="Mus musculus"  
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 /db\_xref="taxon:10090"  
 /clone="IMAGE:555444"  
 /clone\_lib="Life Tech mouse embryo 13 5dpc 10666014"  
 /tissue\_type="embryo"  
 /dev\_stage="13.5dpc embryos"  
 /lab\_host="DH10B"  
 /note="Organ: whole embryo; Vector: pCMV-SPORT2; Site\_1: SalI; Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT. 13.5dpc embryos. pCMV-SPORT2 vector."

alignment\_scores:  
 Quality: 14.00 Length: 14  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
 US-09-155-076-1 x AA118440 ..  
 Align seg 1/1 to: AA118440 from: 1 to: 514

1 AlaGluPheHisArgTrpSerSeryrMetValHisTrpLys 14  
 |||||  
 202 GCGGAGTTCACCGCTGGAGCTCCTACATGTGCTGCTGGAAG 243

seq\_name: gb\_est2:AA118440  
 seq\_documentation\_block:

us-09-155-076-1.rst

Wed Sep 13 08:11:29 2000



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 13, 2000, 02:19:17 ; Search time 17.65 Seconds  
(without alignments)  
18.788 Million cell updates/sec

Title: US-09-155-076-1

Perfect score: 87

Sequence: 1 AEFHRWSSYVHWK 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_36:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87	100.0	14	W35340	Human acetylcholin
2	87	100.0	39	R77010	Alternative human
3	87	100.0	45	W48800	C-terminal fragmen
4	87	100.0	45	W68144	Human AChE splice
5	87	100.0	45	W74586	Amino acid sequenc
6	87	100.0	500	R06990	Human foetal acety
7	87	100.0	613	R06989	Human acetylcholin
8	87	100.0	614	R80726	Human acetylcholin
9	80	92.0	575	W39078	Torpedo californic
10	80	92.0	575	W39079	Torpedo californic
11	62	71.3	602	R37442	Full-length human
12	62	71.3	635	P60097	Sequence of protei
13	62	71.3	635	R41509	Full-length foetal
14	40.5	46.6	510	R41195	Yeast delta 9 desa
15	40	46.0	124	R15441	Heavy chain variab
16	40	46.0	124	R54335	Anti-HIV gp120 imm
17	40	46.0	124	R54244	Anti-HIV gp120 imm
18	40	46.0	124	R54245	Anti-HIV gp120 imm
19	40	46.0	124	R54246	Anti-HIV gp120 imm
20	40	46.0	124	W01309	VH region of HIV n
21	40	46.0	124	W01247	VH region of HIV n
22	40	46.0	124	W01227	VH region of HIV n
23	40	46.0	124	W01228	VH region of HIV n
24	40	46.0	146	R75617	VH Fab M556-13 bin
25	39	44.8	124	R75616	VH Fab M556-5 bind
26	39	44.8	124	R75615	VH Fab M556-16 bin
27	39	44.8	124	R75614	VH Fab M556-15 bin
28	39	44.8	124	R75613	VH Fab M556-10 bin
29	39	44.8	124	R75612	VH Fab M556-7 bind
30	39	44.8	124	R75611	VH Fab M556-3 bind
31	39	44.8	124	R75610	VH Fab M556-2 bind
32	39	44.8	124	R75609	VH Fab M556-1 bind
33	39	44.8	124	R75608	VH Fab M556-0 bind

34	39	44.8	124	1	R75570	VH Fab 3b3 binds t
35	39	44.8	124	1	R75572	VH Fab 3b9 binds t
36	39	44.8	137	1	R62445	81C6 heavy chain v
37	39	44.8	144	1	R08346	Heavy chain variab
38	38	43.7	121	1	R28806	5A8 VH. New anti-C
39	38	43.7	124	1	R54330	Anti-HIV gp120 imm
40	38	43.7	124	1	R54332	Anti-HIV gp120 imm
41	38	43.7	124	1	R54336	Anti-HIV gp120 imm
42	38	43.7	124	1	R54269	Anti-HIV gp120 imm
43	38	43.7	124	1	W01306	VH region of HIV n
44	38	43.7	124	1	W01310	VH region of HIV n
45	38	43.7	124	1	W01311	VH region of HIV n

ALIGNMENTS

RESULT 1  
W35340  
ID W35340 standard; peptide; 14 AA.  
AC W35340:  
DT 17-APR-1998 (first entry)  
DE Human acetylcholinesterase 14-mer peptide.  
KW Acetylcholinesterase; AChE; neuronal degeneration;  
KW Parkinson's disease; Alzheimer's disease; stroke; cancer;  
KW calcium channel modulator; antibody; inhibitor.  
OS Homo sapiens.  
PN W09735962-A1.  
PD 02-OCT-1997.  
PF 21-MAR-1997; G00796.  
PR 22-MAR-1996; GB-006040.  
PA (ISIS-) ISIS INNOVATION LTD.  
PI Greenfield SA, Vaux DJ;  
DR WPI; 97-489626/45.  
PT Peptide(s) from acetylcholine esterase which open calcium channels -  
PT used for treating disorders of the central nervous system, cancer  
PT and stroke  
PS Claim 1; Page 20; 27pp; English.  
CC This 14-mer peptide corresponds to residues 535-548 of the  
CC Acetylcholinesterase mature protein. This peptide is known to  
CC act alone or in synergism with a fragment of beta-amyloid to  
CC contribute to neuronal degeneration. Compounds that inhibit the  
CC biological activity of the novel peptides, and antibodies, can be  
CC used to control cytoplasmic calcium ion currents in vivo, and are  
CC useful for treating disorders of the central nervous system  
CC (e.g. Parkinson's and Alzheimer's diseases), stroke and cancer.  
SQ Sequence 14 AA;

Query Match 100.0% Score 87; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.8e-07;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AEFHRWSSYVHWK 14  
|||||  
DB 1 AEFHRWSSYVHWK 14

RESULT 2  
R77010  
ID R77010 standard; Protein; 39 AA.  
AC R77010;  
DT 31-MAR-1996. (first entry)  
DE Alternative human acetylcholinesterase (AChE) protein.  
KW Acetylcholinesterase; acetyl cholinesterase; EC-3.1.1.7;  
KW chromosome-7q22; acetylcholine-hydrolyzing enzyme.  
OS Homo sapiens.  
PN W09523158-A1.  
PD 31-AUG-1995.  
PF 28-FEB-1995; U02806.  
PR 28-FEB-1994; US-202755.  
PR 09-JAN-1995; US-370156.  
PA (KOHN/) KOHN K I.



PA (YISS ) YISSUM RES & DEV CO.  
 PI Shani M, Soreq H, Zakut H;  
 DR WPI: 95-311499/40.  
 PT Alternative forms of human acetyl cholinesterase (ChE) gene -  
 PT expressed in transgenic animal assay system for evaluating anti-ChE  
 PT activity of organophosphate(s), etc. or as model of ChE imbalance  
 PS Disclosure; Fig.6; 5pp; English.  
 CC Human acetylcholinesterase (EC-3.1.1.7) is accumulated at  
 CC neuromuscular junctions where it serves a vital function in  
 CC modulating cholinergic neurotransmission. This alternatively  
 CC spliced form of human AChE may be expressed in transgenic animals  
 CC which are used in an assay system for determining the anti-ChE  
 CC activity of organophosphates, carbamates, anti-ChE drugs, plant  
 CC glycoalkaloids and snake venoms.  
 SQ Sequence 39 AA;

Query Match 100.0%; Score 87; DB 1; Length 39;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRSSVMVHWK 14  
 | | | | | | | | | | | | | | | |  
 Db 11 AEFHRSSVMVHWK 24

RESULT 3  
 ID W48800 standard; protein; 45 AA.  
 AC W48800.  
 DT 07-OCT-1998 (first entry)  
 DE C-terminal fragment of human acetylcholine esterase variant EI-4.6.  
 KW Human acetylcholine esterase-I4 readthrough splice variant; AChE-I4; CNS;  
 KW blood/brain barrier; BBB; I4 peptide; antibiotic; brain tumour; glioma;  
 KW chemotherapeutic drug; central nervous system.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT Region 1..5  
 FT /note= "This region is encoded by the 3' end of  
 FT AChE exon 4"

FT Region 6..45  
 FT /note= "Residues encoded by AChE exon 6"  
 FN WO9822132-A2.  
 PD 28-MAY-1998.  
 PE 20-NOV-1997; U21696.  
 PR 21-JUL-1997; US-053200.  
 PR 20-NOV-1996; US-031194.  
 PR 12-DEC-1996; US-035266.  
 PA (KOHN/) KOHN K I.  
 PI (YISS ) YISSUM RES & DEV CO.  
 PI Friedman A, Kaufer D, Seidman S, Soreq H;  
 DR WPI: 98-312172/27.  
 FT Increasing the permeability of the blood/brain barrier - using e.g.  
 FT adrenaline, atropine or acetylcholine esterase I4 splice variant  
 FT peptide, useful for imaging and/or treatment of central nervous  
 FT system disorders  
 PS Disclosure; Fig 2; 71pp; English.

CC The present sequence represents a C-terminal fragment of the human  
 CC acetylcholine esterase splice variant EI-4.6. The AChE EI-4.6 variant  
 CC comprises of residues encoded by exons 1-4 of AChE linked to residues  
 CC encoded by the alternatively spliced AChE exon 6. The invention claims  
 CC for the human acetylcholine esterase-I4 (AChE-I4) readthrough splice  
 CC variant (W48797). The invention provides a pharmaceutical composition,  
 CC for facilitating passage of compounds through the blood/brain barrier  
 CC (BBB), comprising of AChE-I4, I4 peptide (see W48797) or AChE-I4  
 CC analogues (such as the AChE EI-4.6 variant) together with a  
 CC pharmaceutically acceptable carrier. The pharmaceutical composition  
 CC is claimed to facilitate a reversible disruption of the BBB allowing  
 CC transport of compounds through the BBB. The compounds, e.g. imaging  
 CC agents, antibiotics or chemotherapeutic drugs, are claimed to be useful  
 CC for the diagnosis and treatment of diseases or disorders of the CNS such  
 CC as infections, neurochemical disorders, brain tumours, gliomas, etc.  
 SQ Sequence 45 AA;

Query Match 100.0%; Score 87; DB 1; Length 45;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRSSVMVHWK 14  
 | | | | | | | | | | | | | | | |  
 Db 17 AEFHRSSVMVHWK 30

RESULT 4  
 ID W68144 standard; Protein; 45 AA.  
 AC W68144;  
 DT 05-OCT-1998 (first entry)  
 DE Human AChE splice variant EI-4. 6.  
 KW Nuclease resistant; acetylcholinesterase; human; myasthenia gravis;  
 KW AChE; Parkinson's disease; Alzheimer's disease; central nervous system;  
 KW neuromuscular junction; cholinergic signalling; brain.  
 OS Homo sapiens.  
 PN WO9826062-A2.  
 PD 18-JUN-1998.  
 PE 12-DEC-1997; U23598.  
 PR 21-JUL-1997; US-053334.  
 PR 12-DEC-1996; US-035266.  
 PR 13-FEB-1997; US-037777.  
 PR 02-MAY-1997; US-850347.  
 PA (KOHN/) KOHN K I.  
 PI (YISS ) YISSUM RES & DEV CO.  
 PI Eckstein F, Friedman A, Kaufer D, Seidman S, Soreq H;  
 DR WPI: 98-348522/30.  
 PT Synthetic nuclease resistant antisense oligodeoxynucleotides -  
 PT directed against acetylcholinesterase, useful for treating  
 PT Parkinson's and Alzheimer's diseases and myasthenia gravis  
 PS Disclosure; Fig 12; 89pp; English.

CC This represents the amino acid sequence of a human acetylcholinesterase  
 CC (AChE) splice variant. The invention provides sequences shown in V41278  
 CC to V41285 that represent synthetic nuclease resistant antisense  
 CC oligodeoxynucleotides which are capable of selectively modulating human  
 CC acetylcholinesterase (AChE) production. These oligonucleotides are  
 CC targeted to a splice junction in a splice variant of AChE mRNA and are  
 CC capable of selectively modulating human AChE production in the central  
 CC nervous system and neuromuscular junction. The invention also provides a  
 CC method for determining the efficacy of these human AChE specific  
 CC antisense oligonucleotides. These antisense oligonucleotides can be used  
 CC to restore balanced cholinergic signalling in the brain, particularly  
 CC related to learning and memory as well as stress disorders, Parkinson's  
 CC and Alzheimer's disease. They can also be used to reduce production and  
 CC therefore deposition of AChE in the neuromuscular junctions of patients  
 CC with e.g. myasthenia gravis. The oligonucleotides work effectively at low  
 CC doses while avoiding many of the side effects associated with Tacrine and  
 CC related cholinergic drugs for Alzheimer's disease and pyridostigmine and  
 CC related drugs for myasthenia gravis.  
 SQ Sequence 45 AA;

Query Match 100.0%; Score 87; DB 1; Length 45;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRSSVMVHWK 14  
 | | | | | | | | | | | | | | | |  
 Db 17 AEFHRSSVMVHWK 30

RESULT 5  
 ID W74586 standard; Protein; 45 AA.  
 AC W74586;  
 DT 21-DEC-1998 (first entry)  
 DE Amino acid sequence of the human AChE variant 1.  
 KW Nuclease resistance; inhibition; human; acetyl-cholinesterase; AChE;

KW Central nervous system; CNS.

OS Homo sapiens.  
 PN WO9829486-A1.  
 PD 11-SEP-1998.  
 PF 06-MAR-1998; U04503.  
 PR 06-MAR-1997; US-040203.  
 PA (KOHN/) KOHN K I.  
 PA (YISS ) YISSUM RES & DEV CO.  
 PI Seidman S, Shohami E, Soreq H;  
 DR WPI; 98-506377/43.  
 PT Treatment of injury to central nervous system - by administration of  
 PT inhibitor of acetylcholinesterase production  
 PS Disclosure; Page 61; 88pp; English.  
 CC This is the amino acid sequence of a human acetylcholinesterase  
 CC (ACHE) variant used in the method of the invention, where inhibitors  
 CC of ACHE are used to treat injury to the central nervous system (CNS).  
 CC The ACHE inhibitor can also be used to facilitate transplantation of  
 CC neuronal cells to the CNS of a patient. The inhibitor can also be  
 CC used to improve hippocampal neuron survival following injury to the  
 CC CNS. The CNS injuries that can be treated with the method include  
 CC epilepsy, stroke, Huntington's disease, head injury, spinal injury,  
 CC Pain, Parkinson's disease, myelin deficiencies, neuromuscular  
 CC disorders, neurological pain, amyotrophic lateral sclerosis,  
 CC Alzheimer's disease, and affective disorders of the brain.  
 SQ Sequence 45 AA;

Query Match 100.0%; Score 87; DB 1; Length 45;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSVMVHWK 14  
 |||||

DB 17 AEFHRWSSVMVHWK 30

# RESULT 6

R06990  
 ID R06990 standard; protein; 500 AA.  
 AC R06990;  
 DT 16-JAN-1991 (first entry)  
 DE Human foetal acetylcholinesterase (hACHE) primary transcript.  
 DE Organophosphorous poisoning; OP; cancer; leukaemia;  
 KW megakaryocytopoiesis; ovarian cancer.  
 OS Homo sapiens.  
 PN EP-388906-A.  
 PD 26-SEP-1990.  
 PR 20-MAR-1990; 105274.  
 PR (YISS ) YISSUM RES DEV CO.  
 PI Soreq H, Zakut H;  
 DR WPI; 90-291865/39.  
 DR N-PSDB; Q05999.  
 PT Human acetylcholinesterase DNA and prodn. of recombinant hACHE -  
 PT for treatment of organo-phosphorous poisoning and diagnosis of haemo-  
 PT cytopoietic disorders and ovarian carcinomas.  
 PS Disclosure; Fig 1c; 47pp; English.  
 CC Gene product is useful as an active pharmacological component for the  
 CC prophylaxis and treatment of organophosphorous poisoning, and post-  
 CC surgical apnea due to succinylcholine administration.  
 CC cDNA probe to the sequence may be used in diagnosis of various  
 CC leukaemias, abnormal megakaryocytopoiesis and ovarian carcinomas.  
 SQ Sequence 500 AA;

Query Match 100.0%; Score 87; DB 1; Length 500;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSVMVHWK 14  
 |||||

DB 472 AEFHRWSSVMVHWK 485

# RESULT 7

R06989  
 ID R06989 standard; protein; 613 AA.  
 AC R06989;  
 DT 16-JAN-1991 (first entry)  
 DE Human acetylcholinesterase (hACHE) primary transcript.  
 DE Organophosphorous poisoning; OP; cancer; leukaemia;  
 KW megakaryocytopoiesis; ovarian cancer.  
 OS Homo sapiens.  
 PN EP-388906-A.  
 PD 26-SEP-1990.  
 PR 20-MAR-1990; 105274.  
 PR (YISS ) YISSUM RES DEV CO.  
 PI Soreq H, Zakut H;  
 DR WPI; 90-291865/39.  
 DR N-PSDB; Q05998.  
 PT Human acetylcholinesterase DNA and prodn. of recombinant hACHE -  
 PT for treatment of organo-phosphorous poisoning and diagnosis of haemo-  
 PT cytopoietic disorders and ovarian carcinomas.  
 PS Claim 5; Page 25; 47pp; English.  
 CC Gene product is useful as an active pharmacological component for the  
 CC prophylaxis and treatment of organophosphorous poisoning, and post-  
 CC surgical apnea due to succinylcholine administration.  
 CC cDNA probe to the sequence may be used in diagnosis of various  
 CC leukaemias, abnormal megakaryocytopoiesis and ovarian carcinomas.  
 SQ Sequence 613 AA;

Query Match 100.0%; Score 87; DB 1; Length 613;  
 Best Local Similarity 100.0%; Pred. No. 2e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSVMVHWK 14  
 |||||

DB 585 AEFHRWSSVMVHWK 598

# RESULT 8

R0726  
 ID R0726 standard; protein; 614 AA.  
 AC R0726;  
 DT 31-MAR-1996 (first entry)  
 DE Human acetylcholinesterase (ACHE) protein.  
 DE Acetylcholinesterase; acetyl cholinesterase; EC-3.1.1.7;  
 KW chromosome-7q22; acetylcholine-hydrolyzing enzyme.  
 OS Homo sapiens.  
 PN WO9523158-A1.  
 PD 31-AUG-1995.  
 PF 28-FEB-1995; U02806.  
 PR 28-FEB-1994; US-202755.  
 PR 09-JAN-1995; US-370156.  
 PA (KOHN/) KOHN K I.  
 PA (YISS ) YISSUM RES & DEV CO.  
 PI Shani M, Soreq H, Zakut H;  
 DR WPI; 95-311499/40.  
 DR N-PSDB; Q99002.  
 PT Alternative forms of human acetyl cholinesterase (ChE) gene -  
 PT expressed in transgenic animal assay system for evaluating anti-ChE  
 PT activity of organo:phosphate(s), etc. or as model of ChE imbalance  
 PS Claim 3; Fig.1B; 55pp; English.  
 CC Human acetylcholinesterase (EC-3.1.1.7) is accumulated at  
 CC neuromuscular junctions where it serves a vital function in  
 CC modulating cholinergic neurotransmission. Alternately spliced  
 CC forms of human ACHE may be expressed in transgenic animals which  
 CC are used in an assay system for determining the anti-ChE activity  
 CC of organophosphates, carbamates, anti-ChE drugs, plant glycoalkaloids  
 CC and snake venoms.  
 SQ Sequence 614 AA;

Query Match 100.0%; Score 87; DB 1; Length 614;

```

Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRSSYVHWK 14
    | | | | | | | | | |
Db 586 AEFHRSSYVHWK 599

RESULT 9
W39078
ID W39078 standard; protein; 575 AA.
AC W39078;
DE 08-APR-1998 (first entry)
KW Torpedo californica acetylcholinesterase AChE.
KW Acetylcholinesterase; AChE; organophosphate; detoxification; oxime;
KW ray; chemical agent; treatment; prevention; aging; mutant.
OS Torpedo californica.
FH Key
FH Location/Qualifiers
FT Region
FT /note= "region as indicated in specification."
FT Modified_site
FT 59. .61
FT /note= "site as indicated in specification."
FT Region
FT /note= "region as indicated in specification."
FT Modified_site
FT 199
FT /note= "region as indicated in specification."
FT Region
FT /note= "region as indicated in specification."
FT Modified_site
FT 254. .265
FT /note= "wild-type Glu is replaced by Gln"
FT Region
FT /note= "region as given in specification"
FT Modified_site
FT 402. .521
FT /note= "region as given in specification"
FT Region
FT /note= "region as given in specification"
FT Modified_site
FT 416. .418
FT /note= "site as given in specification"
FT Modified_site
FT 457. .459
FT /note= "site as given in specification"
FT Modified_site
FT 533. .535
FT /note= "site as given in specification"
FT US5695750-A.
PN Location/Qualifiers
PD 09-DEC-1997.
PF 25-NOV-1994; 348920.
PR 25-NOV-1994; US-348920.
PA (USSA ) US SEC OF ARMY.
PI Doctor BP, Maxwell D, Radic Z, Saxena A, Taylor P;
DR WPI; 98-041233/04.
PT Mutant Torpedo acetylcholinesterase - useful for detoxifying
PT organo-phosphate compounds
PS Claim 1; Fig 2; 12pp; English.
CC This sequence represents a variant of the enzyme acetylcholinesterase
CC (AChE) from Torpedo californica which is capable of detoxifying
CC organophosphates. This E199Q mutant has greater resistance to aging
CC than the wild-type AChE and can destroy organophosphates in an
CC environmentally friendly manner. When combined with an oxime, this
CC mutant's ability to detoxify several organophosphates is amplified
CC and is predicted to have applications for the detoxification of chemical
CC warfare agents such as sarin or as a means of treating or preventing the
CC deleterious effects of organophosphate exposure in organisms.
SQ Sequence 575 AA;

Query Match 92.0%; Score 80; DB 1; Length 575;
Best Local Similarity 92.3%; Pred. No. 0.0002;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EFHRSSYVHWK 14
    | | | | | | | | | |
Db 548 EFHRSSYVHWK 560

RESULT 11
R37442
ID R37442 standard; protein; 602 AA.
AC R37442;
DE 06-OCT-1993 (first entry)
DE Full-length human pseudocholinesterase.
KW butylcholinesterase; acetylcholine acylhydrolase; EC3.1.1.8; psi-ChE;
KW pseudo-Ch; neurotransmitter; organophosphorus insecticide; OP-poison;
KW antidote.
OS Homo sapiens.
FH Key
FH Location/Qualifiers
FT peptide
FT 1. .24
FT /note= "putative leader peptide"
FT modified_site
FT 45. .47
FT /note= "potential N-glycosylation site"
FT modified_site
FT 134. .136
FT /note= "potential N-glycosylation site"
FT modified_site
FT 269. .271
FT /note= "potential N-glycosylation site"
FT modified_site
FT 284. .286
FT /note= "potential N-glycosylation site"
FT modified_site
FT 369. .371
FT /note= "potential N-glycosylation site"
FT modified_site
FT 509. .511
FT /note= "potential N-glycosylation site"

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FT modified\_site 514..516  
 FT /note= "potential N-glycosylation site"  
 FT active\_site 226  
 FT /note= "active site Serine"

US5215909-A.  
 PD 01-JUN-1993.  
 PF 18-JUN-1986; 875737.  
 PR 21-AUG-1987; US-875737.  
 PR 15-AUG-1990; US-572911.  
 PA (YEDA ) YEDA RES & DEV CO LTD.  
 PI Soreq H;  
 DR WPI; 93-188509/23.  
 DR N-PSDB; Q42496.  
 PT Recombinant human gene encoding human pseudo-cholinesterase -  
 PT used to treat organo-phosphorus poisoning  
 PS Disclosure; Columns 35-40; 34pp; English.  
 CC A cDNA library prepared from foetal brain mRNA was screened with  
 CC degenerate probe pools based on the organophosphorus binding site of  
 CC cholinesterases. A 764 nucleotide insert (designated FBChE12) was  
 CC isolated from one positive clone and sequenced. This insert (Q42495),  
 CC containing an ORF large enough to code for about half the subunit  
 CC size of human cholinesterase, was used as a probe to obtain the full-  
 CC length pseudo-cholinesterase sequence (Q42496).  
 SQ Sequence 602 AA;

Query Match 71.3%; Score 62; DB 1; Length 602;  
 Best Local Similarity 64.3%; Pred. No. 0.087;  
 Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14  
 | | | | | : | | : | |  
 DB 573 AGFHRWNNYMDWK 586

## RESULT 12

P60097  
 ID P60097 standard; Protein; 635 AA.  
 DT 27-JUN-1991 (first entry)  
 DE Sequence of protein having human cholinesterase (ChE)  
 DE activity.  
 KW Organophosphorus poisoning; therapy; prophylaxis; diagnosis;  
 KW pseudo-cholinesterase deficiency.  
 OS Homo sapiens.  
 PN EP-205200-A.  
 PD 30-DEC-1986.  
 PF 16-JUN-1986; 108189.  
 PR 18-JUN-1985; IL-075553.  
 PA (YEDA ) YEDA RES & DEV CO LTD.  
 PI Soreq H;  
 DR WPI; 86-340581/52.  
 DR N-PSDB; N60111.  
 PT Human cholinesterase-type proteins - produced by host cell contg.  
 PT recombinant vector which contains DNA fragment coding for the  
 PT enzyme  
 PS Claim 17; Page 38-40; 44pp; English.  
 CC Human cholinesterase-type proteins can be used for the prophylaxis  
 CC or for the treatment of the effects of organophosphorus cpd.  
 CC poisoning. Other uses include clinical detection of  
 CC pseudo-cholinesterase deficiencies, elucidation of the active site  
 CC topography and the AA sequence of AChE for the development of rapid  
 CC simple clinical methods to detect poisoning or disease-related  
 CC changes in ChEs, and for detecting mutations in ChE genes.  
 SQ Sequence 635 AA;

Query Match 71.3%; Score 62; DB 1; Length 635;  
 Best Local Similarity 64.3%; Pred. No. 0.092;  
 Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14

Db 606 AGFHRWNNYMDWK 619  
 | | | | | : | | : | |

## RESULT 13

R41509  
 ID R41509 standard; Protein; 635 AA.  
 AC R41509;  
 DT 06-OCT-1993 (first entry)  
 DE Full-length foetal human pseudo-cholinesterase.  
 KW butyrylcholinesterase; acetylcholine acylhydrolase; EC3.1.1.8; psi-ChE;  
 KW pseudo-ChE; neurotransmitter; organophosphorus insecticide; OP-poison;  
 KW antidote.  
 OS Homo sapiens.  
 DR WPI; 93-188509/23.  
 DR N-PSDB; Q42496.  
 FT Key  
 FT Location/Qualifiers  
 FT peptide 35..58  
 FT /note= "putative leader peptide"  
 FT modified\_site 79..81  
 FT /note= "potential N-glycosylation site"  
 FT modified\_site 168..170  
 FT /note= "potential N-glycosylation site"  
 FT modified\_site 303..305  
 FT /note= "potential N-glycosylation site"  
 FT modified\_site 318..320  
 FT /note= "potential N-glycosylation site"  
 FT modified\_site 403..405  
 FT /note= "potential N-glycosylation site"  
 FT modified\_site 506..508  
 FT /note= "potential N-glycosylation site"  
 FT modified\_site 543..545  
 FT /note= "potential N-glycosylation site"  
 FT active\_site 260  
 FT /note= "active site serine"  
 PN US5215909-A.  
 PD 01-JUN-1993.  
 PR 18-JUN-1986; 875737.  
 PR 18-JUN-1986; US-875737.  
 PR 21-AUG-1987; US-087724.  
 PR 15-AUG-1990; US-572911.  
 PA (YEDA ) YEDA RES & DEV CO LTD.  
 PI Soreq H;  
 DR WPI; 93-188509/23.  
 DR N-PSDB; Q48393.  
 PT Recombinant human gene encoding human pseudo-cholinesterase -  
 PT used to treat organo-phosphorus poisoning  
 PS Claim 4; Columns 41-46; 34pp; English.  
 CC A cDNA library prepared from foetal brain mRNA was screened with  
 CC degenerate probe pools based on the organophosphorus binding site of  
 CC cholinesterases. A 764 nucleotide insert (designated FBChE12) was  
 CC isolated from one positive clone and sequenced. This insert (Q42495),  
 CC containing an ORF large enough to code for about half the subunit  
 CC size of human cholinesterase, was used as a probe to obtain the full-  
 CC length pseudo-cholinesterase sequence by screening a foetal liver  
 CC cDNA library and a primary glioblastoma cDNA library (Q48393).  
 CC This sequence differs from sequence Q42496, particularly in the  
 CC 3'-UTR.  
 SQ Sequence 635 AA;

Query Match 71.3%; Score 62; DB 1; Length 635;  
 Best Local Similarity 64.3%; Pred. No. 0.092;  
 Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14

Db 606 AGFHRWNNYMDWK 619  
 | | | | | : | | : | |

## RESULT 14

R41195  
 ID R41195 standard; Protein; 510 AA.  
 AC R41195;  
 DT 18-MAR-1994 (first entry)

DE Yeast delta 9 desaturase gene.  
 KW Delta-9 desaturase; fatty acids; seed oil; Zea maize;  
 KW Brassica rapa; Brassica napus; yeast; crops; ss.  
 OS Saccharomycetes cerevisiae.  
 PN EP-561569-A.  
 PD 22-SEP-1993.  
 PF 12-MAR-1993; 301895.  
 PR 13-MAR-1992; US-850714.  
 PA (LUBR ) LUBRIZOL CORP.  
 PI Mehra-palta A, Poutre CG;  
 DR WPI; 93-296843/38.  
 DR N-PSDB; Q48731.  
 PT Plant seed contg. yeast delta-9 desaturase gene - used to produce  
 PT oil with lower proportion of saturated fatty acids  
 PS Disclosure; Page 21-22; 32pp; English.  
 CC The yeast delta-9 desaturase gene was placed under the control of a  
 CC phaseolin promoter (normal or truncated) or 35S promoter to drive  
 CC expression in plant seeds transformed with the gene. Plant seeds  
 CC preferably used are Zea maize (a monocot plant) and Brassica rapa or  
 CC Brassica napus (dicots). Expression of the yeast delta-9 saturase  
 CC gene in any plant seed tissue could result in a decrease in  
 CC saturated fatty acids and an increase in monounsaturated fatty acids  
 CC in the seed oil.  
 SQ Sequence 510 AA;

Query Match 46.6%; Score 40.5; DB 1; Length 510;  
 Best Local Similarity 56.2%; Pred. NO. 99;  
 Matches 9; Conservative 1; Mismatches 3; Indels 3; Gaps 2;

QY 1 AEFHR-WS--SYMVHW 13  
 | : | | | | | | |  
 DB 158 AGYHRLWHSRYSNAHW 173

RESULT 15  
 R15441  
 ID R15441 standard; Protein; 124 AA.  
 AC R15441;  
 DT 25-FEB-1992 (first entry)  
 DE Heavy chain variable region of MAb 18B9.  
 KW HRV; ICAM-1; antigen-binding fragment; inflammation;  
 KW auto-immune disease.  
 OS Homo sapiens.  
 PN EP-459577-A.  
 PD 04-DEC-1991.  
 PF 25-MAY-1991; 201243.  
 PR 01-JUN-1990; US-532001.  
 PA (MERI ) MERCK & CO INC.  
 PI Colonna RJ, Condra JH, Tomassini JE, Sardana VV;  
 DR WPI; 91-355850/49.  
 PT Microbially expressed portions of monoclonal antibody - can block  
 PT attachment of rhinovirus ligands to inter-cellular adhesion  
 PT molecule (ICAM-1)  
 PS Claim 1; Page 20; 28pp; English.  
 CC This is one of six antibody fragments from MAb's specific for domain  
 CC 1 of ICAM-1. The peptide fragments can be used to treat or prevent  
 CC rhinovirus infection. See R15437-R15443.  
 SQ Sequence 124 AA;

Query Match 46.0%; Score 40; DB 1; Length 124;  
 Best Local Similarity 38.5%; Pred. NO. 27;  
 Matches 5; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 AEFHRWSSYMWVHW 13  
 | : | : | : | : |  
 DB 24 ASGHFTSFVHW 36

us-09-155-076-l\_1.rag

Wed Sep 13 08:11:29 2000





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 13, 2000, 02:19:42 ; Search time 14.59 Seconds  
(without alignments)  
14.709 Million cell updates/sec

Title: US-09-155-076-1  
Perfect score: 87  
Sequence: 1 AEFHRWSSYMHVK 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 152396 seqs, 15329161 residues  
Total number of hits satisfying chosen parameters: 152396

Minimum DB seq length: 0  
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/PCFUS\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	87	100.0	40	2	US-08-370-156-25
2	87	100.0	45	2	US-08-370-156-7
3	87	100.0	45	2	US-08-370-156-8
4	87	100.0	614	1	US-07-732-962A-2
5	87	100.0	614	2	US-08-370-156-2
6	87	100.0	614	3	US-08-446-100-19
7	87	100.0	614	3	US-08-446-100-20
8	87	100.0	614	3	US-08-446-100-21
9	87	100.0	614	3	US-08-446-100-22
10	87	100.0	614	3	US-08-446-100-23
11	87	100.0	614	3	US-08-446-100-25
12	87	100.0	614	3	US-08-814-095-2
13	87	100.0	614	4	PCT-US92-08106-2
14	80	92.0	575	1	US-08-348-920-1
15	80	92.0	575	1	US-08-348-920-2
16	62	71.3	572	5	5200183-5
17	62	71.3	573	5	5215909-12
18	62	71.3	602	3	US-08-446-100-1
19	62	71.3	602	3	US-08-446-100-2
20	62	71.3	602	3	US-08-446-100-3
21	62	71.3	602	3	US-08-446-100-4
22	62	71.3	602	3	US-08-446-100-5
23	62	71.3	602	3	US-08-446-100-6
24	62	71.3	602	3	US-08-446-100-7
25	62	71.3	602	3	US-08-446-100-8
26	62	71.3	602	3	US-08-446-100-9
27	62	71.3	602	3	US-08-446-100-10
28	62	71.3	602	3	US-08-446-100-11

29 71.3 602 3 US-08-446-100-12 Sequence 12, Appl  
30 71.3 602 3 US-08-446-100-13 Sequence 13, Appl  
31 71.3 602 3 US-08-446-100-14 Sequence 14, Appl  
32 71.3 602 3 US-08-446-100-15 Sequence 15, Appl  
33 71.3 602 3 US-08-446-100-16 Sequence 16, Appl  
34 71.3 602 3 US-08-446-100-17 Sequence 17, Appl  
35 71.3 602 3 US-08-446-100-18 Sequence 18, Appl  
36 71.3 602 3 US-08-446-100-24 Sequence 24, Appl  
37 71.3 602 5 5215909-11 Patent No. 5215909  
38 71.3 635 5 5215909-10 Patent No. 5215909  
39 42 48.3 1788 2 US-08-962-284-2 Sequence 2, Appl  
40 42 48.3 1792 2 US-08-962-284-4 Sequence 4, Appl  
41 40.5 46.6 510 1 US-08-742-273-2 Sequence 2, Appl  
42 40 46.0 124 1 US-08-276-852-66 Sequence 66, Appl  
43 40 46.0 124 1 US-08-276-852-67 Sequence 67, Appl  
44 40 46.0 124 1 US-08-276-852-68 Sequence 68, Appl  
45 40 46.0 124 1 US-08-276-852-130 Sequence 130, Appl

## ALIGNMENTS

RESULT 1  
US-08-370-156-25  
; Sequence 25, Application US/08370156  
; Patent No. 5932780  
; GENERAL INFORMATION:  
; APPLICANT: Soreq, Hermona  
; APPLICANT: Zakut, Haim  
; APPLICANT: Shani, Moshe  
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR  
; TITLE OF INVENTION: ANTICHOLINESTERASE SUBSTANCES  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Reising, Ethington, Barnard & Perry  
; STREET: P.O. Box 4390  
; CITY: Troy  
; STATE: Michigan  
; COUNTRY: US  
; ZIP: 48099  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/370,156  
; FILING DATE:  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kohn, Kenneth I.  
; REGISTRATION NUMBER: 30,955  
; REFERENCE/DOCKET NUMBER: P-307 (Mullford)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (810) 689-3500  
; TELEFAX: (810) 689-4071  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 40 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-370-156-25

Query Match 100.0%; Score 87; DB 2; Length 40;  
Best Local Similarity 100.0%; Pred. No. 5.2e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYMHVK 14

DB 12 AEFHRWSSYMHVK 25

RESULT 2  
US-08-370-156-7  
; Sequence 7, Application US/08370156  
; Patent No. 5932780  
; GENERAL INFORMATION:  
; APPLICANT: Soreq, Hermona  
; APPLICANT: Zakut, Haim  
; APPLICANT: Shani, Moshe  
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR  
; ANTICHOLINESTERASE SUBSTANCES  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Reising, Ethington, Barnard & Perry  
; STREET: P.O. Box 4390  
; CITY: Troy  
; STATE: Michigan  
; COUNTRY: US  
; ZIP: 48099  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/370,156  
; FILING DATE:  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kohn, Kenneth I.  
; REGISTRATION NUMBER: 30,955  
; REFERENCE/DOCKET NUMBER: P-307 (Mulford)  
; TELEPHONE: (810) 689-3500  
; TELEFAX: (810) 689-4071  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 45 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-370-156-7

Query Match 100.0%; Score 87; DB 2; Length 45;  
Best Local Similarity 100.0%; Pred. No. 5.8e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYVHWK 14  
Db 17 AEFHRWSSYVHWK 30

RESULT 3  
US-08-370-156-8  
; Sequence 8, Application US/08370156  
; Patent No. 5932780  
; GENERAL INFORMATION:  
; APPLICANT: Soreq, Hermona  
; APPLICANT: Zakut, Haim  
; APPLICANT: Shani, Moshe  
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR  
; ANTICHOLINESTERASE SUBSTANCES  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Reising, Ethington, Barnard & Perry  
; STREET: P.O. Box 4390  
; CITY: Troy  
; STATE: Michigan  
; COUNTRY: US  
; ZIP: 48099  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/370,156  
; FILING DATE:  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kohn, Kenneth I.  
; REGISTRATION NUMBER: 30,955  
; REFERENCE/DOCKET NUMBER: P-307 (Mulford)  
; TELEPHONE: (810) 689-3500  
; TELEFAX: (810) 689-4071  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 45 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-370-156-8

Query Match 100.0%; Score 87; DB 2; Length 45;  
Best Local Similarity 100.0%; Pred. No. 5.8e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYVHWK 14  
Db 17 AEFHRWSSYVHWK 30

RESULT 4  
US-07-732-962A-2  
; Sequence 2, Application US/07732962A  
; Patent No. 5248604  
; GENERAL INFORMATION:  
; APPLICANT: Fischer, Meir  
; TITLE OF INVENTION: EXPRESSION OF ENZYMATICALLY ACTIVE  
; TITLE OF INVENTION: RECOMBINANT HUMAN ACETYLCHOLINESTERASE  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: John P. White, Esq.  
; STREET: 30 Rockefeller Plaza  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10112  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/732,962A  
; FILING DATE: 19910722  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 39304/JPW/LSW  
; TELEPHONE: (212) 977-9550  
; TELEFAX: (212) 664-0525  
; TELEX: 422523 COOP UI  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 614 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-732-962A-2

Query Match 100.0%; Score 87; DB 1; Length 614;  
Best Local Similarity 100.0%; Pred. No. 6.3e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYVHWK 14  
| | | | | | | | | | | | | | | |  
Db 586 AEFHRWSSYVHWK 599

## RESULT 5

US-08-370-156-2  
; Sequence 2, Application US/08370156  
; Patent No. 5932780  
; GENERAL INFORMATION:  
; APPLICANT: Soreq, Hermona  
; APPLICANT: Zakut, Haim  
; APPLICANT: Shani, Moshe  
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR  
; TITLE OF INVENTION: ANTICHLINESTERASE SUBSTANCES  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Reising, Ethlington, Barnard & Perry  
; STREET: P.O. Box 4390  
; CITY: Troy  
; STATE: Michigan  
; COUNTRY: US  
; ZIP: 48099  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/370,156  
; FILING DATE:  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kohn, Kenneth I.  
; REGISTRATION NUMBER: 30,955  
; REFERENCE/DOCKET NUMBER: P-307 (Mullford)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (810) 689-3500  
; TELEFAX: (810) 689-4071  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 614 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-370-156-2

Query Match 100.0%; Score 87; DB 2; Length 614;  
Best Local Similarity 100.0%; Pred. No. 6.3e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYVHWK 14  
| | | | | | | | | | | | | | | |  
Db 586 AEFHRWSSYVHWK 599

## RESULT 6

US-08-446-100-19  
; Sequence 19, Application US/08446100  
; Patent No. 6001625  
; GENERAL INFORMATION:  
; APPLICANT: Broomfield, Clarence A  
; APPLICANT: Millard, Charles B  
; APPLICANT: Lockridge, Oksana  
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hendricks and Assoc.  
; STREET: 9669 A Main Street, P.O. Box 2509  
; CITY: Fairfax  
; STATE: VA  
; COUNTRY: US  
; ZIP: 22031  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/446,100  
; FILING DATE: 19-MAY-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:

; ADDRESSEE: Hendricks and Assoc.  
; STREET: 9669 A Main Street, P.O. Box 2509  
; CITY: Fairfax  
; STATE: VA  
; COUNTRY: US  
; ZIP: 22031  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/446,100  
; FILING DATE: 19-MAY-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hendricks, Glenna  
; REGISTRATION NUMBER: 32,535  
; REFERENCE/DOCKET NUMBER: Broomfield  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 425-4250  
; TELEFAX: (703) 425-2767  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 614 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: YES  
; ANTI-SENSE: YES  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:  
; ORGANISM: human esterases  
; US-08-446-100-19

Query Match 100.0%; Score 87; DB 3; Length 614;  
Best Local Similarity 100.0%; Pred. No. 6.3e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYVHWK 14  
| | | | | | | | | | | | | | | |  
Db 586 AEFHRWSSYVHWK 599

## RESULT 7

US-08-446-100-20  
; Sequence 20, Application US/08446100  
; Patent No. 6001625  
; GENERAL INFORMATION:  
; APPLICANT: Broomfield, Clarence A  
; APPLICANT: Millard, Charles B  
; APPLICANT: Lockridge, Oksana  
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hendricks and Assoc.  
; STREET: 9669 A Main Street, P.O. Box 2509  
; CITY: Fairfax  
; STATE: VA  
; COUNTRY: US  
; ZIP: 22031  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/446,100  
; FILING DATE: 19-MAY-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:

NAME: Hendricks, Glenna  
REGISTRATION NUMBER: 32,535  
REFERENCE/DOCKET NUMBER: broomfield  
TELEPHONE: (703) 425-4250  
TELEFAX: (703) 425-2767  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 614 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
HYPOTHETICAL: YES  
ANTI-SENSE: YES  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE: human esterases  
US-08-446-100-20

Query Match 100.0%; Score 87; DB 3; Length 614;  
Best Local Similarity 100.0%; Pred. No. 6.3e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14  
|||||  
DB 586 AEFHRWSSYVHWK 599

## RESULT 8

US-08-446-100-21  
Sequence 21, Application US/08446100  
Patent No. 6001625  
GENERAL INFORMATION:  
APPLICANT: Broomfield, Clarence A  
APPLICANT: Millard, Charles B  
APPLICANT: Lockridge, Oksana  
TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hendricks and Assoc.  
STREET: 9669 A Main Street, P.O. Box 2509  
CITY: Fairfax  
STATE: VA  
COUNTRY: US  
ZIP: 22031  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/446.100  
FILING DATE: 19-MAY-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Hendricks, Glenna  
REGISTRATION NUMBER: 32,535  
REFERENCE/DOCKET NUMBER: broomfield  
TELEPHONE: (703) 425-4250  
TELEFAX: (703) 425-2767  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 614 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
HYPOTHETICAL: YES  
ANTI-SENSE: YES  
FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:  
ORGANISM: human esterases  
US-08-446-100-21

Query Match 100.0%; Score 87; DB 3; Length 614;  
Best Local Similarity 100.0%; Pred. No. 6.3e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14  
|||||  
DB 586 AEFHRWSSYVHWK 599

## RESULT 9

US-08-446-100-22  
Sequence 22, Application US/08446100  
Patent No. 6001625  
GENERAL INFORMATION:  
APPLICANT: Broomfield, Clarence A  
APPLICANT: Millard, Charles B  
APPLICANT: Lockridge, Oksana  
TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hendricks and Assoc.  
STREET: 9669 A Main Street, P.O. Box 2509  
CITY: Fairfax  
STATE: VA  
COUNTRY: US  
ZIP: 22031  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/446.100  
FILING DATE: 19-MAY-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Hendricks, Glenna  
REGISTRATION NUMBER: 32,535  
REFERENCE/DOCKET NUMBER: broomfield  
TELEPHONE: (703) 425-4250  
TELEFAX: (703) 425-2767  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 614 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
HYPOTHETICAL: YES  
ANTI-SENSE: YES  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE: human esterases  
US-08-446-100-22

Query Match 100.0%; Score 87; DB 3; Length 614;  
Best Local Similarity 100.0%; Pred. No. 6.3e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14  
|||||  
DB 586 AEFHRWSSYVHWK 599

## RESULT 10

US-08-446-100-23

; Sequence 23, Application US/08446100  
; Patent No. 6001625  
; GENERAL INFORMATION:  
; APPLICANT: Broomfield, Clarence A  
; APPLICANT: Millard, Charles B  
; APPLICANT: Lockridge, Oksana  
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hendricks and Assoc.  
; STREET: 9669 A Main Street, P.O. Box 2509  
; CITY: Fairfax  
; STATE: VA  
; COUNTRY: US  
; ZIP: 22031  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/446,100  
; FILING DATE: 19-MAY-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hendricks, Glenna  
; REGISTRATION NUMBER: 32,535  
; REFERENCE/DOCKET NUMBER: Broomfield  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 425-4250  
; TELEFAX: (703) 425-2767  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 614 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: YES  
; ANTI-SENSE: YES  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:  
; ORGANISM: human esterases  
; US-08-446-100-23

Query Match 100.0%; Score 87; DB 3; Length 614;  
Best Local Similarity 100.0%; Pred. No. 6.3e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYMHVK 14  
|||||  
Db 586 AEFHRWSSYMHVK 599

RESULT 11  
US-08-446-100-25  
; Sequence 25, Application US/08446100  
; Patent No. 6001625  
; GENERAL INFORMATION:  
; APPLICANT: Broomfield, Clarence A  
; APPLICANT: Millard, Charles B  
; APPLICANT: Lockridge, Oksana  
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hendricks and Assoc.  
; STREET: 9669 A Main Street, P.O. Box 2509  
; CITY: Fairfax  
; STATE: VA  
; COUNTRY: US  
; ZIP: 22031  
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/446,100  
; FILING DATE: 19-MAY-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hendricks, Glenna  
; REGISTRATION NUMBER: 32,535  
; REFERENCE/DOCKET NUMBER: Broomfield  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 425-4250  
; TELEFAX: (703) 425-2767  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 614 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: YES  
; ANTI-SENSE: YES  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:  
; ORGANISM: human esterases  
; US-08-446-100-25

Query Match 100.0%; Score 87; DB 3; Length 614;  
Best Local Similarity 100.0%; Pred. No. 6.3e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYMHVK 14  
|||||  
Db 586 AEFHRWSSYMHVK 599

RESULT 12  
US-08-814-095-2  
; Sequence 2, Application US/08814095  
; Patent No. 6025183  
; GENERAL INFORMATION:  
; APPLICANT: Soreq, Hermona  
; APPLICANT: Zakut, Haim  
; APPLICANT: Shani, Moshe  
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR  
; TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTANCES  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: KOHN & ASSOCIATES  
; STREET: 30500 No. 6025183thwestern Highway, Suite 410  
; CITY: Farmington Hills  
; STATE: Michigan  
; COUNTRY: U.S.  
; ZIP: 48334  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/814,095  
; FILING DATE:  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Montgomery, Ilene N.  
; REGISTRATION NUMBER: 38,972  
; REFERENCE/DOCKET NUMBER: 2391.00066  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (248) 539-5050  
; TELEFAX: (248) 539-5055

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 614 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-08-814-095-2

Query Match 100.0%; Score 87; DB 3; Length 614;  
Best Local Similarity 100.0%; Pred. No. 6.3e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14  
|||||  
DB 586 AEFHRWSSYVHWK 599

## RESULT 13

PCT-US92-06106-2

Sequence 2, Application PC/TUS9206106  
GENERAL INFORMATION:

APPLICANT: Fischer, Melr  
TITLE OF INVENTION: ENZYMATICALLY ACTIVE RECOMBINANT HUMAN  
TITLE OF INVENTION: ACETYLCHOLINESTERASE AND USES THEREOF  
NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: John P. White, Esq.

STREET: 30 Rockefeller Plaza

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10112

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/06106

FILING DATE: 19920722

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 39304-B-PCT/JPW/EAB

TELEPHONE: (212) 977-9550

TELEFAX: (212) 664-0525

TELEX: 422523 COOP UI

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 614 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US92-06106-2

Query Match 100.0%; Score 87; DB 4; Length 614;  
Best Local Similarity 100.0%; Pred. No. 6.3e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14  
|||||  
DB 586 AEFHRWSSYVHWK 599

## RESULT 14

US-08-348-920-1

Sequence 1, Application US/08348920  
Patent No. 5695750  
GENERAL INFORMATION:  
APPLICANT: Doctor, Bhupandra P.  
APPLICANT: Maxwell, Donald  
APPLICANT: Saxena, Ashima  
APPLICANT: Radic, Zoran  
APPLICANT: Taylor, Palmer  
TITLE OF INVENTION: Compositions for Use to Deactivate  
TITLE OF INVENTION: Organophosphates  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John F. Moran  
STREET: Off. Of Command Judge Adv., HQ USAMRDC, Fort  
STREET: Detrick  
CITY: Frederick  
STATE: MD  
COUNTRY: US  
ZIP: 21702-5012

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/348.920  
FILING DATE: 25-NOV-1994  
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Hendricks, Glenna

REGISTRATION NUMBER: 32,535

REFERENCE/DOCKET NUMBER: doc348,920

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 619-7807

TELEFAX: 301-619-7714

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 575 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: internal

US-08-348-920-1

Query Match 92.0%; Score 80; DB 1; Length 575;  
Best Local Similarity 92.3%; Pred. No. 0.00054;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 EFRWSSYVHWK 14  
|||||  
DB 548 EFRWSSYVHWK 560

## RESULT 15

US-08-348-920-2

Sequence 2, Application US/08348920  
Patent No. 5695750

GENERAL INFORMATION:

APPLICANT: Doctor, Bhupandra P.

APPLICANT: Maxwell, Donald

APPLICANT: Saxena, Ashima

APPLICANT: Radic, Zoran

APPLICANT: Taylor, Palmer

TITLE OF INVENTION: Compositions for Use to Deactivate

TITLE OF INVENTION: Organophosphates

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: John F. Moran

STREET: Off. Of Command Judge Adv., HQ USAMRDC, Fort

```

; STREET: Detrick
; CITY: Frederick
; STATE: MD
; COUNTRY: US
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/348,920
; FILING DATE: 25-NOV-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: doc348,920
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-7807
; TELEFAX: 301-619-7714
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 575 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
;
US-08-348-920-2

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Query Match          92.0%; Score 80; DB 1; Length 575;
Best Local Similarity 92.3%; Pred.No. 0.00054;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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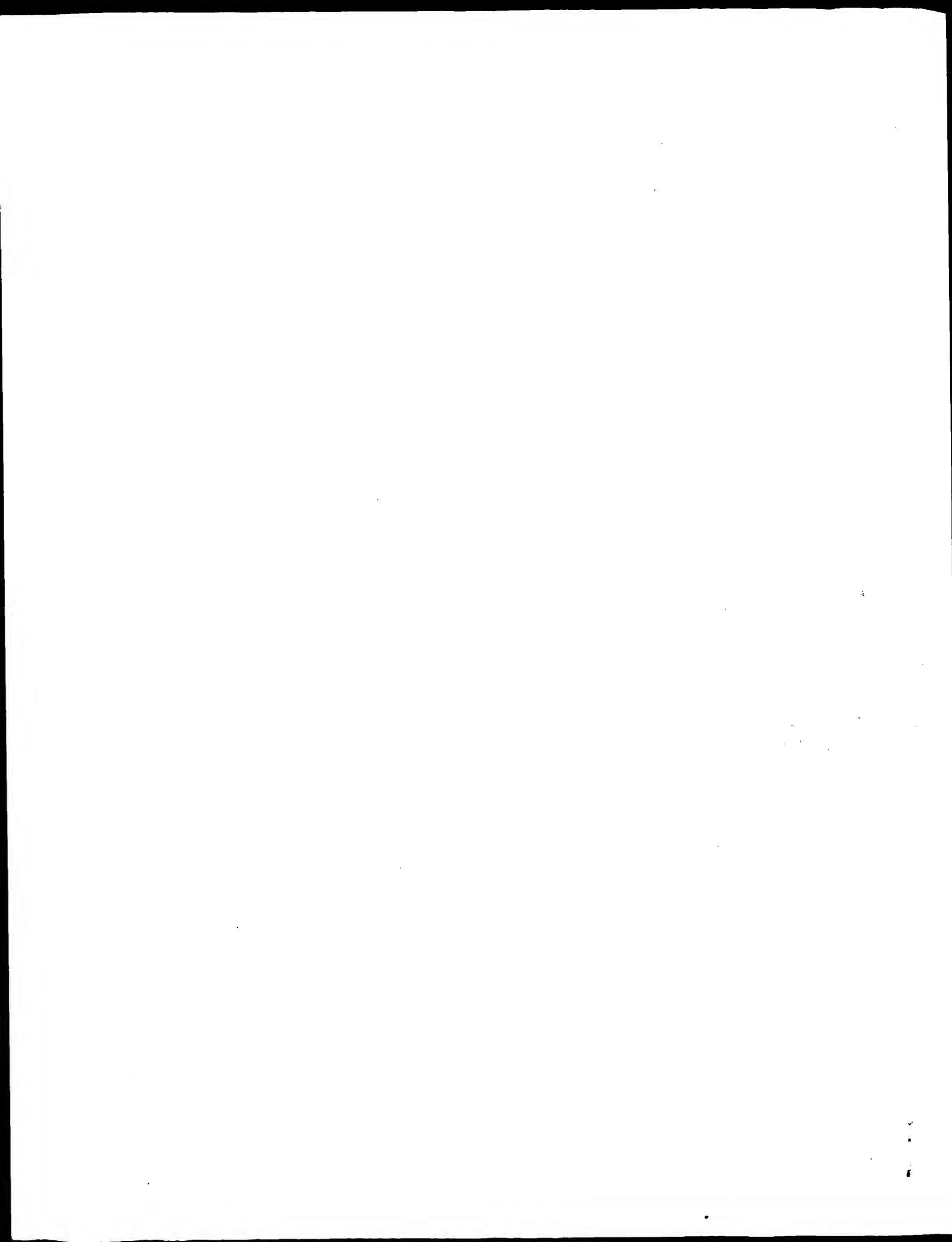
QY      2 EFHRWSSYMYVHWK 14
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Db      548 EFHRWSSYMMHWK 560

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Search completed: September 13, 2000, 02:22:01
Job time: 139 sec

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seq\_name: gb\_pr3:HUMACHE04

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seq_documentation_block:
LOCUS HUMACHE04 475 bp DNA PRI 14-JUN-1995
DEFINITION Human acetylcholinesterase (ACHE) gene, exon 6.
ACCESSION L22562
VERSION L22562.1 GI:862302
KEYWORDS acetylcholinesterase.
SEGMENT 4 of 4
SOURCE Homo sapiens DNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS Soreq,H.E., Ben-Aziz,R., Prody,C.A., Seidman,S., Gnatt,A.,
Neville,L., Lieman-Hurwitz,J., Lev-Lehman,E., Ginzberg,D.,
Lapidot-Lifson,Y. and Zakut,H.
TITLE Molecular cloning and construction of the coding region for human
acetylcholinesterase reveals a G + C-rich attenuating structure
Proc. Natl. Acad. Sci. U.S.A. 87 (24), 9688-9692 (1990)
JOURNAL 91088577
MEDLINE
REFERENCE 2 (sites)
AUTHORS Li,Y., Camp,S., Rachinsky,T.L., Getman,D. and Taylor,P.
TITLE Gene structure of mammalian acetylcholinesterase. Alternative exons
dictate tissue-specific expression
J. Biol. Chem. 266 (34), 23083-23090 (1991)
JOURNAL 92078174
MEDLINE
REFERENCE 3 (bases 1 to 475)
AUTHORS Bartels,C.F., Zelinski,T. and Lockridge,O.
TITLE Mutation at codon 322 in the human acetylcholinesterase (ACHE) gene
accounts for vt blood group polymorphism
Am. J. Hum. Genet. 52 (5), 928-936 (1993)
JOURNAL 93256075
MEDLINE
COMMENT On Jun 15, 1995 this sequence version replaced gi:857448.
**Reference [1] reports bases 142-480;
Reference [J. Biol. Chem. 266, 23083-23090 (1991)] reports bases
132-141;
Reference [3] reports bases 1-131**.
FEATURES
Location/Qualifiers
1..475
/organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="blood"
/map="7q22"
join(L22559.1..1355,L22560.1..1.779,L22561.1..1.510,
1..475)
/gene="ACHE"
<1..136
/intron /gene="ACHE"
/note="UTR (retained intron or exon); G00-118-746"
137..>475
/exon /gene="ACHE"
/note="hydrophilic form; G00-118-746"
/number=6
BASE COUNT 77 a 195 c 113 g 90 t
ORIGIN

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alignment\_scores:  
Quality: 87.00 Length: 14  
Ratio: 6.214 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-155-076-1 x HUMACHE04 ..

Align seg 1/1 to: HUMACHE04 from: 1 to: 475

1 AlaGlupHeHisArgTrpSerSeryrMetValHisTrpLys 14

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169 GCGAGTTCACCGCTGGAGCTCCTACATGGTGCACCTGGAAG 210

seq\_name: gb\_om:OCU05036

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seq_documentation_block:
LOCUS OCU05036 1947 bp mRNA MAM 28-NOV-1994
DEFINITION Oryctolagus cuniculus acetylcholinesterase mRNA, partial cds.
ACCESSION U05036
VERSION U05036.1 GI:576446
KEYWORDS
SOURCE Oryctolagus cuniculus.
ORGANISM Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE 1 (bases 1 to 1947)
AUTHORS Jbilo,O., Lhermite,Y., Toutant,J. and Chatonnet,A.
TITLE Acetylcholinesterase and butyrylcholinesterase expression in adult
rabbit tissues and during development
Eur. J. Biochem. 225, 115-124 (1994)
JOURNAL 95010036
MEDLINE
REFERENCE 2 (bases 1 to 1947)
AUTHORS Chatonnet,A.
TITLE Direct Submission
JOURNAL
SUBMITTED (13-JAN-1994) Arnaud Chatonnet, Physiologie Animale,
Institut National de la Recherche Agronomique, Place Viala,
Montpellier, 34060 France
FEATURES
Location/Qualifiers
1..1947
/organism="Oryctolagus cuniculus"
/db_xref="taxon:9986"
/clone="epiph"
/tissue_type="muscle"
/dev_stage="adult"
<1..1755
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/codon_start=1
/product="acetylcholinesterase"
/protein_id="AAA53235.1"
/db_xref="GI:576447"
/translation="AEGREDPELVTVGRGLRLKAPGVPVSFLGIPFEEPPVVG
PRRLPEPKRPWAGVLDATAFQSCYQYVDLYPGFETEMNPNRELSDCGLYNV
WTPRPSTPPTPLVLIYGGFYSGASLDVYIGRELVAQEGVLVAMNYRVGAFET
CLPGSRAPNGVGLDLQWENVAFGDPDPATVILFGESAGASVGLHLLSFP
SRGLFHRVLSQSGAPNGFWATVGVGEARRATLLARLVCPGPGAGNDTELACLT
RPAQDLVDHEWRVLPQESIFRSFVYVDGLSDTPEALINAGDFGLQVLGVVKD
EGTYFLVYGAPGFSKDNESFTSRAQFLAGVRGVPOASDLAAEAVLHYTDWLHPEDP
ARLDALSDVVDHNVCPVAOLAGLAAOGARVYAVFEHRASTLSWPLMWGVPHCY
EIEFTGLPESLNTYEERIEFQRLMYRWFANFATGDNEPRDAKAPQWPVYTAG
QQYVSLNLRPLEVRGLRAQCAFWNRFLLSATDTLDEAERQWKAEFHRWSSYNV
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polyA_signal
polyA_site 1946
BASE COUNT 299 a 655 c 660 g 333 t
ORIGIN

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alignment\_scores:  
Quality: 87.00 Length: 14  
Ratio: 6.214 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-155-076-1 x OCU05036 ..

Align seg 1/1 to: OCU05036 from: 1 to: 1947

1 AlaGlupHeHisArgTrpSerSeryrMetValHisTrpLys 14

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1666 GCGAGTTCACCGCTGGAGCTCCTACATGGTGCACCTGGAAG 1707

seq\_name: gb\_ro:S50879

seq\_documentation\_block:

LOCUS S50879 2066 bp mRNA

DEFINITION acetylcholinesterase T subunit [rats, mRNA Partial, 2066 nt].

ROD

08-MAY-1993

!

TITLE Molecular cloning and construction of the coding region for human acetylcholinesterase reveals a G+C-rich attenuating structure

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (24), 9688-9692 (1990)

MEDLINE 91088577

FEATURES

source

1..2218

Location/Qualifiers

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/dev\_stage="21-week-old fetus"

/tissue\_lib="lambda-gt10"

/map="7q22"

1..2218

/gene="ACHE"

/note="G00-118-746"

/product="acetylcholinesterase"

1..2218

/gene="ACHE"

157..2001

/gene="ACHE"

/EC\_number="3.1.1.7"

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/product="acetylcholinesterase"

/protein\_id="AAA68151.1"

/db\_xref="GI:177975"

/translation="MRPQCLHTPSSLASPLLLLLWLLGGVGAEGREDAELLTVVR  
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YVDLYPGFEGTEWNNPNRELSDECLXNVMVPIPRETSPFVLYWYGGFVSGASS  
LDVYDGLFVQARTVLSVMNRYVGAFFGLPGSREAPNGVGLLQRLALQWQENV  
AAGGDPSTVTLFESAGASVGMHLLSPFSRGLFHRVAVLQSGAPNGPWATVGMGEAR  
RATOLAHVCGPCPGTGGNDTELVAQLRTPAQVLVNHWHVLPQESVFRFSFVIV  
DGLSDTFEALINAGDFHGLQVLGVVKGDEGSYFLVYGAPFSKONESLISRAEFLA  
GYRVGYPVSLAAENVLHYVDNLHPEDPARLEALSDVVDHNVVCPVAQLAGRLA  
AQGARVAYFEHRASTLWPMGVPHGHEIEFIFGIPIDPSRNTAEKIKFAQRLM  
RYWANFATGPEPRDPKAPWPPYTAGAQQVYVLDLRLPLEVRGLRAQAQAFWNR  
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229..291

sig\_peptide

/gene="ACHE"

/note="G00-118-746; does not fit consensus"

310..1998

/gene="ACHE"

/EC\_number="3.1.1.7"

/note="G00-118-746"

/product="acetylcholinesterase"

BASE COUNT

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ORIGIN

alignment\_scores:

Quality: 87.00 Length: 14  
Ratio: 6.214 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-155-076-1 x HUMACHE ..

Align seg 1/1 to: HUMACHE from: 1 to: 2218

1 AlaCluPheHisArgTrpSerSerTyrMetValHisTrpLys 14

1912 GCCGAGTTCACCGCTGGAGCTCTACATGCTGCTGGAAG 1953

seq\_name: gb\_pat:AR070205

seq\_documentation\_block:

LOCUS AR070205 2256 bp DNA PAT 18-FEB-2000

DEFINITION Sequence 5 from patent US 5891725.

ACCESSION AR070205

VERSION AR070205.1 GI:7221093

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 2256)  
Soreq H., Zakut H. and Eckstein, F.  
TITLE Synthetic antisense oligodeoxynucleotides and pharmaceutical compositions containing them  
JOURNAL Patent: US 5891725-A 5 06-APR-1999;  
FEATURES Location/Qualifiers  
1..2256  
source /organism="unknown"

BASE COUNT 390 a 757 c 680 g 429 t

ORIGIN

alignment\_scores:

Quality: 87.00 Length: 14  
Ratio: 6.214 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-155-076-1 x AR070205 ..

Align seg 1/1 to: AR070205 from: 1 to: 2256

1 AlaCluPheHisArgTrpSerSerTyrMetValHisTrpLys 14

1915 GCCGAGTTCACCGCTGGAGCTCTACATGCTGCTGGAAG 1956

seq\_name: gb\_pat:AR070207

seq\_documentation\_block:

LOCUS AR070207 3016 bp DNA PAT 18-FEB-2000

DEFINITION Sequence 7 from patent US 5891725.

ACCESSION AR070207

VERSION AR070207.1 GI:7221095

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 3016)

Soreq H., Zakut H. and Eckstein, F.

TITLE Synthetic antisense oligodeoxynucleotides and pharmaceutical compositions containing them

JOURNAL Patent: US 5891725-A 7 06-APR-1999;

FEATURES Location/Qualifiers

1..3016

/organism="unknown"

BASE COUNT 497 a 1065 c 840 g 614 t

ORIGIN

alignment\_scores:

Quality: 87.00 Length: 14  
Ratio: 6.214 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-155-076-1 x AR070207 ..

Align seg 1/1 to: AR070207 from: 1 to: 3016

1 AlaCluPheHisArgTrpSerSerTyrMetValHisTrpLys 14

2675 GCCGAGTTCACCGCTGGAGCTCTACATGCTGCTGGAAG 2716

seq\_name: gb\_pat:AR070206

seq\_documentation\_block:

LOCUS AR070206 3096 bp DNA PAT 18-FEB-2000

DEFINITION Sequence 6 from patent US 5891725.

ACCESSION AR070206

VERSION AR070206.1 GI:7221094

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

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Unclassified
1 (bases 1 to 3096)
REFERENCE Sorq,H., Zakut,H. and Eckstein,F.
AUTHORS Synthetic antisense oligodeoxynucleotides and pharmaceutical
TITLE compositions containing them
JOURNAL Patent: US 5891725-A 6 06-APR-1999;
FEATURES Location/Qualifiers
source 1..3096
BASE COUNT 509 a 1089 c 872 g 626 t
ORIGIN

alignment_scores:
Quality: 87.00 Length: 14
Ratio: 6.214 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-1 x AR070206 ..
Align seg 1/1 to: AR070206 from: 1 to: 3096

1 AlaGlupHeHisArgTprSerTyrMetValHisTriPlys 14
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2755 GCCAGATCCACCGCTGAGCTCTACATGCTGCACCTGGAAG 2796

seq_name: gb_om:AF053485

seq_documentation_block:
LOCUS AF053485 3958 bp DNA MAM 01-APR-1998
DEFINITION Felis catus acetylcholinesterase glycopospholipid-anchored form
precursor (ACHE) and acetylcholinesterase collagen-tailed or
globular form precursor (ACHE) genes, complete cds.
ACCESSION AF053485
VERSION AF053485.1 GI:3003019
KEYWORDS cat.
SOURCE Felis catus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Carnivora; Fissipedia; Felidae; Felis.
REFERENCE 1 (bases 1 to 3958)
AUTHORS Bartels,C.F., Xie,W.-H., Miller-Lindholm,A.K. and Lockridge,O.
TITLE Sequence and characterization of domestic cat acetylcholinesterase
and butyrylcholinesterase
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3958)
AUTHORS Bartels,C.F., Xie,W.-H., Miller-Lindholm,A.K. and Lockridge,O.
TITLE Direct Submission
JOURNAL Submitted (12-MAR-1998) Eppley Institute, University of Nebraska
Medical Center, 600 S. 42nd St., Omaha, NE 68198-6805, USA
FEATURES
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/db_xref="taxon:9685"
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/gene="ACHE"
/product="acetylcholinesterase collagen-tailed or globular
form precursor"
join(<92..1150,1517..2001,2768..2937,3051..>3178)
/gene="ACHE"
/product="acetylcholinesterase glycopospholipid-anchored
form precursor"
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/notes="ACHE h-form; encoded by exon 4 spliced to exon 5"
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/db_xref="GI:3003021"

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YDGRFLAQAGTIVLYSMYRVGAFGLALPGSREAPGVGLDQRLALQWQDNVATF
GGDPMSTVLFSGSAGASVGMHLLSPPSRGLFHRVLAQSGAPNGVATVGVGEARRRA
TLLARLVGCPGGAGNDTELVACLTRPAQDLVDHEWHVLPQESVFRSFVVDGD
FLSDTPEALINAGDFHGLQVLGVVKGDESYFLVYGAPGSKDNESLSIQAQFLAGVR
VGVPOASDLAAEAAYLVHTDNLNPDPAKLREAMSDVVDGHNVCVPAQLAGRLAAQ
ARVAYIFEHRASTLSWPLMGVPHGYEIEFIFGLPLESLNTAEERFAQRLMRYW
ANFATGDPNDPRDPKVPQWPPYTAGAQYVSLDLRLPLEVRGLRAQACAFWNRFLPK
LLSATSKAPSTCSGPAGEAARPRPGLSLLLELLLSRLRL"
join(92..1150,1517..2001,2768..2937,3785..3906)
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/notes="ACHE t-form; encoded by exon 4 spliced to exon 6"
/codon_start=1
/product="acetylcholinesterase collagen-tailed or globular
form precursor"
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VGVPOASDLAAEAAYLVHTDNLNPDPAKLREAMSDVVDGHNVCVPAQLAGRLAAQ
ARVAYIFEHRASTLSWPLMGVPHGYEIEFIFGLPLESLNTAEERFAQRLMRYW
ANFATGDPNDPRDPKVPQWPPYTAGAQYVSLDLRLPLEVRGLRAQACAFWNRFLPK
LLSATDLDLDEPRQKAEFRHSWSTWVHMKNFQDHYSKQDRCSDL"
LUSATDLDLDEPRQKAEFRHSWSTWVHMKNFQDHYSKQDRCSDL"
BASE COUNT 723 a 1256 c 1205 g 772 t 2 others
ORIGIN

alignment_scores:
Quality: 87.00 Length: 14
Ratio: 6.214 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-1 x AF053485 ..
Align seg 1/1 to: AF053485 from: 1 to: 3958

1 AlaGlupHeHisArgTprSerTyrMetValHisTriPlys 14
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3817 GCAGATTCACCGCTGAGCTCTACATGCTGCACCTGGAAG 3858

seq_name: gb_pr3:HUMACHEB

seq_documentation_block:
LOCUS HUMACHEB 4185 bp DNA PRI 23-JUN-1995
DEFINITION Homo sapiens acetylcholinesterase (ACHE) gene, exons 2-6.
ACCESSION U42812
VERSION U42812.1 GI:854682
KEYWORDS acetylcholinesterase.
SOURCE Homo sapiens DNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS Bartels,C.F., Zelinski,T. and Lockridge,O.
TITLE Mutation at codon 322 in the human acetylcholinesterase (ACHE) gene
accounts for Yt blood group polymorphism
JOURNAL Am. J. Hum. Genet. 52 (5), 928-936 (1993)
MEDLINE 93256075
REFERENCE 2 (bases 1 to 4185)
AUTHORS Bartels,C.F., Morlearty,P.L., Becker,R.E., Robbs,R.S.,
Sorenson,R.C., Mountjoy,C.P. and Lockridge,O.
TITLE Polymorphic sites in the acetylcholinesterase gene of patients with
Alzheimer's disease
JOURNAL Unpublished (1995)
FEATURES Location/Qualifiers

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CDS



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2005..2119
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2597..2675
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3170..3528
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/evidence=not_experimental
3529..3585
/Note="MZEFF, score = 100%"
/evidence=not_experimental
3539..3764
/Note="CpG island score = 0.82, GC = 62.80%, CpGs = 18"
/Note="Region: CpG island"
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3703..3780
/Note="Alignment: CDS, | Intron"
/evidence=not_experimental
3781..3934
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/Note="Xpound exon prediction, score = 99% (0%)"
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3781..3927
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3812..3960
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/Note="Region: Data base match"
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4191..4220
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mRNA,"
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4809..4840
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mRNA,"
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5119..5208
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5209..5264
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complement(5238..5431)
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chromosome 7 STS SWSS3840; single read."
/Note="Region: Data base match"
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5757..54176
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/Note="Region: GC content"
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5844..7208
/Note="CpG island score = 0.79, GC = 69.50%, CpGs = 126"
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6019..6471
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6454..6508
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/rpt_unit=cctcc
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complement(6738..7007)
/Note="Alignment: CDS,
|HSACHE3|98.9|69|339|OC050362|86.6|1|167|MMACHE2|96.1|1|177
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complement(6781..7047)
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 Quality: 87.00 Length: 14
 Ratio: 6.214 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

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alignment_block:
US-09-155-076-1 x HSAF002993/rev

Align seg 1/1 to reverse of: HSAF002993 from: 1 to: 34921

1 AlaGluPheHisArgTrpSerSerTyrMetValHisTrpLys 14
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6975 GCCGAGTTCACCGCTGGAGCTCTACATGTCACCTGGAG 6934

seq_name: gb_hgt29:AC011895

seq_documentation_block:
LOCUS AC011895 175155 bp DNA HTG 21-APR-2000
DEFINITION Homo sapiens chromosome 7 clone RP11-126L15, WORKING DRAFT
SEQUENCE, 3 unordered pieces.
ACCESSION AC011895
VERSION AC011895.3 GI:7630854
KEYWORDS HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 175155)
Waterston,R.H.
The sequence of Homo sapiens clone
Unpublished
2 (bases 1 to 175155)
Waterston,R.H.
Direct Submission
Submitted (15-OCR-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Apr 21, 2000 this sequence version replaced gi:6136444.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H.NH0126L15
----- Summary Statistics -----
Sequencing vector: M13; 74%
Sequencing method: plasmid; 26%
Chemistry: Dye-primer ET; 67% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 173580 bases at least Q40
Consensus quality: 173920 bases at least Q30
Consensus quality: 174136 bases at least Q20
Insert size: 184000; agarose-fp
Insert coverage: 7.01 in Q20 bases; agarose-fp
Quality coverage: 7.40 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 28804: contig of 28804 bp in length
* 28805 28904: gap of unknown length
* 28905 93340: contig of 64436 bp in length
* 93341 93440: gap of unknown length
* 93441 175155: contig of 81715 bp in length.
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* Location/Qualifiers
* 1. 175155
* /organism="Homo sapiens"
* /db_xref="taxon:9606"
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* /clone="RP11-126L15"

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Ratio: 6.214 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-1 x AC011895/rev

Align seg 1/1 to reverse of: AC011895 from: 1 to: 175155

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seq_name: gb_ov:AF030422

seq_documentation_block:
LOCUS AF030422 4472 bp DNA VRT 20-NOV-1997
DEFINITION Electrophorus electricus acetylcholinesterase catalytic subunit
precursor gene, complete cds.
ACCESSION AF030422
VERSION AF030422.1 GI:2613035
KEYWORDS electric eel.
SOURCE Electrophorus electricus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Ostariophysi; Gymnotiformes;
Gymnotidae; Electrophoridae; Electrophorus.
1 (bases 1 to 4472)
Simon,S. and Massoulie,J.
Cloning and expression of acetylcholinesterase from Electrophorus
J. Biol. Chem. (1997) In press
2 (bases 1 to 4472)
Simon,S. and Massoulie,J.
Direct Submission
Submitted (15-OCR-1997) Neurobiology, Ecole Normale Supérieure, 45
Rue d'Ulm, Paris 75005, France
Location/Qualifiers
1. 4472
/organism="Electrophorus electricus"
/db_xref="taxon:8005"
118. 1186
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/db_xref="GI:2613036"
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SGTEWNPENRMWSEDCLYANVVPATPRPHNLTVMWYGGYSGSSSLDVTGRL
AHSEKVVSNRYVSFAFLANGSAEACNVGLLDQRLALQWQDNHFFGNGPKQ
VTFEFGSAGASVGHLLSPDSRPFKTRAILQSGVPGNPWRTVSFDEARRRAIKLGR
VCGPDNDTILLCLRSKQPDLDQEWLVLPFSGLFRSFVFDGVVFPDTPPEAML
NSGNFKDTQILLGVNNEGYSFLTYGAGFSKDNESLITREDFLOGVKMSVPHANETG
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RLNVTLEEKLSRMKMYANFARTGNPNINVDGSDSRRWPFVFTSEQKHVGLNTD
SLKRVHGLKSGQFCALMNRFLPRLNLVTENIDDAERQWKAFFHRWSYMMHMRNQFDHY
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precursor="
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/note="acetylcholinesterase catalytic subunit"
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139 GAGTTTCATCGGTGGAGTTCTCATGATGACACTGGAAG 177

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Quality: 84.00 Length: 14  
Ratio: 6.000 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 92.857

alignment\_block:  
US-09-155-076-1 x AF030422 ..  
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3614 GCAGAGTTCACCGAGTTCATGATGACACTGGAAG 3655

seq\_name: gb\_ov:TMACHE2

seq\_documentation\_block: 605 bp mRNA VET 14-JUL-1995  
LOCUS TMACHE2  
DEFINITION Torpedo marmorata mRNA fragment for acetylcholinesterase C-term.  
(pACHE2).  
ACCESSION X13172  
VERSION X13172.1 GI:64416  
KEYWORDS acetylcholinesterase; alternative splicing.  
SOURCE marbled electric ray.  
ORGANISM Torpedo marmorata  
Eukaryota; Metazoa; Chordata; Vertebrata; Chondrichthyes;  
Elasmobranchii; Rajiformes; Torpedinoidei; Torpedinidae; Torpedo.  
1 (bases 1 to 605)  
AUTHORS Sikorav, J.L., Duval, N., Anselmet, A., Bon, S., Krejci, E., Legay, C.,  
Osterlund, M., Reimund, B. and Massoulie, J.  
TITLE Complex alternative splicing of acetylcholinesterase transcripts in  
Torpedo electric organ; primary structure of the precursor of the  
glycolipid-anchored dimeric form  
JOURNAL ENBO J. 7 (10), 2983-2993 (1988)  
MEDLINE 89030590  
COMMENT See also x13173, x13174 and x05497  
Data kindly reviewed (24-May-1989) by Massoulie J.  
FEATURES  
source  
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/tissue\_type="electric organ."  
/clone="pACHE2"  
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BASE COUNT 127 a 228 c 117 g 133 t  
ORIGIN

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Quality: 80.00 Length: 13  
Ratio: 6.154 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 92.308

alignment\_block:  
US-09-155-076-1 x TMACHE2 ..  
Align seg 1/1 to: TMACHE2 from: 1 to: 605  
2 GluPheHisArgTrpSerTyrMetValHisTrpLys 14  
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OM of: US-09-155-076-1 to: N\_Geneseq\_36.\* out\_format : pfs  
 Date: Sep 13, 2000 2:58 AM  
 About: Results were produced by the GenCore software, version 4.5,  
 Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:  
 -MODEL=frame+2n.model -DEV=xlip  
 -Q/cgn2\_1/USPRO\_Spool/US09155076/runat\_29082000\_092505\_15779/app\_query.fasta\_1.144  
 -DB=N\_Geneseq\_36 -OFMT=fastap -SUFFIX=ring -GAPOP=12.000  
 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000  
 -GAPOP=4.500 -OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500  
 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500  
 -DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=bloum62  
 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR\_SCORE=pct  
 -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs  
 -NORM=ext -MINLEN=0 -MAXLEN=100000 -USER=US09155076\_CGNI\_1\_75  
 -NCPU=6 -ICPU=3 -LONGLOG -NO\_XLPXY -WAIT -THREADS=1

## Search information block:

Query: US-09-155-076-1  
 Query length: 14  
 Database: N\_Geneseq\_36.\*  
 Database sequences: 311585  
 Database length: 125096042  
 Search time (sec): 75.680000

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N_Geneseq_36:Q09002	+	87.00	228.95	3.8e+05	2256
N_Geneseq_36:Q04296	+	62.00	156.13	0.4270	2400
N_Geneseq_36:N60111	+	62.00	155.96	0.4364	2445
N_Geneseq_36:Q48393	+	62.00	155.96	0.4364	2445
N_Geneseq_36:V74454	-	55.00	122.57	31.64	10320
N_Geneseq_36:V68847	+	50.50	125.94	20.54	1722
N_Geneseq_36:V29987	+	50.50	125.94	20.54	1722
N_Geneseq_36:V68836	+	50.50	112.46	115.62	7515
N_Geneseq_36:V29985	+	50.50	112.46	115.62	7515
N_Geneseq_36:V21209	02	49.00	83.59	4.7e+03	110000
N_Geneseq_36:V26068	+	48.00	109.21	175.51	4868
N_Geneseq_36:V94023	+	48.00	107.95	206.25	5586
N_Geneseq_36:V52253	+	48.00	105.66	276.50	7172
N_Geneseq_36:Q49460	+	47.50	105.45	283.99	6265
N_Geneseq_36:V60844	+	47.00	114.69	86.85	1948
N_Geneseq_36:Q94313	-	46.50	117.68	59.22	1200
N_Geneseq_36:V78805	+	46.00	129.13	13.64	293
N_Geneseq_36:V13398	-	46.00	115.32	80.14	1326
N_Geneseq_36:V59642	-	45.00	107.00	232.81	2400
N_Geneseq_36:V33247	+	45.00	90.94	1.8e+03	13907
N_Geneseq_36:V53431	-	44.00	112.40	116.56	970
N_Geneseq_36:V79452	-	44.00	110.83	142.60	1152
N_Geneseq_36:Q40502	+	44.00	107.55	217.03	1648
N_Geneseq_36:V62067	+	44.00	104.06	339.75	2415
N_Geneseq_36:V70137	+	44.00	95.15	1.1e+03	6393
N_Geneseq_36:Q24980	-	44.00	94.20	1.2e+03	7100
N_Geneseq_36:Q47380	-	44.00	88.84	2.4e+03	12752
N_Geneseq_36:N81756	-	43.00	109.55	168.04	966
N_Geneseq_36:V20426	-	43.00	105.46	283.75	1510
N_Geneseq_36:Q85245	-	43.00	104.48	321.80	1691
N_Geneseq_36:Q56782	-	43.00	95.80	979.90	4344
N_Geneseq_36:V99986	-	43.00	95.80	979.90	4344
N_Geneseq_36:T44068	-	43.00	95.26	984.14	4360
N_Geneseq_36:V74474	+	43.00	94.77	1.2e+03	5132
N_Geneseq_36:X13176	+	43.00	91.13	1.8e+03	7237
N_Geneseq_36:X12956	+	43.00	79.58	7.8e+03	2580
N_Geneseq_36:V11174	+	42.00	120.40	41.79	215
N_Geneseq_36:Q60004	+	42.00	114.81	85.54	396
N_Geneseq_36:X09020	-	42.00	108.45	193.42	794

N\_Geneseq\_36:Q12851 + 42.00 108.14 201.16 821 ! A.niger PGII promoter, signa  
 N\_Geneseq\_36:Q36662 - 42.00 100.05 568.22 1990 ! Full length GP01 cDNA. DNA  
 N\_Geneseq\_36:Q87171 - 42.00 96.39 907.75 2967 ! Natural resistance-associat  
 N\_Geneseq\_36:T05501 + 42.00 96.22 928.24 3024 ! Bfrr1-PvuII fragment contg. a

seq\_name: N\_Geneseq\_36:Q05999

seq\_documentation\_block:

ID Q05999 standard; DNA; 1800 BP.  
 AC Q05999;  
 DT 16-JAN-1991 (first entry)  
 DE Sequence encoding foetal human acetylcholinesterase (hACHE).  
 KW Organophosphorous poisoning; OP; cancer; leukaemia;  
 KW megakaryocytopoiesis; ovarian cancer; ds.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT cds 1..1500  
 FT 3'utr 1501..1800  
 FT /\*tag= a  
 FT /\*tag= b  
 PN EP-388906-A.  
 PF 26-SEP-1990.  
 PP 20-MAR-1990; 105274.  
 PR 21-MAR-1989; IL-089703.  
 PA (YISS ) YISSUM RES DEV CO.  
 PI Soreq H, Zakut H;  
 DI WPI: 90-291865/39.  
 DR P-PSDB; R06990.  
 PT Human acetylcholinesterase DNA and prodn. of recombinant hACHE -  
 PT for treatment of organo-phosphorous poisoning and diagnosis of haemo-  
 PT cytopoietic disorders and ovarian carcinomas.  
 PS Disclosure; Fig 1c; 47pp; English.  
 CC hACHE is useful as an active pharmacological component for the  
 CC prophylaxis and treatment of organophosphorous poisoning, and  
 CC post-surgical apnea due to succinylcholine administration.  
 CC cDNA probe to the sequence may be used in diagnosis of various  
 CC leukaemias, abnormal megakaryocytopoiesis and ovarian carcinomas.  
 CC Bases given as N are obscured in the patent specification.  
 SQ Sequence 1800 BP; 330 A; 602 C; 539 G; 326 T;

## alignment\_scores:

Quality: 87.00 Length: 14  
 Ratio: 6.214 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

## alignment\_block:

US-09-155-076-1 x Q05999 ..  
 Align seg 1/1 to: Q05999 from: 1 to: 1800

1 AlaGluPheHisArgTrpSerSerTyrMetValHisTrpLys 14  
 |||||  
 1414 GCCGAGTCCAGCTGAGCTCTACATGCTGCTGGAAG 1455

seq\_name: N\_Geneseq\_36:Q05998

seq\_documentation\_block:

ID Q05998 standard; DNA; 2253 BP.  
 AC Q05998;  
 DT 16-JAN-1991 (first entry)  
 DE Sequence encoding human acetylcholinesterase (hACHE).  
 KW Organophosphorous poisoning; OP; cancer; leukaemia;  
 KW megakaryocytopoiesis; ovarian cancer; ds.  
 OS Homo sapiens.  
 PN EP-388906-A.  
 PF 26-SEP-1990.  
 PP 20-MAR-1990; 105274.  
 PR 21-MAR-1989; IL-089703.  
 PA (YISS ) YISSUM RES DEV CO.  
 PI Soreq H, Zakut H;  
 DI WPI: 90-291865/39.  
 DR P-PSDB; R06989.

PT Human acetylcholinesterase DNA and prodn. of recombinant hAChE -  
PT for treatment of organo-phosphorous poisoning and diagnosis of haemo-  
PS cytopoietic disorders and ovarian carcinomas.

CC Gene product is useful as an active pharmacological component for the  
CC prophylaxis and treatment of organophosphorous poisoning, and post-  
CC surgical apnea due to succinylcholine administration.  
CC cDNA probe to the sequence may be used in diagnosis of various  
CC leukaemias, abnormal megakaryocytopoiesis and ovarian carcinomas.  
SQ Sequence 2253 BP; 390 A; 740 C; 694 G; 429 T;

alignment\_scores:  
Quality: 87.00 Length: 14  
Ratio: 6.214 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
US-09-155-076-1 x Q05998 ..

Align seg 1/1 to: Q05998 from: 1 to: 2253

1 AlaGluPheHisArgTrpSerSerTyrMetValHisTrpLys 14  
|||||  
1912 GCCGAGTTCACCGCTGGAGCTCTACATGTCGACGTGGAAG 1953

seq\_name: N\_Geneseq\_36:Q99002

seq\_documentation\_block:

ID Q99002 standard; DNA; 2256 BP.  
AC Q99002;  
DT 31-MAR-1996 (first entry)  
DE Human acetylcholinesterase (AChE) gene.  
KW Acetylcholinesterase; acetyl cholinesterase; EC-3.1.1.7;  
KW chromosome-7q22; acetylcholine-hydrolyzing enzyme; ss.  
OS Homo sapiens.

FT Key Location/Qualifiers  
FT cds 160..2206  
FT /\*tag= a

PN W09523158-A1.

PD 31-AUG-1995.

PF 28-FEB-1995; U02806.

PR 28-FEB-1994; US-202755.

PR 09-JAN-1995; US-370156.

PA (KOHN/) KOHN K I.

PA (YISS ) YISSUM RES & DEV CO.

PI Shani M, Soreq H, Zakut H;

DR P-PSDB; R80726.

PT Alternative forms of human acetyl cholinesterase (ChE) gene -

PT expressed in transgenic animal assay system for evaluating anti-ChE  
PT activity of organo:phosphate(s), etc. or as model of ChE imbalance

PS Claim 3; Fig.1A; 5pp; English.

CC This DNA sequence encoding human acetylcholinesterase is useful

CC for producing transgenic animals which express AChE. The

CC transgenic animals are in turn useful as an assay system for

CC determining the anti-ChE activity of organophosphates, carbamates,

CC anti-ChE drugs, plant glycoalkaloids and snake venoms. This gene

CC contains a promoter region, 6 exons (E1 to E6) and 4 introns (I1-

CC I4).

alignment\_scores:  
Quality: 87.00 Length: 14  
Ratio: 6.214 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
US-09-155-076-1 x Q99002 ..

Align seg 1/1 to: Q99002 from: 1 to: 2256

1 AlaGluPheHisArgTrpSerSerTyrMetValHisTrpLys 14  
|||||  
1915 GCCGAGTTCACCGCTGGAGCTCTACATGTCGACGTGGAAG 1956

seq\_name: N\_Geneseq\_36:Q42496

seq\_documentation\_block:

ID Q42496 standard; cDNA; 2400 BP.

AC Q42496;

DT 06-OCT-1993 (first entry)

DE Full-length human pseudochoolinesterase gene.

KW butylcholinesterase; acylcholine acylhydrolase; EC3.1.1.8; psi-ChE;

KW pseudo-ChE; neurotransmitter; organophosphorus insecticide; OP-poison;

KW antidote; ss.

OS Homo sapiens.

FT Key Location/Qualifiers

FT cds 76..1884

FT /\*tag= a

FT /note= "full-length ChE gene"

FT signal\_peptide 76..147

FT /\*tag= b

FT /note= "putative leader peptide"

PN US5215909-A.

PD 01-JUN-1993.

PF 18-JUN-1986; 875737.

PR 21-JUN-1986; US-875737.

PR 18-AUG-1987; US-087724.

PR 15-AUG-1990; US-572911.

PA (YEDA ) YEDA RES & DEV CO LTD.

PI Soreq H;

DR WPI; 93-188509/23.

DR P-PSDB; R37442.

PT Recombinant human gene encoding human pseudo-cholinesterase -

PT used to treat organo-phosphorus poisoning

PS Disclosure; Columns 33-40; 34pp; English.

CC A cDNA library prepared from foetal brain mRNA was screened with

CC degenerate probe pools based on the organophosphorus binding site of

CC cholinesterases. A 764 nucleotide insert (designated PchE12) was

CC isolated from one positive clone and sequenced. This insert (Q42495),

CC containing an ORF large enough to code for about half the subunit

CC size of human cholinesterase, was used as a probe to obtain the full-

CC length pseudochoolinesterase sequence (Q42496).

SQ Sequence 2400 BP; 794 A; 419 C; 469 G; 718 T;

alignment\_scores:

Quality: 62.00 Length: 14

Ratio: 5.167 Gaps: 0

Percent Similarity: 85.714 Percent Identity: 64.286

alignment\_block:

US-09-155-076-1 x Q42496 ..

Align seg 1/1 to: Q42496 from: 1 to: 2400

1 AlaGluPheHisArgTrpSerSerTyrMetValHisTrpLys 14  
|||||  
1792 GCAGATTCACCGCTGGACACATTCATGATGACTGGAAA 1833

seq\_name: N\_Geneseq\_36:N60111

seq\_documentation\_block:

ID N60111 standard; cDNA; 2445 BP.

AC N60111;

DT 27-JUN-1991 (first entry)

DE Sequence encoding a protein having human cholinesterase (ChE)

DE activity.

KW Organophosphorous poisoning; therapy; prophylaxis; diagnosis;

OS Pseudochoolinesterase deficiency; ss.

OS Homo sapiens.

FT Key Location/Qualifiers

FT cds 1..1908

FT /\*tag= a



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PR 05-JAN-1996: US-009861.
PA (HUMA-) HUMAN GENOME SCI INC.
PI Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA,
PI Rosen CA;
DR WPI: 97-374922/35.
PT polynucleotide(s) and proteins derived from Staphylococcus aureus
PT stored on computer readable medium and used in the production of
PT anti-S.aureus vaccines
PS Claim 1; Page 745-750; 3271pp; English.
CC This sequence represents one of 5191 Staphylococcus aureus DNA sequences
CC of the invention. The DNA sequences are recorded on a computer readable
CC medium, preferably selected from a floppy or hard disk, random access
CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
CC the S.aureus DNA sequences allows putative functions to be assigned so
CC that protein-encoding or regulatory regions of commercial, therapeutic or
CC industrial importance can be obtained. Specifically, sequences which are
CC likely to encode antigens have been identified and these polypeptides can
CC be used in a vaccine composition against S.aureus infection. The
CC polypeptides can also be used in a kit for the immunodetection of
CC S.aureus in a sample. S.aureus is implicated in numerous human diseases,
CC including cellulitis, eyelid infections, food poisoning, osteomyelitis,
CC skin and surgical wound infections, scalded skin syndrome, toxic shock
CC syndrome, etc. Organisms transformed with the DNA sequences can be used
CC for recombinant production of the polypeptides. The new DNA sequences
CC (and their fragments) are useful as primers or probes for isolating
CC homologues of any of the S.aureus DNA sequences contained on the
CC computer readable medium.
SQ Sequence 10320 BP; 3071 A; 1967 C; 1531 G; 3449 T;

alignment_scores:
  Quality: 55.00 Length: 11
  Ratio: 5.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 45.455

alignment_block:
US-09-155-076-1 x V74454/rev ..

Align seg 1/1 to reverse of: V74454 from: 1 to: 10320

3 PheHisArgTrpSerSerTyrMetValHisTrp 13
:::|||||:|||||:|||||:|||||:
908 TACCACCAATGGACAAAGTATTGTACATTGG 876

seq_name: N_Geneseq_36:T68847

seq_documentation_block:
ID T68847 standard; DNA; 1722 BP.
AC T68847;
DE 30-JAN-1998 (first entry)
KW Photorhabdus luminescens insect toxin TcbA11.
KW Insecticide; insect; toxin; pest control; biological control;
KW Photorhabdus luminescens; TcbA; Southern corn rootworm;
KW Colorado potato beetle; Western corn rootworm; meal worm;
KW boll weevil; turf grub; Coleoptera; beet armyworm; black cutworm;
KW cabbage looper; codling moth; corn earworm; European corn borer;
KW tobacco hornworm; tobacco budworm; Lepidoptera; Hymenoptera;
KW Diptera; Dictyoptera; Acarina; Homoptera; ds.
OS Photorhabdus luminescens strain W-14 (ATCC 55397).
PN WO9717432-A1.
PD 15-MAY-1997.
PF 06-NOV-1996; US-705484.
PR 28-AUG-1996; US-705484.
PR 06-NOV-1995; US-007255.
PR 28-FEB-1996; US-608423.
PA (WISC ) WISCONSIN ALUMNI RES FOUND.
PI Blackburn MB, Bowen DJ, Cliche TA, Ensign JC, Fatig R;
PI Ffrench-Constant RH, Guo L, Hey TD, Merlo DJ, Orr GL;
PI Petell J, Roberts JL, Rocheleau TA, Schoonover S;
PI Strickland JA;
DR WPI: 97-281022/25.
DR P-PSDB; W18303.
PT Photorhabdus sp. insecticidal protein toxins and DNA encoding them -

can be genetically engineered into insect larvae food and plants for
insect control
Claim 38; Page 229-231; 276pp; English.
This genomic DNA sequence encodes the 62.9 kDa TcbA11 insecticidal
toxin protein (see W17899) of Photorhabdus luminescens W-14.
It is derived from a full-length clone (see T68836) obtained from a
genomic library. A 280.6 kDa protein (see W17871) is processed
proteolytically into TcbA11 (see W18302) and TcbA11 components.
Claimed toxins of P. luminescens (see W17871, W17884-89, W17899-900,
W18301-06) can be produced by recombinant DNA methods and applied to,
or genetically engineered into, insect larvae food and plants for
insect control. The Photorhabdus toxins are particularly effective
against Southern corn rootworm, Colorado potato beetle, Western corn
rootworm, meal worm, boll weevil and turf grub (Coleoptera), beet
armyworm, black cutworm, cabbage looper, codling moth, corn earworm,
European corn borer, tobacco hornworm and tobacco budworm
(Lepidoptera), and are also active against insects of the orders
Hymenoptera, Diptera, Dictyoptera, Acarina and Homoptera. (All
claimed).
SQ Sequence 1722 BP; 461 A; 368 C; 446 G; 447 T;

alignment_scores:
  Quality: 50.50 Length: 14
  Ratio: 4.208 Gaps: 1
Percent Similarity: 85.714 Percent Identity: 57.143

alignment_block:
US-09-155-076-1 x T68847 ..

Align seg 1/1 to: T68847 from: 1 to: 1722

1 AlaGluPheHisArgTrpSerTyrMetValHisTrpLys 14
|||||:|||||:|||||:|||||:
1187 GCACGGTTTCAT...TGGCAGTGGTTTATGATTCACGTGAAG 1225

seq_name: N_Geneseq_36:V29987

seq_documentation_block:
ID V29987 standard; DNA; 1722 BP.
AC V29987;
DE 07-AUG-1998 (first entry)
DE tcbA11 gene from the tcb genomic region encoding protein TcbA.
KW Photorhabdus luminescens W-14; nematode; symbiotic;
KW Heterorhabditis; tca; tcb; tcc; insecticidal activity; toxin;
KW Lepidoptera; Coleoptera; Hymenoptera; Diptera; Dictyoptera; Acarina;
KW Homoptera; Southern; Western corn rootworm; Colorado potato beetle;
KW mealworm; boll weevil; turf grub; beetle armyworm; black cutworm;
KW cabbage looper; codling moth; corn earworm; European corn borer;
KW Tobacco hornworm; budworm; ds.
OS Photorhabdus luminescens.
FH Key Location/Qualifiers
FT CDS 1..1722
FT /*tag= a
FT WO9808932-A1.
PN 05-MAR-1998.
PD 05-MAY-1997; U07657.
PF 06-NOV-1996; WO-U18003.
PR 28-AUG-1996; US-705484.
PR 06-NOV-1996; US-743699.
PA (DOMC ) DOWELANCO.
PA (WISC ) WISCONSIN ALUMNI RES FOUND.
PI Blackburn MB, Bowen DJ, Cliche TA, Ensign JC, Fatig R,
PI Ffrench-Constant RH, Guo L, Hey TD, Merlo DJ, Orr GL,
PI Petell J, Roberts JL, Rocheleau TA, Schoonover S,
PI Strickland JA, Sukhupinda K;
DR WPI: 98-179427/16.
DR P-PSDB; W36559.
PT Isolated toxins from Photorhabdus luminescens strains - useful for
PT control of insect pests
PS Claim 38; Pages 259-261; 321pp; English.
CC The present sequence encodes a protein named TcbA11 of the bacterium
CC Photorhabdus luminescens (W-14). This is a symbiotic bacterium of the

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```
alignment_scores:
  Quality: 50.50
  Ratio: 4.208
  Percent similarity: 85.714
  Length: 14
  Gaps: 1
  Percent Identity: 57.143

alignment_block:
  US-09-155-076-1 x T68836 ..
```

```
alignment_scores:      Quality: 50.50      Length: 14
                       Ratio: 4.208      Gaps: 1
                       Percent Similarity: 85.714      Percent Identity: 57.143
```

```
alignment_block:
US-09-155-076-1 x V29985      ..
Align seg 1/1 to: V29985 from: 1 to: 7515

1 AlaGLuPhEHisArTrpSerSerTyMeVaHisTrpLys 14
|||||
6980 GCACGGTTTCAT...TGGCAGTGTTTATGATTCACTCGAAG 7018
```

seq name: N Geneseq 36:v21209 02

seq\_documentation\_block:  
Continuation (3 of 17)  
WP Sequence split into 17 fragments LOCUS V21209 Accession V21209  
Methanococcus jannaschii circular chr

WP	Fragment Name	Begin	End
WP	V21209_00	1	110000
WP	V21209_01	100001	210000
WP	V21209_02	300001	310000
WP	V21209_03	300001	410000
WP	V21209_04	400001	510000
WP	V21209_05	500001	610000
WP	V21209_06	600001	710000
WP	V21209_07	700001	810000
WP	V21209_08	800001	910000
WP	V21209_09	900001	1010000
WP	V21209_10	1000001	1110000
WP	V21209_11	1100001	1210000
WP	V21209_12	1200001	1310000
WP	V21209_13	1300001	1410000
WP	V21209_14	1400001	1510000
WP	V21209_15	1500001	1610000
WP	V21209_16	1600001	1664976

```
alignment_scores:      Quality: 49.00      Length: 13
                       Ratio: 4.900      Gaps: 0
                       Percent Similarity: 76.933      Percent Identity: 53.846
```

```
alignment_block:
US-09-155-076-1 x V21209.02
..
```

Align seq 1/1 to: v21209.02 from: 1 to: 110000

1 AlaLupPheHisArgTrpSerSeryrMetValHistrp 13  
||| |||::: ||| ||||||:::||||||  
40708 GCAGTTTTTATTATGGTGGAATTTATTCATTGG 40746

seq\_name: N\_Geneseq\_36:V26068

seq\_documentation\_block:  
ID V26068 standard; cDNA to mRNA; 4868 BP.  
AC V26068;  
22-JUL-1998 (first entry)  
DE Human canalicular multispecific organic anion transporter gene.  
DE Human; canalicular multispecific organic anion transporter; CMOAT;  
KW K<sub>1</sub> channel  
KW diagnosis: Dubin-Johnson syndrome; Cancer: tumour; ss.  
KW

OS	Homo sapiens.	Location/Qualifiers
FH	Key	38. .4675
FT	CDS	

```
FT /*tag= a
FT /product= "CMOAT"
FT /note= "canalicular multispecific organic anion
FT transporter"
```

J10099079-A.

FM 010039073 R.  
PD 21-APR-1998.

PF 30-SEP-1996; 259945.

PR 30-SEP-1996; JP-259945.

(KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
WPI: 98-289872/26.  
P-PSDB: W55966.  
Human cMOAT gene and its cDNA - useful in diagnosis of Dublin-Johnson syndrome  
PT  
PS Claim 1: Page 4-6; 16pp; Japanese.  
CC The present sequence encodes the human canalicular multispecific organic anion transporter (cMOAT). The human cMOAT gene expresses a mRNA of 6.5 kb and is present in the band 4 of the region 2 in the long arm of the tenth human chromosome. The cMOAT gene and the cDNA can be used for the diagnosis and the treatment of Dublin-Johnson syndrome.  
CC Sequence 4868 BP; 1322 A; 1148 C; 1135 G; 1263 T.  
SQ

```
alignment_scores:
  Quality: 48.00
  Ratio: 5.333
  Percent Similarity: 69.231
  Percent Identity: 46.154
  Length: 13
  Gaps: 0
```

```
alignment_block:
US-09-155-076-1 x V26068 ..
```

Align seq 1/1 to: V26068 from: 1 to: 4868

1 AlaGluPheHisArgTrpSerSerTyrMetValHisTrp 13  
:::~::~~:: ~~~~~ ~~~ ~~~~~  
4105 TCAGATTATCATTTGATGGTAGTATTGGTTCCTGG 4143

seq\_name: N Geneseq 36:T94023

seq\_documentation\_block:  
ID T94023 standard: cdNA: 5586 BP.

AC 134023, 01-APR-1998 (first entry)  
DE Human canalicular multispecific organic anion transporter cDNA.  
KW Canalicular multispecific organic anion transporter protein;  
KW cMOAT protein; ATP-binding cassette transporter family; ABC transporter;  
KW hepatobiliary excretion; multidrug resistance-associated protein; 1  
KW cMOAT protein activity; multidrug resistance-related protein; MDR-1;  
KW Dubin-Johnson disease; Rotor disease; ss.

CS	nono suppress.	Location/Qualifiers
FH	key	102. .4739
FT	CDS	/*tag= a
FT		

PN	WO9731111-A2.
PD	28-AUG-1997.
PF	21-FEB-1997. NL0079.
PR	21-FEB-1996; EP-200460.
PA	(MED.) ACAD MEDISCH CENT AMSTERDAM.
PA	(HETR.) HET NEDERLANDS KANKER INST.
PA	(INTR.) INTROGENE BV.
PI	Borst P, Bosma PJ, Evers R, Oude Elferink RPJ,
PI	Paulusma CC.
DR	WPI: 97-435163/40.
DR	P-PSDB: W33362.

P-F505; W35502.  
PT DNA encoding human and rat canalicular multispecific organic anion  
PT transporter proteins - useful for diagnosis and treatment of  
PT Dubin-Johnson disease and Rotor disease  
PS Claim 4; Fig 1A; 106pp; English.  
CC The present cDNA sequence encodes a novel canalicular multispecific  
CC organic anion transporter (cMOAT) protein, isolated from a human lambda  
CC gtil liver cDNA library. The protein is a new member of the ATP-binding  
CC cassette (ABC) transporter family. The ATP dependent cMOAT transporter  
CC system mediates hepatobiliary excretion in the liver. cMOAT may be a  
CC liver-specific homologue of multidrug resistance-associated protein.  
CC The nucleic acids are used to provide cells with cMOAT protein activity.  
CC cMOAT protein activity in cells can be enhanced by increasing the level  
CC of glutathione, glucuronide and/or sulphate. Antisense constructs,  
CC especially derived from another multidrug resistance (MDR)-related  
CC protein, e.g. MDR-1, to the nucleic acids and vectors can be used to  
CC decrease the level of cMOAT in a cell. The nucleic acids and proteins  
CC can be used especially in diagnosis of Dubin-Johnson disease, Rotor  
CC disease or another disease involving cMOAT. The cMOAT gene may also be



CC used as a selectable marker gene.  
SQ Sequence 5586 BP; 1533 A; 1278 C; 1244 G; 1524 T;

alignment\_scores:  
Quality: 48.00 Length: 13  
Ratio: 5.333 Gaps: 0  
Percent Similarity: 69.231 Percent Identity: 46.154

alignment\_block:  
US-09-155-076-1 x T94023 ..

Align seg 1/1 to: T94023 from: 1 to: 5586

1 AlaGluPheHisArgTrpSerSerTyrMetValHisTrp 13  
4169 TCAGATTATCATGTGATGGATAGATATTGCTTCATTGG 4207

seq\_name: N\_Geneseq\_36:V52253

seq\_documentation\_block:  
ID\_V52253 standard; DNA; 7172 BP.  
AC V52253;  
DE 23-OCT-1998 (first entry)  
DE Streptococcus pneumoniae genome fragment SEQ ID NO:120.  
KW Streptococcus pneumoniae; S. pneumoniae; genome; diagnosis; assay;  
KW computer readable medium; vaccine; pharmaceutical composition; ds.  
OS Streptococcus pneumoniae.  
PN W09818931-A2.  
PD 07-MAY-1998.  
PF 30-OCT-1997; U19588.  
PR 31-OCT-1996; US-029960.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PI Barash SC, Choi GH, Dillon PV, Dougherty BA, Fannon M,  
PI Kunsch CA, Rosen CA;  
PI WPI: 98-272225/24.  
DR Computer-readable medium with recorded Streptococcus pneumoniae  
PT polynucleotide sequences - useful in diagnostic kits and assays, and  
PT pharmaceutical compositions and vaccines for Streptococcus  
PT pneumoniae  
FS Claim 1; Page 846-850; 1409pp; English.  
CC The present invention describes a computer readable medium which has  
CC the nucleotide sequences SEQ ID NO:1 to 391 (V52134 to V52524) recorded  
CC on it, or a representative fragment or a sequence at least 95% identical  
CC to SEQ ID NO:1 to 391. The nucleotide sequences depicted in SEQ ID NO:1  
CC to 391 (V52134 to V52524) are genomic fragments from Streptococcus  
CC pneumoniae. The present invention also describes an isolated nucleic acid  
CC molecule encoding a homologue of any of the fragments of the S. pneumoniae  
CC genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced  
CC by a process comprising: (a) screening a genomic DNA library using as a  
CC probe a target sequence defined by any of the sequences in SEQ ID NO:1  
CC to 391, identifying members of the library which contain sequences  
CC that hybridize to the target sequence and isolating the nucleic acid  
CC molecules from the members; or (b) isolating mRNA, DNA or cDNA produced  
CC from an organism, amplifying nucleic acid molecules whose nucleotide  
CC sequence is homologous to amplification primers derived from the  
CC fragment of the S. pneumoniae genome to prime the amplification and  
CC isolating the amplified sequences. The computer readable medium can be  
CC used in a computer-based system for identifying fragments of the  
CC S. pneumoniae genome of commercial importance, or expression modulating  
CC fragments of the S. pneumoniae genome. Products from the present  
CC invention can be used in diagnosis kits and assays, and pharmaceutical  
CC compositions and vaccines for S. pneumoniae.  
SQ Sequence 7172 BP; 1920 A; 1699 C; 1381 G; 2172 T;

alignment\_scores:  
Quality: 48.00 Length: 9  
Ratio: 6.000 Gaps: 0  
Percent Similarity: 88.889 Percent Identity: 66.667

alignment\_block:  
US-09-155-076-1 x V52253 ..

Align seg 1/1 to: V52253 from: 1 to: 7172

5 ArgTrpSerSerTyrMetValHisTrp 13  
|||||:|||||:|||||:|||||  
3765 CGGTGGAACCTCGTATCACAACACTGG 3791



OM of: US-09-155-076-1 to: Issued\_Patents\_NA:\* out\_format : pfs  
 Date: Sep 13, 2000 2:43 AM  
 About: Results were produced by the GenCore software, version 4.5,  
 Copyright (c) 1993-2000 CompuGen Ltd.

## Command line parameters:

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## Search information block:

Query: US-09-155-076-1  
 Query length: 14  
 Database: Issued\_Patents\_NA\*  
 Database sequences: 243080  
 Database length: 6877915  
 Search time (sec): 59.930000

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seq\_name: /cgn2\_6/ptodata/2/ina/5D\_COMB.seq:US-08-370-156-24

## seq\_documentation\_block:

; Sequence 24, Application US/08370156  
 ; Patent No. 5932780  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Soreq, Hermona  
 ; APPLICANT: Zakut, Haim  
 ; APPLICANT: Shani, Moshe  
 ; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR  
 ; NUMBER OF SEQUENCES: 27  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Reising, Ethington, Barnard & Perry  
 ; STREET: P.O. Box 4390  
 ; CITY: Troy  
 ; STATE: Michigan  
 ; COUNTRY: US  
 ; ZIP: 48099  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; FILING DATE: US/08/370,156  
 ; CLASSIFICATION: 536  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Kohn, Kenneth I.  
 ; REGISTRATION NUMBER: 30,955  
 ; REFERENCE/DOCKET NUMBER: P-307 (Mullford)  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (810) 689-3500  
 ; TELEFAX: (810) 689-4071  
 ; INFORMATION FOR SEQ ID NO: 24:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 374 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; US-08-370-156-24

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 Percent Similarity: 100.000 Percent Identity: 100.000

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US-09-155-076-1 x US-08-370-156-24 ..

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seq\_name: /cgn2\_6/ptodata/2/ina/5D\_COMB.seq:US-08-370-156-26

## seq\_documentation\_block:

; Sequence 26, Application US/08370156  
 ; Patent No. 5932780  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Soreq, Hermona  
 ; APPLICANT: Zakut, Haim  
 ; APPLICANT: Shani, Moshe  
 ; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR

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; TITLE OF INVENTION: ANTICHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reising, Ethington, Barnard & Perry
; STREET: P.O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: US
; ZIP: 48099
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/370,156
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: P-307 (Mulford)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 689-3500
; TELEFAX: (810) 689-4071
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1215 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..78
; US-08-370-156-26

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; Patent No. 5248604
; GENERAL INFORMATION:
; APPLICANT: Fischer, Meir
; TITLE OF INVENTION: EXPRESSION OF ENZYMATICALLY ACTIVE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White, Esq.
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/732,962A
; FILING DATE: 19910722
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 39304/JPW/LSW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1845 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1842
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seq_name: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US92-06106-1

seq_documentation_block:
; Sequence 1, Application PC/TUS9206106
; GENERAL INFORMATION:
; APPLICANT: Fischer, Meir
; TITLE OF INVENTION: ENZYMATICALLY ACTIVE RECOMBINANT HUMAN
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White, Esq.
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06106
; FILING DATE: 19920722
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 39304-B-PCT/JPW/EAB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; INFORMATION FOR SEQ ID NO: 1:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1845 base pairs
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; STRANDEDNESS: single
; TOPOLOGY: linear
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; LOCATION: 1..1842
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; Patent No. 5891725
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Eckstein, Fritz
; TITLE OF INVENTION: Synthetic Antisense
; TITLE OF INVENTION: Oligodeoxynucleotides and Pharmaceutical Compositions
; TITLE OF INVENTION: Containing Them
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kohn & Associates
; STREET: 30500 No. 5891725thwestern Hwy., Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: US
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: 2391.00001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
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; TYPE: nucleic acid
; STRANDEDNESS: double
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; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens

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; Patent No. 5932780
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTICHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reising, Ethington, Barnard & Perry
; STREET: P.O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: US
; ZIP: 48099
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; APPLICATION NUMBER: US/08/370,156
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: P-307 (Mulford)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 689-3500
; TELEFAX: (810) 689-4071
; INFORMATION FOR SEQ ID NO: 1:
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; STRANDEDNESS: single
; TOPOLOGY: linear
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Wed Sep 13 08:11:31 2000

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; Patent No. 6025183
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KOHN & ASSOCIATES
; STREET: 30500 No. 6025183thwestern Highway, Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: U.S.
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/814,095
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Montgomery, Ilene N.
; REGISTRATION NUMBER: 38,972
; REFERENCE/DOCKET NUMBER: 2391.00066
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2256 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "ACHE gene comprising exons
; DESCRIPTION: 2, 3, 4 and 6"
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-814-095-1
alignment_scores:
Quality: 87.00 Length: 14
Ratio: 6.214 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-09-155-076-1 x US-08-814-095-1 ..
Align seg 1/1 to: US-08-814-095-1 from: 1 to: 2256
1 AlaGlupHeHisArgTrpSerTyrMetValHisTrpLys 14
|||||
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seq_documentation_block:
; Sequence 1, Application US/0881826A
; Patent No. 5891725
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Eckstein, Fritz
; TITLE OF INVENTION: Synthetic Antisense
; TITLE OF INVENTION: Oligodeoxynucleotides and Pharmaceutical Compositions
; TITLE OF INVENTION: Containing Them
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kohn & Associates
; STREET: 30500 No. 5891725thwestern Hwy., Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: US
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,826A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: 2391.00001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3016 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
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; ORGANISM: Homo sapiens
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; Patent No. 5932780
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
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; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTICHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Reising, Ethington, Barnard & Perry
; STREET: P.O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: US
; ZIP: 48099
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/370,156
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: P-307 (Mulford)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 689-3500
; TELEFAX: (810) 689-4071
; INFORMATION FOR SEQ ID NO: 5:
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; seq_documentation_block:
; Sequence 5, Application US/08814095
; Patent No. 6025183
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: KOHN & ASSOCIATES
; STREET: 30500 No. 6025183thwestern Highway, Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: U.S.
; ZIP: 48334
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; COMPUTER READABLE FORM:
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; APPLICATION NUMBER: US/08/814,095
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Montgomery, Ilene N.
; REGISTRATION NUMBER: 38,972
; REFERENCE/DOCKET NUMBER: 2391.00066
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 5:
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; TOPOLOGY: linear
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; ORGANISM: Homo sapiens
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; Sequence 6, Application US/08318826A
; Patent No. 5891725
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Eckstein, Fritz
; TITLE OF INVENTION: Synthetic Antisense
; TITLE OF INVENTION: Oligodeoxynucleotides and Pharmaceutical Compositions
; TITLE OF INVENTION: Containing Them
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Kohn & Associates
; STREET: 30500 No. 5891725thwestern Hwy., Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: US
; ZIP: 48334
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; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
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; APPLICATION NUMBER: US/08/318,826A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: 2391.00001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 6:
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; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
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; LOCATION: 160..1959
; OTHER INFORMATION: /note= "Splice variant: Exons 1, 2,
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US-08-318-826A-6

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; Sequence 3, Application US/08370156
; Patent No. 5932780
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTICHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reising, Ethington, Barnard & Perry
; STREET: P.O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: US
; ZIP: 48099
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/370,156
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.

; APPLICATION NUMBER: US/08/318,826A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: 2391.00001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
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US-08-318-826A-6

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; Patent No. 6025183
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KOHN & ASSOCIATES
; STREET: 30500 No. 6025183thwestern Highway, Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: U.S.
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/814,095
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Montgomery, Ilene N.
; REGISTRATION NUMBER: 38,972
; REFERENCE/DOCKET NUMBER: 2391.00066
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3096 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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Wed Sep 13 08:11:31 2000

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; DESCRIPTION: comprising exons 2, 3, 4 and 5 as well as the translated portion
; DESCRIPTION: of Intron 4 (readthrough)"
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
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; Patent No. 6025183
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KOHN & ASSOCIATES
; STREET: 30500 No. 6025183Western Highway, Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: U.S.
; ZIP: 48334
; COMPUTER READABLE FORM:
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; OPERATING SYSTEM: PC-DOS/MS-DOS
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/814,095
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Montgomery, Ilene N.
; REGISTRATION NUMBER: 38,972
; REFERENCE/DOCKET NUMBER: 2391.00066
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
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; ANTI-SENSE: NO
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; Patent No. 5891725
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Eckstein, Fritz
; TITLE OF INVENTION: Synthetic Antisense
; TITLE OF INVENTION: Oligodeoxynucleotides and Pharmaceutical Compositions
; TITLE OF INVENTION: Containing Them
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kohn & Associates
; STREET: 30500 No. 5891725thwestern Hwy., Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: US
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,826A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: 2391.00001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2381 base pairs
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; STRANDEDNESS: double
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; MOLECULE TYPE: cDNA to mRNA
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; ANTI-SENSE: NO
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Wed Sep 13 08:11:31 2000

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GenCore version 4.5  
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OM protein - protein search, using sw model

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(without alignments)  
46.505 Million cell updates/sec

Title: US-09-155-076-1

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Total number of hits satisfying chosen parameters: 178050

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_64:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	87	100.0	584	2 S48724	acetylcholinesterase
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4	87	100.0	614	2 A39256	acetylcholinesterase
5	87	100.0	614	2 JH0314	acetylcholinesterase
6	80	92.0	596	1 ACRYE	acetylcholinesterase
7	80	92.0	599	1 A38868	acetylcholinesterase
8	65	74.7	767	2 S47639	acetylcholinesterase
9	62	71.3	602	1 ACHU	cholinesterase (EC
10	61	70.1	581	2 C39768	cholinesterase (EC
11	61	70.1	603	2 S70849	cholinesterase (EC
12	44	50.6	260	2 T12393	NADH dehydrogenase
13	43	48.4	516	2 S67037	SMP3 protein - yea
14	42	48.3	1792	2 T08878	supervillin p205 -
15	41	47.1	397	2 A75137	hypothetical prote
16	41	47.1	1323	2 T30253	spalt protein - mo
17	40.5	46.6	510	1 S64059	stearyl-CoA desat
18	40	46.0	90	2 PH1152	Ig heavy chain v r
19	40	46.0	184	2 JC2104	hypothetical 20.8K
20	40	46.0	245	2 S64351	hypothetical prote
21	40	46.0	450	2 A64546	hypothetical prote
22	40	46.0	1350	2 T30341	zinc finger protei
23	40	46.0	1995	2 T08166	probable membrane
24	39.5	45.4	469	2 S74825	probable Rieske ir
25	39.5	45.4	542	2 T02379	hypothetical prote
26	39	44.8	100	2 T09856	sucrose synthase (
27	39	44.8	138	1 HVMST7	Ig heavy chain pre
28	39	44.8	226	2 D49591	membrane protein M
29	39	44.8	226	2 S37434	membrane glycoprot

## ALIGNMENTS

RESULT 1

S10712

acetylcholinesterase (EC 3.1.1.7) - bovine  
C:Species: Bos primigenius taurus (cattle)

C:Date: 21-Nov-1993 #sequence\_revision 23-Mar-1995 #text\_change 12-May-1995

C:Accession: S10712; A39734; B39734; B25650

R:Doctor, B.P.; Chapman, T.C.; Christner, C.E.; Deal, C.D.; de la Hoz, D.M.; Gentry, F.E. Lett. 266, 123-127, 1990

A:Title: Complete amino acid sequence of fetal bovine serum acetylcholinesterase and

A:Reference number: S10712; MUID:90306335

A:Accession: S10712

A:Molecule type: protein

A:Residues: 1-583 <DOC>

A:Experimental source: fetal serum

R:Roberts, W.L.; Doctor, B.P.; Foster, J.D.; Rosenberry, T.L.

J. Biol. Chem. 266, 7481-7487, 1991

A:Title: Bovine brain acetylcholinesterase primary sequence involved in intersubunit

A:Reference number: A39734; MUID:91210255

A:Accession: A39734

A:Molecule type: protein

A:Residues: 1-15, 'R', 17-38; 225-235, 'X', 237-244; 248-264, 'X', 266-273; 365-380; 396-404, 'X'

A:Experimental source: brain, erythrocyte

A:Accession: B39734

A:Molecule type: protein

A:Residues: 1-38 <ROZ>

A:Experimental source: fetal serum

R:Bon, S.; Chang, J.Y.; Strosberg, A.D.

FEBS Lett. 209, 206-212, 1986

A:Title: Identical N-terminal peptide sequences of asymmetric forms and of low-salt-s

inesterase.

A:Reference number: A91370; MUID:87080761

A:Accession: B25650

A:Molecule type: protein

A:Residues: 'XS', 3-12 <BON>

A:Experimental source: caudate nucleus

C:Superfamily: cholinesterase; cholinesterase homology

F;32-538/Domain: cholinesterase homology <CHE>

F;61,265,350,464,541/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;203/Active site: Ser #status predicted

Query Match 100.0%; Score 87; DB 2; Length 583;

Best Local Similarity 100.0%; Pred. NO. 4.8e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYNVHWK 14

|||||

DB 555 AEFHRWSSYNVHWK 568

RESULT 2

S48724

acetylcholinesterase - rabbit  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C:Date: 07-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 14-Nov-1997  
 C:Accession: S48724  
 R:Chajlani, V.; Derr, D.; Earles, B.; Schnell, E.; August, T.  
 R:Jbilo, O.; L'Hermite, Y.; Talesa, V.; Toutant, J.P.; Chattonnet, A.  
 Eur. J. Biochem. 225, 115-124, 1994  
 A:Title: Acetylcholinesterase and butyrylcholinesterase expression in adult rabbit tissue  
 A:Reference number: S48724; MUID:95010096  
 A:Accession: S48724  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-584 <JBI>  
 C:Superfamily: cholinesterase; cholinesterase homology  
 C:Keywords: glycoprotein  
 F:32-539/Domain: cholinesterase homology <CHE>

Query Match 100.0%; Score 87; DB 2; Length 584;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYNVHWK 14  
 |||||

Db 556 AEFHRWSSYNVHWK 569

RESULT 3

JH0811  
 acetylcholinesterase (EC 3.1.1.7) catalytic chain precursor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 18-Jun-1999  
 C:Accession: JH0811  
 R:Legay, C.; Bon, S.; Vernier, P.; Coussens, F.; Massoulie, J.  
 J. Neurochem. 60, 337-346, 1993  
 A:Title: Cloning and expression of a rat acetylcholinesterase subunit: generation of mul  
 A:Reference number: JH0811; MUID:93107932  
 A:Accession: JH0811  
 A:Molecule type: mRNA  
 A:Residues: 1-614 <LEG>

A:Cross-references: GB:S50879; NID:g262092; PIDN:AB24586.1; PID:g262093  
 A:Experimental source: striatum  
 C:Comment: This protein is responsible for hydrolysis of acetylcholine at cholinergic sy  
 C:Superfamily: cholinesterase; cholinesterase homology  
 C:Keywords: carboxylic ester hydrolase; glycoprotein; membrane protein; muscle; nerve; n  
 F:1-31/Domain: signal sequence #status predicted <SIG>  
 F:32-614/Product: acetylcholinesterase catalytic chain #status predicted <MAT>  
 F:63-569/Domain: cholinesterase homology <CHE>  
 F:100-127,288-303,440-560/Disulfide bonds: #status predicted  
 F:234,365,478/Active site: Ser, Glu, His #status predicted  
 F:296,381,495/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 87; DB 2; Length 614;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYNVHWK 14  
 |||||

Db 586 AEFHRWSSYNVHWK 599

RESULT 4

A3256  
 acetylcholinesterase (EC 3.1.1.7) precursor, brain splice form - human  
 C:Species: Homo sapiens (man)  
 C:Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 18-Jun-1999  
 C:Accession: A3256; S03959  
 R:Soreq, H.; Ben-Aziz, R.; Prody, C.A.; Seidman, S.; Gnatt, A.; Neville, L.; Lieman-Hurw  
 Proc. Natl. Acad. Sci. U.S.A. 87, 9688-9692, 1990  
 A:Title: Molecular cloning and construction of the coding region for human acetylcholine  
 A:Reference number: A3256; MUID:91088577  
 A:Accession: A3256

A:Molecule type: mRNA; DNA  
 A:Residues: 1-614 <SOR>  
 A:Cross-references: GB:M55040; NID:g177974; PIDN:AAA68151.1; PID:g177975  
 A:Note: this sequence represents composite of clones including clone ABGACHE from adu  
 nee should represent an authentic brain splice form  
 R:Chajlani, V.; Derr, D.; Earles, B.; Schnell, E.; August, T.  
 FBS Lett. 247, 279-282, 1989  
 A:Title: Purification and partial amino acid sequence analysis of human erythrocyte a  
 A:Reference number: S03959; MUID:89232136  
 A:Accession: S03959  
 A:Molecule type: protein  
 A:Residues: 256-266, 'Y', '268-273:306-308, 'X', '310-313, 'X', '315-316, 'D', '318-323, 'D', '325-3  
 Y', '532-551 <CHE>  
 A:Experimental source: erythrocytes  
 A:Note: this form was a disulfide-linked homodimer  
 C:Genetics:  
 A:Gene: GDB:ACHE; YT  
 A:Cross-references: GDB:118746; OMIM:100740  
 A:Map position: 7q22-7q22  
 C:Superfamily: cholinesterase; cholinesterase homology  
 C:Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein; phosphati  
 F:63-569/Domain: cholinesterase homology <CHE>

Query Match 100.0%; Score 87; DB 2; Length 614;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYNVHWK 14  
 |||||

Db 586 AEFHRWSSYNVHWK 599

RESULT 5

JH0314  
 acetylcholinesterase (EC 3.1.1.7) precursor - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 18-Jun-1999  
 C:Accession: JH0314  
 R:Rachinsky, T.L.; Camp, S.; Li, Y.; Ekstroem, T.J.; Newton, M.; Taylor, P.  
 Neuron 5, 317-327, 1990  
 A:Title: Molecular cloning of mouse acetylcholinesterase: tissue distribution of alte  
 A:Reference number: JH0314; MUID:90380429  
 A:Accession: JH0314  
 A:Molecule type: mRNA  
 A:Residues: 1-614 <RAC>

A:Cross-references: EMBL:X56518; NID:g49844; PIDN:CAA39867.1; PID:g49845  
 A:Experimental source: brain  
 C:Superfamily: cholinesterase; cholinesterase homology  
 C:Keywords: carboxylic ester hydrolase; glycoprotein; membrane protein; muscle; nerve

F:1-31/Domain: signal sequence #status predicted <SIG>  
 F:32-614/Product: acetylcholinesterase #status predicted <MAT>  
 F:63-569/Domain: cholinesterase homology <CHE>  
 F:100-127,288-303,440-560/Disulfide bonds: #status predicted  
 F:234/Active site: Ser #status predicted  
 F:296,381,495/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 87; DB 2; Length 614;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYNVHWK 14  
 |||||

Db 586 AEFHRWSSYNVHWK 599

RESULT 6

ACRYE  
 acetylcholinesterase (EC 3.1.1.7) precursor, 11s form - Pacific electric ray  
 N:Alternate names: acetylcholinesterase, asymmetric form  
 C:Species: Torpedo californica (Pacific electric ray)  
 C:Date: 17-Mar-1987 #sequence\_revision 08-Nov-1996 #text\_change 26-Feb-1999

C:Accession: A00773; A60820; A31962; B31962; A23902; B41117; S15677  
 R:Schumacher, M.; Camp, S.; Maulet, Y.; Newton, M.; MacPhee-Quigley, K.; Taylor, S.S.; F  
 Nature 319, 407-409, 1986  
 A:Title: Primary structure of Torpedo californica acetylcholinesterase deduced from its  
 A:Reference number: A00773; PMID:86118676  
 A:Accession: A00773  
 A:Molecule type: mRNA  
 A:Residues: 'NS', 11-596 <SCH>  
 A:CROSS-references: GB:X03439; NID:964389  
 A:Experimental source: electric organ  
 A:Note: Parts of this sequence, including the amino and carboxyl ends of the mature prot  
 R:Schumacher, M.; Camp, S.; Maulet, Y.; Newton, M.; MacPhee-Quigley, K.; Taylor, S.S.; F  
 Fed. Proc. 45, 2976-2981, 1986  
 A:Title: Primary structure of acetylcholinesterase: implications for regulation and func  
 A:Reference number: A60820; PMID:87054662  
 A:Accession: A60820  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 22-596 <SC2>  
 R:Schumacher, M.; Maulet, Y.; Camp, S.; Taylor, P.  
 J. Biol. Chem. 263, 18979-18987, 1988  
 A:Title: Multiple messenger RNA species give rise to the structural diversity in acetyl  
 A:Reference number: A92701; PMID:89066695  
 A:Accession: A31962  
 A:Molecule type: mRNA  
 A:Residues: 1-23 <SC3>  
 A:CROSS-references: EMBL:X03439; NID:964389  
 A:Experimental source: clones AChE-11 and AChE-18  
 A:Note: revision to sequence A00773  
 A:Accession: B31962  
 A:Molecule type: DNA; mRNA  
 A:Residues: 499-565 <SC4>  
 A:CROSS-references: GB:X03439; NID:964389  
 A:Experimental source: clone AChE-1  
 R:MacPhee-Quigley, K.; Taylor, P.; Taylor, S.  
 J. Biol. Chem. 260, 12185-12189, 1985  
 A:Title: Primary structures of the catalytic subunits from two molecular forms of acetyl  
 A:Reference number: A23902; PMID:86008285  
 A:Accession: A23902  
 A:Molecule type: protein  
 A:Residues: 22, 7, 24-45; 214-237 <MAC>  
 A:Note: active site Ser identification  
 R:Krenkamp, H.J.; Weise, C.; Raba, R.; Avakisaa, A.; Hucho, F.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 6117-6121, 1991  
 A:Title: Anionic subsites of the catalytic center of acetylcholinesterase from Torpedo a  
 A:Reference number: A41117; PMID:91296772  
 A:Accession: B41117  
 A:Molecule type: protein  
 A:Residues: 100-108 <KRE>  
 A:Note: substrate binding site  
 R:Maulet, Y.; Camp, S.; Gibney, G.; Rachinsky, T.L.; Ekstroem, T.J.; Taylor, P.  
 Neuron 4, 289-301, 1990  
 A:Title: Single gene encodes glycopospholipid-anchored and asymmetric acetylcholinester  
 A:Reference number: PS0113; PMID:90166618  
 A:Accession: S15677  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 557-596 <MAU>  
 A:CROSS-references: EMBL:X56516  
 R:MacPhee-Quigley, K.; Vedvick, T.S.; Taylor, P.; Taylor, S.S.  
 J. Biol. Chem. 261, 13565-13570, 1986  
 A:Title: Profile of the disulfide bonds in acetylcholinesterase.  
 A:Reference number: A43099; PMID:87008586  
 A:Contents: annotation; disulfide bonds  
 R:Sussman, J.L.; Harel, M.; Frolow, F.; Oefner, C.; Goldman, A.; Tokar, L.; Silman, I.  
 Science 253, 872-879, 1991  
 A:Reference number: A50061; PDB:1ACE  
 A:Contents: annotation; X-ray crystallography, 2.8 angstroms, residues 26-481, 511-555 of  
 A:Title: Atomic structure of acetylcholinesterase from Torpedo californica: a prototypic  
 A:Reference number: A43098; PMID:91343928  
 A:Contents: annotation; X-ray crystallography, 2.8 angstroms, residues 26-481, 511-555 of

C:Comment: Synapses usually contain this 115 (asymmetric) form of cholinesterase with  
 holinesterase occurs on the outer surfaces of cell membranes, including those of eryt  
 C:Complex: 11S form is disulfide linked homodimer; 18S form is homotetramer, a dimer  
 C:Function:  
 A:Description: hydrolyzes acetylcholine to choline and acetate  
 A:Pathway: neurotransmitter degradation  
 C:Superfamily: cholinesterase; cholinesterase homology  
 C:Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein; membrane  
 F:1-21/Domain: signal sequence #status predicted <SIG>  
 F:22-596/Product: acetylcholinesterase, 11S form #status experimental <MAT>  
 F:51-551/Domain: cholinesterase homology <CHE>  
 F:80,478,554/Binding site: carbohydrtate (Asn) (covalent) #status predicted  
 F:88-115,275-286,423-542/Disulfide bonds: #status experimental  
 F:105/Binding site: substrate (Trp) #status experimental  
 F:221/Active site: Ser #status experimental  
 F:348,461/Active site: Glu, His #status predicted  
 F:437/Binding site: carbohydrtate (Asn) (covalent) #status experimental  
 F:593/Disulfide bonds: interchain #status experimental

Query Match 92.08; Score 80; DB 1; Length 596;  
 Best Local Similarity 92.3%; Pred. No. 5.9e-05;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EFRHWSYMHVK 14  
 |||||:|||||  
 Db 569 EFRHWSYMHVK 581

RESULT 7  
 A38868  
 acetylcholinesterase (EC 3.1.1.7) precursor - marbled electric ray  
 C:Species: Torpedo marmorata (marbled electric ray)  
 C:Date: 23-Apr-1993 #sequence-revision 15-Nov-1996 #text-change 11-Jun-1999  
 C:Accession: A38868; A29682; S15696; A25650  
 R:Massoulié, J.; Bon, S.  
 submitted to the EMBL Data Library, June 1992  
 A:Reference number: A38868  
 A:Accession: A38868  
 A:Molecule type: mRNA  
 A:Residues: 1-599 <MAS>  
 A:CROSS-references: EMBL:X05497; NID:964414; PIDN:CAA29047.1; PID:964415  
 R:Sikorav, J.L.; Krejci, E.; Massoulié, J.  
 EMBO J. 6, 1865-1873, 1987  
 A:Title: cDNA sequences of Torpedo marmorata acetylcholinesterase: primary structure  
 A:Reference number: A29682; MUID:88004392  
 A:Accession: A29682  
 A:Molecule type: mRNA  
 A:Residues: 1-40, 'G', 42-226, 'G', 228-272, 'G', 274-284, 'E', 286-420, 'N', 422-599 <SIK>  
 A:CROSS-references: EMBL:X05497  
 R:Sikorav, J.L.; Duval, N.; Anselmet, A.; Bon, S.; Krejci, E.; Legay, C.; Osterlund,  
 EMBO J. 7, 2983-2993, 1988  
 A:Title: Complex alternative splicing of acetylcholinesterase transcripts in Torpedo  
 A:Reference number: S01293; MUID:89030590  
 A:Accession: S15696  
 A:Molecule type: mRNA  
 A:Residues: 526-599 <SI2>  
 A:CROSS-references: EMBL:X13172; NID:964416; PIDN:CAA31570.1; PID:964417  
 A:Experimental source: clone PACHE2  
 R:Bon, S.; Chang, J.Y.; Strosberg, A.D.  
 FEBS Lett. 209, 206-212, 1986  
 A:Title: Identical N-terminal peptide sequences of asymmetric forms and of low-salt-s  
 inesterase.  
 A:Reference number: A91370; MUID:87080761  
 A:Accession: A25650  
 A:Molecule type: protein  
 A:Residues: 25-40, 'G', 42-47 <BON>  
 C:Genetics:  
 A:Gene: AChE  
 C:Function:  
 A:Description: hydrolyzes acetylcholine to choline and acetate  
 A:Pathway: neurotransmitter degradation  
 C:Superfamily: cholinesterase; cholinesterase homology

C;Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein; neurotransmitter  
 F;1-24/Domain: signal sequence #status predicted <SIG>  
 F;25-599/Product: acetylcholinesterase #status predicted <MAT>  
 F;54-554/Domain: cholinesterase homology <CHE>  
 F;83,440,481,557/Binding site: carboxylate (Asn) (covalent) #status predicted  
 F;91-118,278-289,426-545/Disulfide bonds: #status predicted  
 F;224,351,464/Active site: Ser, Glu, His #status predicted  
 F;596/Disulfide bonds: interchain #status predicted

Query Match 92.0%; Score 80; DB 1; Length 599;  
 Best Local Similarity 92.3%; Pred. No. 5.9e-05;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EFRWSSYMHVK 14  
 |||||  
 Db 572 EFRWSSYMHVK 584

RESULT 8  
 S47639  
 acetylcholinesterase (EC 3.1.1.7) - chicken  
 C;Species: Gallus gallus (chicken)  
 C;Date: 25-Dec-1994 #sequence\_revision 10-Nov-1995 #text\_change 17-Mar-2000  
 C;Accession: S47639  
 R;Randall, W.R.; Rimer, M.; Gough, N.R.  
 Biochim. Biophys. Acta 1218, 453-456, 1994  
 A;Title: Cloning and analysis of chicken acetylcholinesterase transcripts from muscle and brain  
 A;Reference number: S47639; MUID:94325359  
 A;Accession: S47639  
 A;Molecule type: mRNA  
 A;Residues: 1-767 <RAN>  
 A;Cross-references: EMBL:U03472; NID:9623031; PID:9424115  
 C;Superfamily: cholinesterase; cholinesterase homology  
 C;Keywords: carboxylic ester hydrolase

Query Match 74.7%; Score 65; DB 2; Length 767;  
 Best Local Similarity 76.9%; Pred. No. 0.015;  
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 EFRWSSYMHVK 14  
 |||||  
 Db 740 EFRWSSYMHVK 752

RESULT 9  
 ACHU  
 cholinesterase (EC 3.1.1.8) precursor - human  
 N;Alternate names: acylcholine acylhydrolase; butyrylcholinesterase; choline esterase II  
 C;Species: Homo sapiens (man)  
 C;Date: 30-Jun-1987 #sequence\_revision 23-Feb-1996 #text\_change 02-Sep-1997  
 C;Accession: A33769; A26613; A33887; A34668; A00772  
 R;Arpagaus, M.; Kott, M.; Vatsis, K.P.; Bartels, C.F.; La Du, B.N.; Lockridge, O.  
 Biochemistry 29, 124-131, 1990  
 A;Title: Structure of the gene for human butyrylcholinesterase. Evidence for a single copy  
 A;Reference number: A33769; MUID:90212557  
 A;Accession: A33769  
 A;Molecule type: DNA  
 A;Residues: 'MSVQSNLQAGAAASCISPKYIMFTPKLHLCRCRESEIN', 1-602 <ARP>  
 A;Cross-references: GB:M32391; GB:J02879  
 A;Note: two ATG codons found upstream of Met-1 do not lie in a favorable context for translation  
 R;Prod'y, C.A.; Zevin-Sonkin, D.; Ghatt, A.; Goldberg, O.; Soreq, H.  
 Proc. Natl. Acad. Sci. U.S.A. 84, 3555-3559, 1987  
 A;Title: Isolation and characterization of full-length cDNA clones coding for cholinesterase  
 A;Reference number: A26613; MUID:87231856  
 A;Accession: A26613  
 A;Molecule type: mRNA  
 A;Residues: 1-133, 'D', 135-602 <PRO>  
 R;McInternan, C.; Adkins, S.; Chattonnet, A.; Vaughan, T.A.; Bartels, C.F.; Kott, M.; Rose  
 Proc. Natl. Acad. Sci. U.S.A. 84, 6682-6686, 1987  
 A;Title: Brain cDNA clone for human cholinesterase.  
 A;Reference number: A33887; MUID:88016155

A;Accession: A33887  
 A;Molecule type: mRNA  
 A;Residues: 'MSVQSNLQAGAAASCISPKYIMFTPKLHLCRCRESEIN', 1-602 <MCT>  
 A;Note: two ATG codons found upstream of Met-1 do not lie in a favorable context for translation  
 R;Nogueira, C.P.; McGuire, M.C.; Graeser, C.; Bartels, C.F.; Arpagaus, M.; Van der Sp  
 Am. J. Hum. Genet. 46, 934-942, 1990  
 A;Title: Identification of a frameshift mutation responsible for the silent phenotype  
 A;Reference number: A34668; MUID:90252779  
 A;Accession: A34668  
 A;Molecule type: DNA  
 A;Residues: 143-145, 'VSNWNIIFTCL' <NOG>  
 A;Note: frameshift mutant in codon for residue 145 (Gly)  
 R;Lockridge, O.; Bartels, C.F.; Vaughan, T.A.; Wong, C.K.; Norton, S.E.; Johnson, L.L  
 J. Biol. Chem. 262, 549-557, 1987  
 A;Title: Complete amino acid sequence of human serum cholinesterase.  
 A;Reference number: A00772; MUID:87109144  
 A;Accession: A00772  
 A;Molecule type: protein  
 A;Residues: 29-602 <LOC>  
 A;Experimental source: Plasma  
 C;Comment: Cholinesterase is present in most cells (except erythrocytes).  
 C;Genetics:  
 A;Gene: GDB:BCHE; CHE1  
 A;Cross-references: GDB:120558; OMIM:177400  
 A;Map position: 3q26.1-3q26.2  
 A;Introns: 506/2; 562/1  
 C;Function:  
 A;Description: hydrolyzes acylcholines to choline and a carboxylic acid  
 A;Note: This cholinesterase is highly reactive with organophosphate esters  
 C;Superfamily: cholinesterase; cholinesterase homology  
 C;Keywords: carboxylic ester hydrolase; glycoprotein; homotetramer  
 F;1-28/Domain: signal sequence #status predicted <SIG>  
 F;29-602/Product: cholinesterase #status experimental <MAT>  
 F;56-556/Domain: cholinesterase homology <CHE>  
 F;45,85,134,269,284,369,483,509,514/Binding site: carboxylate (Asn) (covalent) #stat  
 F;226/Active site: Ser #status experimental

Query Match 71.3%; Score 62; DB 1; Length 602;  
 Best Local Similarity 64.3%; Pred. No. 0.035;  
 Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYMHVK 14  
 |||||  
 Db 573 AGFHRWSSYMHVK 586

RESULT 10  
 C39768  
 cholinesterase (EC 3.1.1.8) - rabbit  
 N;Alternate names: butyrylcholinesterase  
 C;Species: Oryctolagus cuniculus (domestic rabbit)  
 C;Date: 14-Feb-1992 #sequence\_revision 01-Mar-1996 #text\_change 18-Jun-1999  
 C;Accession: S10255; C39768  
 R;Jbilo, O.; Chattonnet, A.  
 Nucleic Acids Res. 18, 3990, 1990  
 A;Title: Complete sequence of rabbit butyrylcholinesterase.  
 A;Reference number: S10255; MUID:90326526  
 A;Accession: S10255  
 A;Status: translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-581 <JBI>  
 A;Cross-references: EMBL:X52090; NID:g1476; PIDN:CAA36308.1; PID:e247309; PID:g137027  
 R;Arpagaus, M.; Chattonnet, A.; Masson, P.; Newton, M.; Vaughan, T.A.; Bartels, C.F.;  
 J. Biol. Chem. 266, 6966-6974, 1991  
 A;Title: Use of the polymerase chain reaction for homology probing of butyrylcholines  
 A;Reference number: A39768; MUID:91201348  
 A;Accession: C39768  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 75-215 <ARP>  
 A;Cross-references: GB:M62779; NID:g164788; PIDN:AAA31169.1; PID:g164789  
 C;Genetics:





A.Status: preliminary; translated from GB/EMBL/DBJ  
A.Molecule type: mRNA  
A.Residues: 1-1792 <PES>  
A.Cross-references: EMBL:AF025996; NID:g2668622; PID:g2668623  
A.Experimental source: cell line MDBK (Madin Darby Bovine Kidney); ATCC CCL-22  
C.Superfamily: villin headpiece homology  
C.keywords: actin binding; cell adhesion; membrane-associated protein  
F.1792-1792/Domain: villin headpiece homology <VHH>

Query Match	48.3%	Score 42;	DB 2;	Length 1792;
Best Local Similarity	46.2%	Pred. No.	1.2e+02;	
Matches	6;	Conservative	3;	Mismatches 4; Indels 0; Gaps 0;

QY 2 EFHRSSYVHWK 14  
:  
Db 1352 QFHEGDAYVVKWK 1364

RESULT 15

A75137

hypothetical protein PAB0600 - *Pyrococcus abyssi* (strain Orsay)

C:Species: *Pyrococcus abyssi*

C:Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 20-Aug-1999

C:Accession: A75137

R:anonymous, Genoscope

submitted to the EMBL Data Library, July 1999

A:Description: *Pyrococcus abyssi* genome sequence: insights into archaeal chromosome structure

A:Reference number: A75001

A:Accession: A75137

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-337 <KAW>

A:Cross-References: GB:AJ248285; GB:AL096836; MID:g5458067; PIDN:CAB49810.1; PID:e151570

A:Experimental source: strain Orsay

C:Genetics:

A:Gene: PAB0600

Query Match 47.1%; Score 41; DB 2; Length 397;  
Best Local Similarity 40.0%; Pred. No. 40;  
Matches 6; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

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QY      2 EFH--RWSSYMVHWK 14
          ::|||:||||
Db     18 DYHVKRWKEOKLHWK 32
```

Search completed: September 13, 2000, 02:22:33  
Job time: 131 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 13, 2000, 02:21:42 ; Search time 10.66 Seconds  
(without alignments)  
40.699 Million cell updates/sec

Title: US-09-155-076-1  
Perfect score: 87  
Sequence: 1 AEFHRWSSVMVHWK 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 85661 seqs, 30989116 residues

Total number of hits satisfying chosen parameters: 85661

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_38:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87	100.0	583	1 ACES_BOVIN	P23795 bos taurus
2	87	100.0	584	1 ACES_RABIT	Q29499 oryctolagus
3	87	100.0	614	1 ACES_HUMAN	P22303 homo sapien
4	87	100.0	614	1 ACES_MOUSE	P21836 mus musculus
5	87	100.0	614	1 ACES_RAT	P37136 rattus norv
6	65	74.7	767	1 ACES_CHICK	P36196 gallus gall
7	62	71.3	602	1 CHLE_HUMAN	P06276 homo sapien
8	61	70.1	581	1 CHLE_RABIT	P21927 oryctolagus
9	61	70.1	603	1 CHLE_MOUSE	Q03311 mus musculus
10	44	50.6	746	1 NU5C_ARATH	P56752 arabidopsis
11	43	49.4	516	1 SMP3_YEAST	Q04174 saccharomyc
12	40.5	46.6	510	1 ACOL_YEAST	P31237 saccharomyc
13	40	46.0	245	1 YG24_YEAST	P31369 influenza a
14	40	46.0	716	1 RRP2_IARTE	P36495 chlamydomon
15	40	46.0	1995	1 YCX7_CHLRE	P03980 mus musculus
16	39	44.8	138	1 HV48_MOUSE	P32825 schizosacch
17	39	44.8	507	1 SXA2_SCHPO	P25215 epstein-bar
18	39	44.8	575	1 UL87_EBV	O13683 schizosacch
19	39	44.8	1237	1 YD12_SCHPO	P19127 drosophila
20	38.5	44.3	318	1 AG0D_DROME	P18930 drosophila
21	38	43.7	117	1 NU3M_DROME	P51940 drosophila
22	38	43.7	117	1 NU3M_DROVA	P07705 drosophila
23	38	43.7	117	1 Y770_MYCTRU	P17825 mycobacteri
24	38	43.7	295	1 Y770_MYCTRU	P23998 vaccinia vi
25	38	43.7	351	1 VB19_VACCD	P25213 vaccinia vi
26	38	43.7	351	1 VB19_VACCV	P21077 vaccinia vi
27	38	43.7	353	1 VB19_VACCC	P23347 rattus norv
28	38	43.7	1234	1 B3A2_RAT	P13808 mus musculus
29	38	43.7	1237	1 B3A2_MOUSE	P48746 oryctolagus
30	38	43.7	1237	1 B3A2_RABIT	P20241 drosophila
31	38	43.7	1239	1 NRG_DROME	P52063 mycobacteri
32	37.5	43.1	285	1 YD41_MYCLE	P34849 apis mellifi
33	37.5	43.1	333	1 NU2M_APILI	

34 37.5 43.1 494 1 GPPA\_ECOLI  
35 37 42.5 137 1 HV11\_MOUSE  
36 37 42.5 185 1 YH00\_YEAST  
37 37 42.5 327 1 DHBL\_HUMAN  
38 37 42.5 551 1 AAP2\_NEUCR  
39 37 42.5 661 1 MX1\_HUMAN  
40 37 42.5 686 1 FREI\_YEAST  
41 37 42.5 901 1 VGLB\_GPCMV  
42 37 42.5 1350 1 XFIN\_XENLA  
43 37 42.5 1357 1 XJ03\_YEAST  
44 36.5 42.0 1407 1 CYAA\_DICDI  
45 36 41.4 218 1 NUVM\_NEUCR

## ALIGNMENTS

RESULT 1  
ACES\_BOVIN STANDARD; PRT; 583 AA.  
ID ACES\_BOVIN  
AC P23795;  
DT 01-NOV-1991 (Rel. 20, Created)  
DT 01-NOV-1991 (Rel. 20, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE ACETYLCHOLINESTERASE (EC 3.1.1.7).  
GN ACHE.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
RN [1]  
RP SEQUENCE.  
RC TISSUE=FETAL SERUM;  
RX MEDLINE: 90306335.  
RA Doctor B.P., Chapman T.C., Christner C.E., Deal C.D., de la Hoz D.M.,  
RA Gentry M.K., Ogert R.A., Rush R.S., Smyth K.K., Wolfe A.D.;  
RA "Complete amino acid sequence of fetal bovine serum  
RT acetylcholinesterase and its comparison in various regions with other  
RT cholinesterases.";  
RL FEBS Lett. 266:123-127(1990).  
CC -1- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.  
CC -1- CATALYTIC ACTIVITY: ACETYLCHOLINE + H(2)O = CHOLINE + ACETATE.  
CC -1- SUBUNIT: OLIGOMER COMPOSED OF DISULFIDE-LINKED HOMODIMERS.  
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
DR PIR: S10712; S10712.  
DR HSP; P22303; 2CLJ.  
DR PFAM: PF00135; Coesterase; 1.  
DR PRINTS: PR00878; CHOLNESTRASE.  
DR PROSITE: PS00122; CARBOXYLESTERASE\_B\_1; 1.  
DR PROSITE: PS00941; CARBOXYLESTERASE\_B\_2; 1.  
DR Hydrolase; Serine esterase; Synapse; Membrane; Nerve; Muscle;  
KW Neurotransmitter degradation; Glycoprotein.  
FT ACT\_SITE 203 203 BY SIMILARITY.  
FT ACT\_SITE 334 334 BY SIMILARITY.  
FT ACT\_SITE 447 447 BY SIMILARITY.  
FT DISULFID 69 96 BY SIMILARITY.  
FT DISULFID 257 272 BY SIMILARITY.  
FT DISULFID 409 529 BY SIMILARITY.  
FT DISULFID 580 580 INTERCHAIN (BY SIMILARITY).  
FT CARBOHYD 61 61 POTENTIAL.  
FT CARBOHYD 265 265 POTENTIAL.  
FT CARBOHYD 350 350 POTENTIAL.  
FT CARBOHYD 464 464 POTENTIAL.  
FT CARBOHYD 541 541 POTENTIAL.  
SQ SEQUENCE 583 AA; 64238 MW; 78655017E494279F CRC64;

Query Match 100.0%; Score 87; DB 1; Length 583;

Best Local Similarity 100.0%; Pred. No. 6e-06; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 0;

QY 1 AEFHRWSSVMVHWK 14

|||||

Db 555 AEFHRSSYVHWK 568

RESULT 2  
 ACES\_RABBIT STANDARD; PRT; 584 AA.  
 ID ACES\_RABBIT  
 AC Q29499;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE ACETYLCOLINESTERASE PRECURSOR (EC 3.1.1.7) (FRAGMENT).  
 GN ACHE.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Lagomorpha; Leporidae; Oryctolagus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-MUSCLE;  
 RX MEDLINE; 95010096.  
 RA Jbilo O., Lhermite Y., Toutant J., Chatonnet A.;  
 RT "Acetylcholinesterase and butyrylcholinesterase expression in adult  
 rabbit tissues and during development.";  
 RL Eur. J. Biochem. 225:115-124(1994).  
 CC -1- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.  
 CC -1- CATALYTIC ACTIVITY: ACETYLCHOLINE + H(2)O = CHOLINE + ACETATE.  
 CC -1- SUBUNIT: OLIGOMER COMPOSED OF DISULFIDE-LINKED HOMODIMERS.  
 CC -1- MISCELLANEOUS: SYNAPSES USUALLY CONTAIN ASYMMETRIC MOLECULES OF  
 CC CHOLINESTERASE, WITH A COLLAGEN-LIKE PART DISULFIDE-BONDED TO THE  
 CC CATALYTIC PART. A DIFFERENT, GLOBULAR TYPE OF CHOLINESTERASE  
 CC OCCURS ON THE OUTER SURFACES OF CELL MEMBRANES, INCLUDING THOSE OF  
 CC ERYTHROCYTES.  
 CC -1- MISCELLANEOUS: THIS IS THE CATALYTIC SUBUNIT OF AN ASYMMETRIC OR  
 CC SOLUBLE FORM OF ACHE.  
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
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 CC -----  
 CC EMBL; U05036; AAA53235.1; -  
 CC HSP; P22303; 2CLJ.  
 CC PFAM; PF00135; Coesterase; 1.  
 CC PROSITE; PS00122; CARBOXYLESTERASE\_B.1; 1.  
 CC PROSITE; PS00941; CARBOXYLESTERASE\_B.2; 1.  
 CC Hydrolase; Serine esterase; synapse; Membrane; Nerve; Muscle; Signal;  
 CC Neurotransmitter degradation; Glycoprotein.  
 CC NON\_TER 1 1  
 CC SIGNAL <1 1  
 CC CHAIN 2 584  
 CC ACT\_SITE 204 204  
 CC ACT\_SITE 335 335  
 CC ACT\_SITE 448 448  
 CC DISULFID 70 97  
 CC DISULFID 258 273  
 CC DISULFID 410 530  
 CC DISULFID 581 581  
 CC CARBOHYD 266 266  
 CC CARBOHYD 351 351  
 CC CARBOHYD 465 465  
 CC SEQUENCE 584 AA; 64630 MW; 2AE157F3063649FE CRC64;

Query Match 100.0%; Score 87; DB 1; Length 584;  
 Best Local Similarity 100.0%; Pred. No. 6e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRSSYVHWK 14

|||||||

Db 556 AEFHRSSYVHWK 569

RESULT 3  
 ACES\_HUMAN STANDARD; PRT; 614 AA.  
 ID ACES\_HUMAN  
 AC P22303;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE ACETYLCOLINESTERASE PRECURSOR (EC 3.1.1.7).  
 GN ACHE.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Homidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 91088577.  
 RA Soreq H., Ben-Aziz R., Prody C.A., Seidman S., Gnatt A., Neville L.,  
 RA Lieman-Hurwitz J., Lev-Lehman E., Ginzberg D., Lipidot-Lifson Y.,  
 RA Zakut H.;  
 RT "Molecular cloning and construction of the coding region for human  
 RT acetylcholinesterase reveals a G + C-rich attenuating structure.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:9688-9692(1990).  
 CC [2]  
 CC PARTIAL SEQUENCE.  
 CC TISSUE-ERYTHROCYTE;  
 CC MEDLINE; 89232136.  
 CC CHAJJANI V., DERR D., EARLES B., SCHMELL E., AUGUST T.;  
 RT "Purification and partial amino acid sequence analysis of human  
 RT erythrocyte acetylcholinesterase.";  
 RL FEBS Lett. 247:279-282(1989).  
 CC [3]  
 CC MUTAGENESIS OF CYS-611.  
 CC MEDLINE; 92084699.  
 CC VELAN B., GROSFELD H., KRONMAN C., LEITNER M., GOZES Y., LAZAR A.,  
 CC FLASHNER Y., MARCUS D., COHEN S., SHAFERMAN A.;  
 RT "The effect of elimination of intersubunit disulfide bonds on the  
 RT activity, assembly, and secretion of recombinant human  
 RT acetylcholinesterase. Expression of acetylcholinesterase Cys-580-->Ala  
 RT mutant.";  
 RL J. Biol. Chem. 266:23977-23984(1991).  
 CC [4]  
 CC MUTAGENESIS OF ACTIVE-SITE RESIDUES AND OF ASP-206 AND ASP-435.  
 CC MEDLINE; 92388112.  
 CC SHAFFERMAN A., KRONMAN C., FLASHNER Y., LEITNER M., GROSFELD H.,  
 CC ORIENTLICH A., GOZES Y., COHEN S., ARIEL N., BARAK D.;  
 RT "Mutagenesis of human acetylcholinesterase. Identification of  
 RT residues involved in catalytic activity and in polypeptide folding.";  
 RL J. Biol. Chem. 267:17640-17648(1992).  
 CC [5]  
 CC VARIANT BLOOD GROUP YT(B).  
 CC MEDLINE; 93256075.  
 CC BARTELS C.F., ZELINSKI T., LOCKRIDGE O.;  
 RT "Mutation at codon 322 in the human acetylcholinesterase (ACHE) gene  
 RT accounts for YT blood group polymorphism.";  
 RL Am. J. Hum. Genet. 52:928-936(1993).  
 CC -1- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.  
 CC -1- CATALYTIC ACTIVITY: ACETYLCHOLINE + H(2)O = CHOLINE + ACETATE.  
 CC -1- SUBUNIT: OLIGOMER COMPOSED OF DISULFIDE-LINKED HOMODIMERS.  
 CC -1- POLYMORPHISM: ACHE IS RESPONSIBLE FOR THE YT BLOOD GROUP SYSTEM.  
 CC THE MOLECULAR BASIS OF THE YT(A)-YT(B)-YT2 BLOOD GROUP  
 CC ANTIGENS IS A SINGLE VARIATION IN POSITION 353; HIS-353  
 CC CORRESPONDS TO YT(A) AND THE RARE VARIANT WITH ASN-353 TO YT(B).  
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
 CC -----  
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```

DR EMBL; M55040; AAA68151.1; -.
DR PIR; S03959; S03959.
DR PIR; A39256; A39256.
DR PDB; 2CLJ; 04-MAR-98.
DR CARBANK; CCSD:29374; -.
DR CARBANK; CCSD:32958; -.
DR CARBANK; CCSD:35085; -.
DR CARBANK; CCSD:36427; -.
DR SWISS-2DPAGE; P22303; HUMAN.
DR MIM; 100740; -.
DR MIM; 112100; -.
DR PFAM; PF00135; Coesterase; 1.
DR PRINTS; PR00878; CHOLINESTERASE.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase; Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal;
KW Neurotransmitter degradation; Glycoprotein; Polymorphism;
KW Blood group antigen; Alternative splicing; 3D-structure.
FT SIGNAL 1 31
FT CHAIN 32 614
FT ACT_SITE 234 234
FT ACT_SITE 365 365
FT ACT_SITE 478 478
FT DISULFID 100 127
FT DISULFID 288 303
FT DISULFID 440 560
FT DISULFID 611 611
FT CARBOHYD 296 296
FT CARBOHYD 381 381
FT CARBOHYD 495 495
FT VARIAT 353 353
FT MUTAGEN 234 234
FT MUTAGEN 365 365
FT MUTAGEN 478 478
FT MUTAGEN 206 206
FT MUTAGEN 435 435
FT MUTAGEN 611 611
SQ SEQUENCE 614 AA; 67796 MW; B9A84C77831C302 CRC64;

Query Match 100.0%; Score 87; DB 1; Length 614;
Best Local Similarity 100.0%; Pred. No. 6.3e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYMWVHK 14
Db 586 AEFHRWSSYMWVHK 599

RESULT 4
AC ACES_MOUSE STANDARD; PRT; 614 AA.
AC P21836;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7).
GN ACHE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP MEDLINE; 90380429.
RA Rachinsky T.L., Camp S., Li Y., Ekstroem T.J., Newton M., Taylor P.;
RT "Molecular cloning of mouse acetylcholinesterase: tissue distribution
of alternatively spliced mRNA species.";
RL Neuron 5:317-327(1990).
[2]
RP X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS) OF COMPLEX WITH FASCICULIN.
RX MEDLINE; 96067648.

```

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RA Bourne Y., Taylor P., Marchot P.;
RT "Acetylcholinesterase inhibition by fasciculin: crystal structure of
the complex.";
RL Cell 83:503-512(1995).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX MEDLINE; 99115643.
RA Bourne Y., Taylor P., Bougis P.E., Marchot P.;
RT "Crystal structure of mouse acetylcholinesterase. A peripheral site-
occluding loop in a tetrameric assembly.";
RL J. Biol. Chem. 274:2963-2970(1999).
CC -|- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.
CC -|- CATALYTIC ACTIVITY: ACETYLCHOLINE + H(2)O = CHOLINE + ACETATE.
CC -|- SUBUNIT: OLIGOMER COMPOSED OF DISULFIDE-LINKED HOMODIMERS.
CC -|- ALTERNATIVE PRODUCTS: THE DIFFERENT CATALYTIC SUBUNITS ARE ENCODED
BY ALTERNATIVELY SPLICED MRNAS THAT ARISE FROM A SINGLE GENE.
CC THE T (ASYMMETRIC) FORM IS SHOWN HERE.
CC -|- TISSUE SPECIFICITY: PREDOMINATES IN MOST EXPRESSING TISSUES
EXCEPT ERYTHROCYTES WHERE A GLYCOPHOSPHOLIPID-ATTACHED FORM OF
ACHE PREDOMINATES.
CC -|- MISCELLANEOUS: SYNAPSES USUALLY CONTAIN ASYMMETRIC MOLECULES OF
CHOLINESTERASE, WITH A COLLAGEN-LIKE PART DISULFIDE-BONDED TO THE
CATALYTIC PART. A DIFFERENT, GLOBULAR TYPE OF CHOLINESTERASE
OCCURS ON THE OUTER SURFACES OF CELL MEMBRANES, INCLUDING THOSE OF
ERYTHROCYTES.
CC -|- MISCELLANEOUS: THIS IS THE CATALYTIC SUBUNIT OF AN ASYMMETRIC OR
SOLUBLE FORM OF ACHE.
CC -|- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
CC -----
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CC -----
DR EMBL; X56518; CAA39867.1; -.
DR PIR; JH0314; JH0314.
DR PDB; 1MAH; 03-APR-96.
DR PDB; 1MAA; 20-APR-99.
DR MGD; MGI:87876; ACHE.
DR PFAM; PF00135; Coesterase; 1.
DR PRINTS; PR00878; CHOLINESTERASE.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase; Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal;
KW Neurotransmitter degradation; Glycoprotein; Alternative splicing;
KW 3D-structure.
FT SIGNAL 1 31
FT CHAIN 32 614
FT ACT_SITE 234 234
FT ACT_SITE 365 365
FT ACT_SITE 478 478
FT DISULFID 100 127
FT DISULFID 288 303
FT DISULFID 440 560
FT DISULFID 611 611
FT CARBOHYD 296 296
FT CARBOHYD 381 381
FT CARBOHYD 495 495
FT SEQUENCE 614 AA; 68168 MW; 66E2512463C21172 CRC64;

Query Match 100.0%; Score 87; DB 1; Length 614;
Best Local Similarity 100.0%; Pred. No. 6.3e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYMWVHK 14
Db 586 AEFHRWSSYMWVHK 599

```

RESULT 5  
 ID ACES\_RAT STANDARD; PRT; 614 AA.  
 AC P37136;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 15-FEB-2000 (Rel. 39, Last annotation update)  
 DE ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7).  
 GN ACHE.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN [1]  
 RP SEQUENCE FROM N.A. (T FORM).  
 RX MEDLINE; 93107932.  
 RA Legay C., Bon S., Vernier P., Cousens F., Massoulie J.;  
 RT "Cloning and expression of a rat acetylcholinesterase subunit:  
 generation of multiple molecular forms and complementarity with a  
 Torpedo collagenic subunit.";  
 RL J. Neurochem. 60:337-346(1993).  
 [2]  
 RP SEQUENCE FROM N.A. (H AND R FORMS).  
 RX MEDLINE; 93114454.  
 RA Legay C., Bon S., Massoulie J.;  
 RT "Expression of a cDNA encoding the glycolipid-anchored form of rat  
 acetylcholinesterase.";  
 RL FEBS Lett. 315:163-166(1993).  
 CC -1- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.  
 CC -1- CATALYTIC ACTIVITY: ACETYLCHOLINE + H(2)O = CHOLINE + ACETATE.  
 CC -1- SUBUNIT: OLIGOMER COMPOSED OF DISULFIDE-LINKED HOMODIMERS.  
 CC CATALYTIC FORMS H (GPI-ANCHOR DIMER) AND T (ASYMMETRIC COLLAGEN-  
 TAILED), WHICH DIFFER IN THEIR C-TERMINUS, ACCOUNT FOR ALL TYPES  
 OF KNOWN ACHE FORMS.  
 CC -1- ALTERNATIVE PRODUCTS: THE DIFFERENT CATALYTIC SUBUNITS ARE ENCODED  
 BY ALTERNATIVELY SPLICED MRNAS THAT ARISE FROM A SINGLE GENE.  
 CC IT IS NOT KNOWN WHETHER THE R FORM REPRESENTS A FUNCTIONAL  
 SPECIES. THE T (ASYMMETRIC) FORM IS SHOWN HERE.  
 CC -1- TISSUE SPECIFICITY: HAS BEEN FOUND IN CENTRAL NERVOUS SYSTEM AND  
 MUSCLE. FOUND IN EMBRYONIC LIVER AND SPLEEN BUT NOT IN ADULT  
 LIVER.  
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
 -----  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 -----  
 DR EMBL; S50879; AAB24586.1; -;  
 DR EMBL; X70140; CAA49717.1; -;  
 DR EMBL; X70141; CAA49718.1; -;  
 DR PIR; JH0811; JH0811.  
 DR HSP; P21836; IMAH.  
 DR PFAM; PF00135; Coesterase; 1.  
 DR PRINTS; PR00878; CHOLNESTRASE.  
 DR PROSITE; PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 DR PROSITE; PS00941; CARBOXYLESTERASE\_B\_2; 1.  
 KW Hydrolase; Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal;  
 KW Neurotransmitter degradation; Glycoprotein; Alternative splicing.  
 FT SIGNAL 1 31  
 FT CHAIN 32 614  
 FT ACETYLCHOLINESTERASE.  
 FT ACT\_SITE 234 334  
 FT BY SIMILARITY.  
 FT ACT\_SITE 365 365  
 FT BY SIMILARITY.  
 FT ACT\_SITE 478 478  
 FT BY SIMILARITY.  
 FT DISULFID 100 127  
 FT BY SIMILARITY.  
 FT DISULFID 288 303  
 FT BY SIMILARITY.  
 FT DISULFID 440 560  
 FT INTERCHAIN (BY SIMILARITY).  
 FT DISULFID 611 611  
 FT INTERCHAIN (BY SIMILARITY).  
 FT CARBOHYD 296 296  
 FT CARBOHYD 381 381  
 FT CARBOHYD 495 495  
 FT CARBOHYD 495 495

FT VARSPLIC 570 614  
 FT LLSATDTLDEARQWKAERHSSWSSYVMVHKNQFDHYSKOER  
 FT CSDL -> LLSATATEVPTCTPSPARHGEAARPGPALSLSL  
 FT LFLFLHLSGLRWL (IN ISOFORM H).  
 FT LLSATDTLDEARQWKAERHSSWSSYVMVHKNQFDHYSKOER  
 FT CSDL -> LLSATGRRGVGQGMHKAARVGTGRRGGKRR  
 FT M (IN ISOFORM R).  
 SQ SEQUENCE 614 AA; 68196 MW; 2EDAE7D46282E7C0 CRC64;  
 Query Match 100.0%; Score 87; DB 1; Length 614;  
 Best Local Similarity 100.0%; Pred. No. 6.3e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AEFHRSWSSYVMVHVK 14  
 |||||||||  
 DB 586 AEFHRSWSSYVMVHVK 599  
 |||||||||  
 RESULT 6  
 ID ACES\_CHICK STANDARD; PRT; 767 AA.  
 AC P36196;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7).  
 GN ACHE.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 CC Gallus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-MUSCLE.  
 RX MEDLINE; 94325359.  
 RA Randall W.R., Rimer M., Gough N.R.;  
 RT "Cloning and analysis of chicken acetylcholinesterase transcripts  
 from muscle and brain.";  
 RL Biochim. Biophys. Acta 1218:453-456(1994).  
 CC -1- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.  
 CC -1- CATALYTIC ACTIVITY: ACETYLCHOLINE + H(2)O = CHOLINE + ACETATE.  
 CC -1- SUBUNIT: OLIGOMER COMPOSED OF DISULFIDE-LINKED HOMODIMERS.  
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
 -----  
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 -----  
 DR EMBL; U03472; AAB60456.1; -;  
 DR HSP; P21836; IMAH.  
 DR PFAM; PF00135; Coesterase; 2.  
 DR PRINTS; PR00878; CHOLNESTRASE.  
 DR PROSITE; PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 DR PROSITE; PS00941; CARBOXYLESTERASE\_B\_2; 1.  
 KW Hydrolase; Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal;  
 KW Neurotransmitter degradation; Glycoprotein.  
 FT SIGNAL 1 19  
 FT CHAIN 20 767  
 FT ACETYLCHOLINESTERASE.  
 FT ACT\_SITE 227 227  
 FT BY SIMILARITY.  
 FT ACT\_SITE 520 520  
 FT BY SIMILARITY.  
 FT ACT\_SITE 633 633  
 FT BY SIMILARITY.  
 FT DISULFID 94 121  
 FT BY SIMILARITY.  
 FT DISULFID 281 292  
 FT BY SIMILARITY.  
 FT DISULFID 595 713  
 FT BY SIMILARITY.  
 FT DISULFID 764 764  
 FT INTERCHAIN (BY SIMILARITY).  
 FT CARBOHYD 285 285  
 FT CARBOHYD 536 536  
 FT CARBOHYD 650 650  
 FT CARBOHYD 725 725  
 FT CARBOHYD 725 725

RP VARIANT ATYPICAL GLY-98.

FT VARIANT 98 98 D -> G (IN ATYPICAL FORM, DIBUCAINE-  
RESISTANT).  
FT FTID-VAR\_002360.  
FT T -> M (IN FLUORIDE-1).  
FT FTID-VAR\_002361.  
FT L -> I (IN HYPOCHOLINESTERASEMIA).  
FT FTID-VAR\_002362.  
FT G -> V (IN FLUORIDE-2).  
FT FTID-VAR\_002363.  
FT A -> T (IN K VARIANT, WITH REDUCED ENZYME  
ACTIVITY).  
FT FTID-VAR\_002364.  
FT SEQUENCE 602 AA; 68418 MW; C9836409D9057F27 CRC64;  
SQ

Query Match 71.3%; Score 62; DB 1; Length 602;  
Best Local Similarity 64.3%; Pred. No. 0.031;  
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AEFHRSWSSVMVHWK 14  
I | | | | : | | : | |  
Db 573 AGFHRNNYMDWK 586

RESULT 8  
CHLE\_RABIT STANDARD; PRT; 581 AA.  
ID CHLE\_RABIT  
AC P21927;  
DT 01-MAY-1991 (Rel. 18, Created)  
DT 01-MAY-1991 (Rel. 18, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE CHOLINESTERASE PRECURSOR (EC 3.1.1.8) (ACYLCHOLINE ACYLHYDROLASE)  
DE (CHOLINE ESTERASE II) (BUTYRYLCHOLINE ESTERASE)  
DE (PSEUDOCOLINESTERASE).  
GN BCHE.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=LAGOMORPHA;  
RX MEDLINE; 90326526.  
RA Jbilo O., Roudani S., Chatonnet A.;  
RT "Complete sequence of rabbit butyrylcholinesterase.";  
RL Nucleic Acids Res. 18:3990-3990(1990).  
RN [2]  
RP SEQUENCE OF 75-215 FROM N.A.  
RX TISSUE=LIVER;  
RX MEDLINE; 91201348.  
RA Arpagaus M., Chatonnet A., Masson P., Newton M., Vaughan T.A.,  
RT Bartels C.F., Nogueira C.P., la Du B.N., Lockridge O.;  
RT "Use of the polymerase chain reaction for homology probing of  
butyrylcholinesterase from several vertebrates.";  
RL J. Biol. Chem. 266:6966-6974(1991).  
CC -1- CATALYTIC ACTIVITY: AN ACYLCHOLINE + H2(O) = CHOLINE + A  
CARBOXYLIC ACID ANION.  
CC -1- SUBUNIT: HOMOTETRAMER. THE TETRAMER IS COMPOSED  
OF TWO DIMERS. THE TWO SUBUNITS IN A DIMER ARE LINKED BY A  
DISULFIDE BOND.  
CC -1- TISSUE SPECIFICITY: PRESENT IN MOST CELLS EXCEPT ERYTHROCYTES.  
CC -1- MISCELLANEOUS: CHOLINESTERASE IS HIGHLY REACTIVE WITH  
ORGANOPHOSPHATE ESTERS.  
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
CC  
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CC  
CC EMBL; X52090; CAA36308.1; -.

DR EMBL; X52091; CAA36308.1; JOINED.  
DR EMBL; X52092; CAA36308.1; JOINED.  
DR EMBL; M62779; AAA31169.1; -.  
DR PIR; S10255; S10255.  
DR PIR; C39768; C39768.  
DR HSP; P21836; 1MAH.  
DR PRMT; PF00135; Coesterase; 1.  
DR PRINTS; PR00878; CHOLNESTRASE.  
DR PROSITE; PS00122; CARBOXYLESTERASE\_B\_1; 1.  
DR PROSITE; PS00941; CARBOXYLESTERASE\_B\_2; 1.  
KW Hydrolase; Serine esterase; Glycoprotein; Signal.  
FT SIGNAL 1 8  
FT CHAIN 9 581  
FT ACT\_SITE 205 205  
FT ACT\_SITE 332 332  
FT ACT\_SITE 445 445  
FT DISULFID 72 99  
FT DISULFID 259 270  
FT DISULFID 407 526  
FT DISULFID 578 578  
FT CARBOHYD 64 64  
FT CARBOHYD 113 113  
FT CARBOHYD 248 248  
FT CARBOHYD 263 263  
FT CARBOHYD 348 348  
FT CARBOHYD 462 462  
FT CARBOHYD 488 488  
FT CARBOHYD 492 492  
FT CARBOHYD 493 493  
SQ SEQUENCE 581 AA; 66156 MW; FE8B199E7B32EB0A CRC64;

Query Match 70.1%; Score 61; DB 1; Length 581;  
Best Local Similarity 64.3%; Pred. No. 0.042;  
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AEFHRSWSSVMVHWK 14  
I | | | | : | | : | |  
Db 552 AGFHRNNYMDWK 565

RESULT 9  
CHLE\_MOUSE STANDARD; PRT; 603 AA.  
ID CHLE\_MOUSE  
AC Q03311;  
DT 01-OCT-1993 (Rel. 27, Created)  
DT 01-OCT-1993 (Rel. 27, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE CHOLINESTERASE PRECURSOR (EC 3.1.1.8) (ACYLCHOLINE ACYLHYDROLASE)  
DE (CHOLINE ESTERASE II) (BUTYRYLCHOLINE ESTERASE)  
DE (PSEUDOCOLINESTERASE).  
GN BCHE.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 90380429.  
RA Rachinsky T.L., Camp S., Li Y., Ekstroem T.J., Newton M., Taylor P.;  
RT "Molecular cloning of mouse acetylcholinesterase: tissue distribution  
of alternatively spliced mRNA species.";  
RL Neuron 5:317-327(1990).  
RN [2]  
RP SEQUENCE OF 97-237 FROM N.A.  
RX TISSUE=LIVER;  
RX MEDLINE; 91201348.  
RA Arpagaus M., Chatonnet A., Masson P., Newton M., Vaughan T.A.,  
RA Bartels C.F., Nogueira C.P., la Du B.N., Lockridge O.;  
RT "Use of the polymerase chain reaction for homology probing of  
butyrylcholinesterase from several vertebrates.";  
RL J. Biol. Chem. 266:6966-6974(1991).  
CC -1- CATALYTIC ACTIVITY: AN ACYLCHOLINE + H2(O) = CHOLINE + A  
CARBOXYLIC ACID ANION.







DT 15-FEB-2000 (Rel. 39, Last annotation update)  
 DE RNA-DIRECTED RNA POLYMERASE SUBUNIT P2 (EC 2.7.7.48) (POLYMERASE  
 DE ACIDIC PROTEIN) (PA).  
 OS Influenza A virus (strain A/Equine/Tennessee/5/86).  
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenza virus A and B group.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 90021190.  
 RA Okazaki K., Kawakita Y., Webster R.G.;  
 RT "Evolutionary pathways of the PA genes of influenza A viruses.";   
 RL Virology 172:601-608(1989).  
 CC -!- SUBUNIT: INFLUENZA RNA POLYMERASE IS COMPOSED OF THREE SUBUNITS:  
 CC P1 (OR PB1), P2 (OR PA), AND P3 (OR PB2).  
 CC -!- SIMILARITY: BELONGS TO THE INFLUENZA VIRUSES POLYMERASE PA FAMILY.  
 CC  
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 CC  
 CC EMBL; M26082; AAA43113.1; -  
 DR PFAM; PF00603; Flu\_PA; 1.  
 KW Transferase; RNA-directed RNA polymerase.  
 SQ SEQUENCE 716 AA; 82724 MW; 9922E3E3995B0C96 CRC64;

Query Match 46.0%; Score 40; DB 1; Length 716;  
 Best Local Similarity 54.5%; Pred. No. 65;  
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 QY 2 EPHRWSSYMHV 12  
 Db 533 EPHWKEYCVH 543  
 | | | | | | | | | |

RESULT 15  
 YCX7-CHLRE STANDARD; PRT; 1995 AA.  
 ID YCX7-CHLRE STANDARD; PRT; 1995 AA.  
 AC P36495; Q37303.  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE 232.2 KDA PROTEIN (ORF1995) (ORF-S) (ORFA).  
 OS Chlamydomonas reinhardtii.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;  
 OC Chlamydomonadaceae; Chlamydomonas.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 97218038.  
 RA Boudreau E., Turmel M., Goldschmidt-Clermont M., Rochaix J.-D.,  
 RA Sivan S., Michaels A., Leu S.;  
 RT "A large open reading frame (orf1995) in the chloroplast DNA of  
 RT Chlamydomonas reinhardtii encodes an essential protein.";   
 RL Mol. Gen. Genet. 253:649-653(1997).  
 RN [2]  
 RP SEQUENCE OF 1573-1995 FROM N.A.  
 RC STRAIN-CW15;  
 RA Sivan S., Michaels A.;  
 RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE OF 1925-1995 FROM N.A.  
 RX MEDLINE; 87031585.  
 RA Woessner J.P., Gilham N.W., Boynton J.E.;  
 RT "The sequence of the chloroplast atpB gene and its flanking regions  
 RT in Chlamydomonas reinhardtii.";   
 RL Gene 44:17-28(1986).  
 RN [4]  
 RP PARTIAL SEQUENCE FROM N.A.

RX MEDLINE; 94207185.  
 RA Boudreau E., Otis C., Turmel M.;  
 RT "Conserved gene clusters in the highly rearranged chloroplast genomes  
 RT of Chlamydomonas moewusii and Chlamydomonas reinhardtii.";   
 RL Plant Mol. Biol. 24:585-602(1994).  
 CC -!- FUNCTION: ESSENTIAL FOR CELL GROWTH. MAY BE INVOLVED IN BINDING  
 CC CHLOROPLAST DNA TO EITHER THE CHLOROPLAST ENVELOPE OR THE  
 CC THYLAKOID MEMBRANE.  
 CC  
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).  
 CC -!- SIMILARITY: TO C.VULGARIS ORF819.  
 CC  
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 CC

DR EMBL; X92726; CAA63385.1; -  
 DR EMBL; X76934; CAA54257.1; -  
 DR PIR; S41289; S41289.  
 KW Chloroplast; transmembrane.  
 FT TRANSMEM 31 51 POTENTIAL.  
 FT TRANSMEM 53 73 POTENTIAL.  
 FT TRANSMEM 106 126 POTENTIAL.  
 FT TRANSMEM 157 177 POTENTIAL.  
 FT TRANSMEM 212 232 POTENTIAL.  
 FT TRANSMEM 254 274 POTENTIAL.  
 FT TRANSMEM 307 327 POTENTIAL.  
 FT CONFLICT 1588 1588 K -> R (IN REF. 2).  
 SQ SEQUENCE 1995 AA; 232194 MW; E5A3F167EAF5FC8A CRC64;

Query Match 46.0%; Score 40; DB 1; Length 1995;  
 Best Local Similarity 60.0%; Pred. No. 1.7e+02;  
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 RWSSYMHVK 14  
 Db 882 RWYIMOHYK 891  
 | | | | | | | | | |

Search completed: September 13, 2000, 02:24:31  
 Job time: 169 sec



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OM protein - protein search, using sw model

Run on: September 13, 2000, 02:22:37 ; Search time 14.59 seconds  
(without alignments)  
14.709 Million cell updates/sec

Title: US-09-155-076-1

Perfect score: 14

Sequence: 1 AEFHRWSSVMVHWK 14

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 152396 seqs, 15329161 residues

Word size: 0

Total number of hits satisfying chosen parameters: 152396

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14	100.0	40	2	US-08-370-156-25
2	14	100.0	45	2	US-08-370-156-7
3	14	100.0	45	2	US-08-370-156-8
4	14	100.0	614	1	US-07-732-962A-2
5	14	100.0	614	2	US-08-370-156-2
6	14	100.0	614	3	US-08-446-100-19
7	14	100.0	614	3	US-08-446-100-21
8	14	100.0	614	3	US-08-446-100-22
9	14	100.0	614	3	US-08-446-100-23
10	14	100.0	614	3	US-08-446-100-25
11	14	100.0	614	3	US-08-446-100-26
12	14	100.0	614	3	US-08-814-095-2
13	14	100.0	614	4	PCT-US92-06106-2
14	9	64.3	575	1	US-08-348-920-1
15	9	64.3	575	1	US-08-348-920-2
16	4	28.6	10	2	US-08-556-597-145
17	4	28.6	13	2	US-08-934-222-66
18	4	28.6	13	2	US-08-933-402-66
19	4	28.6	13	2	US-09-207-621-66
20	4	28.6	13	2	US-08-532-818-66
21	4	28.6	15	1	US-08-551-128A-1
22	4	28.6	15	1	US-08-551-128A-2
23	4	28.6	15	1	US-08-133-271-5
24	4	28.6	20	1	US-08-250-789A-179
25	4	28.6	21	2	US-08-612-840A-3
26	4	28.6	27	1	US-08-384-212-4
27	4	28.6	27	2	US-08-739-819-4
28	4	28.6	32	3	US-08-954-915A-18

29	4	28.6	38	2	US-08-612-840A-1
30	4	28.6	58	3	US-08-676-124-95
31	4	28.6	58	3	US-08-676-124-110
32	4	28.6	58	3	US-09-414-878-95
33	4	28.6	58	3	US-09-414-878-110
34	4	28.6	64	1	US-08-485-971-21
35	4	28.6	64	1	US-08-383-754-21
36	4	28.6	64	2	US-08-485-978-21
37	4	28.6	64	2	US-08-486-814-21
38	4	28.6	64	2	US-08-487-472-21
39	4	28.6	64	4	PCT-US92-00282-17
40	4	28.6	64	4	PCT-US95-08179-21
41	4	28.6	68	2	US-08-637-759B-62
42	4	28.6	68	3	US-08-871-355A-62
43	4	28.6	72	1	US-08-379-538-1
44	4	28.6	72	1	US-08-379-538-6
45	4	28.6	90	1	US-08-085-122-5

ALIGNMENTS

RESULT 1  
US-08-370-156-25  
; Sequence 25, Application US/08370156  
; Patent No. 5932780  
; GENERAL INFORMATION:  
; APPLICANT: Soxeq, Hermona  
; APPLICANT: Zakut, Haim  
; APPLICANT: Shani, Moshe  
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR  
; TITLE OF INVENTION: ANTICHOLINESTERASE SUBSTANCES  
; NUMBER OF SEQUENCE: 27  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Reising, Ethington, Barnard & Perry  
; STREET: P.O. Box 4390  
; CITY: Troy  
; STATE: Michigan  
; COUNTRY: US  
; ZIP: 48099

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/370.156  
FILING DATE:  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Kohn, Kenneth I.  
REGISTRATION NUMBER: 30,955  
REFERENCE/DOCKET NUMBER: P-307 (Mulford)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (810) 689-3500  
TELEFAX: (810) 689-4071  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-370-156-25

Query Match 100.0%; Score 14; DB 2; Length 40;  
Best Local Similarity 100.0%; Pred. No. 6.7e-10;  
Matches 14; Conservative: 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSVMVHWK 14  
Db 12 AEFHRWSSVMVHWK 25

Seal  
Seize  
limited

```

RESULT 2
US-08-370-156-7
; Sequence 7, Application US/08370156
; Patent No. 5932780
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTICHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reising, Ethington, Barnard & Perry
; STREET: P.O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: US
; ZIP: 48099
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/370,156
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: P-307 (Mulford)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 689-3500
; TELEFAX: (810) 689-4071
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-370-156-7

```

```

Query Match 100.0%; Score 14; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 7.3e-10;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 AEFHRWSSYVHWK 14
Db 17 AEFHRWSSYVHWK 30

```

```

RESULT 3
US-08-370-156-8
; Sequence 8, Application US/08370156
; Patent No. 5932780
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTICHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reising, Ethington, Barnard & Perry
; STREET: P.O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: US
; ZIP: 48099
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```

```

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/370,156
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: P-307 (Mulford)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 689-3500
; TELEFAX: (810) 689-4071
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-370-156-8

```

```

Query Match 100.0%; Score 14; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 7.3e-10;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 AEFHRWSSYVHWK 14
Db 17 AEFHRWSSYVHWK 30

```

```

RESULT 4
US-07-732-962A-2
; Sequence 2, Application US/07732962A
; Patent No. 5248604
; GENERAL INFORMATION:
; APPLICANT: Fischer, Meir
; TITLE OF INVENTION: EXPRESSION OF ENZYMATICALLY ACTIVE
; TITLE OF INVENTION: RECOMBINANT HUMAN ACETYLCHOLINESTERASE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White, Esq.
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/732,962A
; FILING DATE: 19910722
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 39304/JPW/LSW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 614 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-732-962A-2

```

Query Match 100.0%; Score 14; DB 1; Length 614;  
Best Local Similarity 100.0%; Pred. No. 5.5e-09; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 0;

QY 1 AEFHRSSYNVHWK 14  
| | | | | | | | | |  
DB 586 AEFHRSSYNVHWK 599

RESULT 5  
US-08-370-156-2  
; Sequence 2, Application US/08370156  
; Patent No. 5932780  
; GENERAL INFORMATION:  
; APPLICANT: Soreq, Hermona  
; APPLICANT: Zakut, Haim  
; APPLICANT: Shani, Moshe  
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR  
; TITLE OF INVENTION: ANTICHOLINESTERASE SUBSTANCES  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Reising, Ethington, Barnard & Perry  
; STREET: P.O. Box 4390  
; CITY: Troy  
; STATE: Michigan  
; COUNTRY: US  
; ZIP: 48099  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/370,156  
; FILING DATE:  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kohn, Kenneth I.  
; REGISTRATION NUMBER: 30,955  
; REFERENCE/DOCKET NUMBER: P-307 (Mulford)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (810) 689-3500  
; TELEFAX: (810) 689-4071  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 614 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-370-156-2

Query Match 100.0%; Score 14; DB 2; Length 614;  
Best Local Similarity 100.0%; Pred. No. 5.5e-09; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 0;

QY 1 AEFHRSSYNVHWK 14  
| | | | | | | | | |  
DB 586 AEFHRSSYNVHWK 599

RESULT 6  
US-08-446-100-19  
; Sequence 19, Application US/08446100  
; Patent No. 6001625  
; GENERAL INFORMATION:  
; APPLICANT: Broomfield, Clarence A  
; APPLICANT: Millard, Charles B  
; APPLICANT: Lockridge, Oksana  
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hendricks and Assoc.  
; STREET: 9669 A Main Street, P.O. Box 2509  
; CITY: Fairfax  
; STATE: VA  
; COUNTRY: US  
; ZIP: 22031  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/446,100  
; FILING DATE: 19-MAY-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hendricks, Glenna  
; REGISTRATION NUMBER: 32,535  
; REFERENCE/DOCKET NUMBER: Broomfield  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 425-4250  
; TELEFAX: (703) 425-2767  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 614 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: YES  
; ANTI-SENSE: YES  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:  
; ORGANISM: human esterases  
; US-08-446-100-19

Query Match 100.0%; Score 14; DB 3; Length 614;  
Best Local Similarity 100.0%; Pred. No. 5.5e-09; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 0;

QY 1 AEFHRSSYNVHWK 14  
| | | | | | | | | |  
DB 586 AEFHRSSYNVHWK 599

RESULT 7  
US-08-446-100-20  
; Sequence 20, Application US/08446100  
; Patent No. 6001625  
; GENERAL INFORMATION:  
; APPLICANT: Broomfield, Clarence A  
; APPLICANT: Millard, Charles B  
; APPLICANT: Lockridge, Oksana  
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hendricks and Assoc.  
; STREET: 9669 A Main Street, P.O. Box 2509  
; CITY: Fairfax  
; STATE: VA  
; COUNTRY: US  
; ZIP: 22031  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/446,100  
; FILING DATE: 19-MAY-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:

```
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 614 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
; US-08-446-100-20

Query Match 100.0%; Score 14; DB 3; Length 614;
Best Local Similarity 100.0%; Pred. No. 5.5e-09;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYMVHWK 14
DB 586 AEFHRWSSYMVHWK 599

RESULT 8
US-08-446-100-21
; Sequence 21, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 614 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
```

```
; ORIGINAL SOURCE:
; ORGANISM: human esterases
; US-08-446-100-21

Query Match 100.0%; Score 14; DB 3; Length 614;
Best Local Similarity 100.0%; Pred. No. 5.5e-09;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYMVHWK 14
DB 586 AEFHRWSSYMVHWK 599

RESULT 9
US-08-446-100-22
; Sequence 22, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 614 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
; US-08-446-100-22

Query Match 100.0%; Score 14; DB 3; Length 614;
Best Local Similarity 100.0%; Pred. No. 5.5e-09;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYMVHWK 14
DB 586 AEFHRWSSYMVHWK 599

RESULT 10
US-08-446-100-23
```



```

; Sequence 23, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446.100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: Broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 614 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
; US-08-446-100-23

```

```

Query Match 100.0%; Score 14; DB 3; Length 614;
Best Local Similarity 100.0%; Pred. No. 5.5e-09;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 AEFHRWSSVMVHWK 14
| | | | | | | | | |
DB 586 AEFHRWSSVMVHWK 599

```

```

RESULT 11
US-08-446-100-25
; Sequence 25, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:

```

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446.100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: Broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 614 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
; US-08-446-100-25

```

```

Query Match 100.0%; Score 14; DB 3; Length 614;
Best Local Similarity 100.0%; Pred. No. 5.5e-09;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 AEFHRWSSVMVHWK 14
| | | | | | | | | |
DB 586 AEFHRWSSVMVHWK 599

```

```

RESULT 12
US-08-814-095-2
; Sequence 2, Application US/08814095
; Patent No. 6025183
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KOHN & ASSOCIATES
; STREET: 30500 No. 6025183thwestern Highway, Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: U.S.
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/814,095
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Montgomery, Ilene N.
; REGISTRATION NUMBER: 38,972
; REFERENCE/DOCKET NUMBER: 2391.00066
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055

```

```
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 614 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   ORIGINAL SOURCE:
;     ORGANISM: Homo sapiens
;   US-08-814-095-2

Query Match          100.0%; Score 14; DB 3; Length 614;
Best Local Similarity 100.0%; Pred. No. 5.5e-09;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

* QY 1 AEFRWSSYMHVK 14
      |||||
Db 586 AEFRWSSYMHVK 599

RESULT 13
PCT-US92-06106-2
; SEQUENCE 2, Application PC/TUS9206106
; GENERAL INFORMATION:
;   APPLICANT: Fischer, Melr
;   TITLE OF INVENTION: ENZYMICALLY ACTIVE RECOMBINANT HUMAN
;   TITLE OF INVENTION: ACETYLCHOLINESTERASE AND USES THEREOF
;   NUMBER OF SEQUENCES: 2
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: John P. White, Esq.
;     STREET: 30 Rockefeller Plaza
;     CITY: New York
;     STATE: New York
;     COUNTRY: USA
;     ZIP: 10112
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: Patent in Release #1.0, Version #1.25
;   CURRENT APPLICATION NUMBER: PCT/US92/06106
;   FILING DATE: 19920722
;   CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;     NAME: White, John P.
;     REGISTRATION NUMBER: 28,678
;     REFERENCE/DOCKET NUMBER: 39304-B-PCT/JPW/EAB
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (212) 977-9550
;       TELEFAX: (212) 664-0525
;       TELEX: 422523 COOP UI
;   INFORMATION FOR SEQ ID NO: 2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 614 amino acids
;       TYPE: AMINO ACID
;       TOPOLOGY: linear
;     MOLECULE TYPE: protein
;   PCT-US92-06106-2

Query Match          100.0%; Score 14; DB 4; Length 614;
Best Local Similarity 100.0%; Pred. No. 5.5e-09;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFRWSSYMHVK 14
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Db 586 AEFRWSSYMHVK 599

RESULT 14
US-08-348-920-1
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; Sequence 1, Application US/08348920
; Patent No. 5695750
; GENERAL INFORMATION:
;   APPLICANT: Doctor, Bhupandra P.
;   APPLICANT: Maxwell, Donald
;   APPLICANT: Saxena, Ashima
;   APPLICANT: Radic, Zoran
;   APPLICANT: Taylor, Palmer
;   TITLE OF INVENTION: Compositions for Use to Deactivate
;   TITLE OF INVENTION: Organophosphates
;   NUMBER OF SEQUENCES: 2
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: John F. Moran
;     STREET: Off. of Command Judge Adv., HQ USAMRDC, Fort
;     CITY: Frederick
;     STATE: MD
;     COUNTRY: US
;     ZIP: 21702-5012
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: Patent in Release #1.0, Version #1.25
;   CURRENT APPLICATION NUMBER: US/08/348,920
;   FILING DATE: 25-NOV-1994
;   CLASSIFICATION: 424
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Hendricks, Glenna
;     REGISTRATION NUMBER: 32,535
;     REFERENCE/DOCKET NUMBER: doc348,920
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (301) 619-7807
;       TELEFAX: 301-619-7714
;   INFORMATION FOR SEQ ID NO: 1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 575 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: unknown
;       MOLECULE TYPE: protein
;       HYPOTHEICAL: NO
;       ANTI-SENSE: NO
;       FRAGMENT TYPE: internal
;   US-08-348-920-1

Query Match          64.3%; Score 9; DB 1; Length 575;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EFHRWSSYM 10
    |||||
Db 548 EFHRWSSYM 556

RESULT 15
US-08-348-920-2
; Sequence 2, Application US/08348920
; Patent No. 5695750
; GENERAL INFORMATION:
;   APPLICANT: Doctor, Bhupandra P.
;   APPLICANT: Maxwell, Donald
;   APPLICANT: Saxena, Ashima
;   APPLICANT: Radic, Zoran
;   APPLICANT: Taylor, Palmer
;   TITLE OF INVENTION: Compositions for Use to Deactivate
;   TITLE OF INVENTION: Organophosphates
;   NUMBER OF SEQUENCES: 2
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: John F. Moran
;     STREET: Off. of Command Judge Adv., HQ USAMRDC, Fort
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; STREET: Detrick
; CITY: Frederick
; STATE: MD
; COUNTRY: US
; ZIP: 21702-5012
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/348,920
; FILING DATE: 25-NOV-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: doc348,920
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-7807
; TELEFAX: 301-619-7714
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 575 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
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US-08-348-920-2

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Query Match      64.3%; Score 9; DB 1; Length 575;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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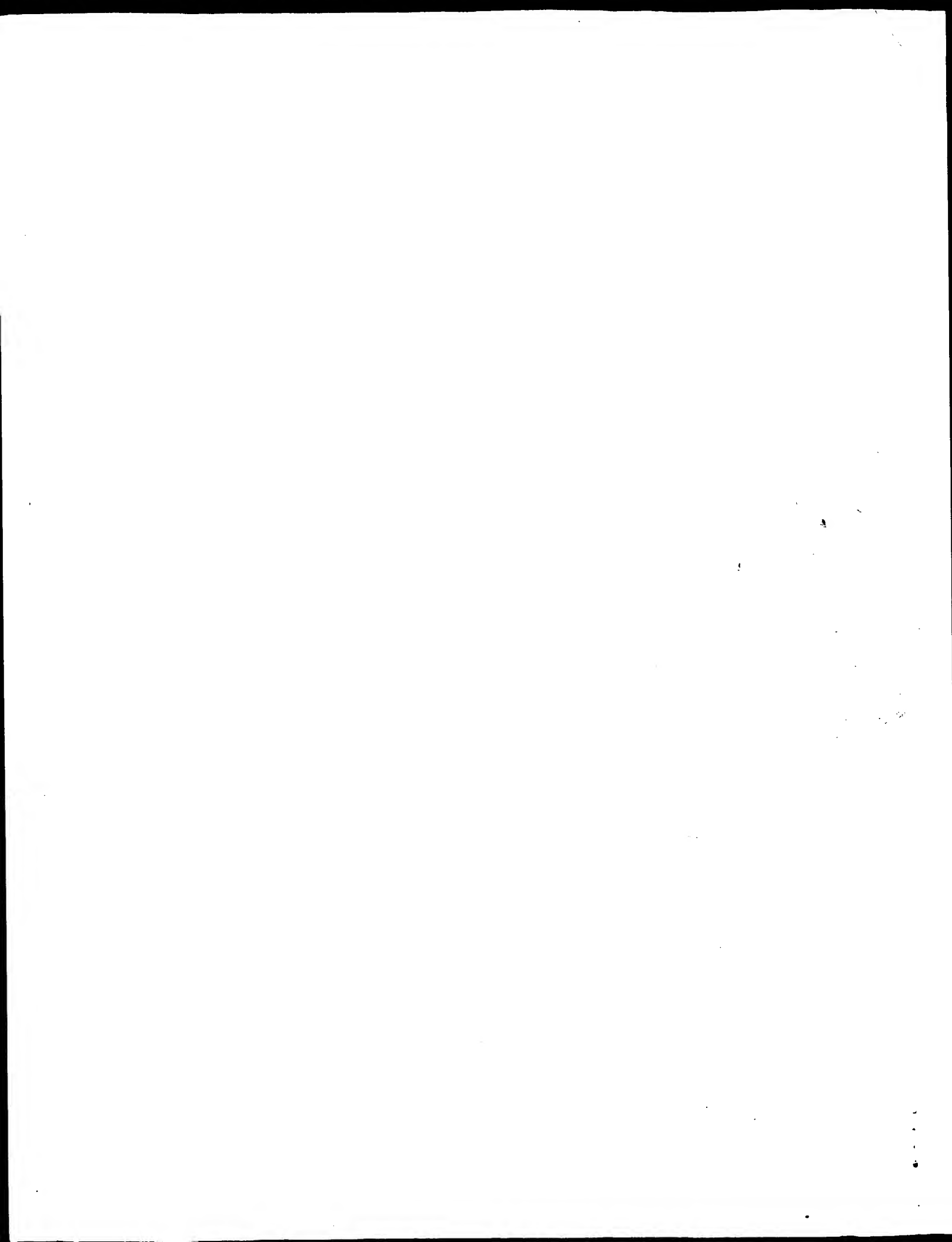
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Search completed: September 13, 2000, 02:25:26
Job time: 169 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 13, 2000, 02:23:37 ; Search time 17.58 Seconds  
(without alignments)  
49.283 Million cell updates/sec

Title: US-09-155-076-1

Perfect score: 14  
Sequence: 1 AEFHRWSSVMVHWK 14

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 178050 seqs, 61884766 residues

Word size : 0

Total number of hits satisfying chosen parameters: 178050

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Listing first 45 summaries

Database : PIR\_64:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14	100.0	583	2	acetylcholinestera
2	14	100.0	584	2	acetylcholinestera
3	14	100.0	614	2	acetylcholinestera
4	14	100.0	614	2	acetylcholinestera
5	14	100.0	614	2	acetylcholinestera
6	9	64.3	596	1	acetylcholinestera
7	9	64.3	599	1	acetylcholinestera
8	9	64.3	767	2	acetylcholinestera
9	6	42.9	330	2	DNA methyltransfer
10	6	42.9	469	2	probable Rieske ir
11	5	35.7	159	2	H811424
12	5	35.7	222	2	H811424
13	5	35.7	236	1	S09256
14	5	35.7	230	1	A36170
15	5	35.7	235	1	WJH04B
16	5	35.7	252	2	T24406
17	5	35.7	282	2	H70078
18	5	35.7	318	2	T05569
19	5	35.7	335	1	B69249
20	5	35.7	338	2	E75576
21	5	35.7	339	2	B70024
22	5	35.7	357	2	D71262
23	5	35.7	365	2	T12040
24	5	35.7	408	2	G65038
25	5	35.7	415	2	D75616
26	5	35.7	428	2	T14419
27	5	35.7	429	2	T07809
28	5	35.7	431	2	T14418
29	5	35.7	440	2	T22699

ALIGNMENTS

RESULT 1

S10712  
acetylcholinesterase (EC 3.1.1.7) - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 21-Nov-1993 #sequence.revision 23-Mar-1995 #text\_change 12-May-1995  
C:Accession: S10712; A39734; B39734; B25650  
R:Doctor, B.P.; Chapman, T.C.; Christner, C.E.; Deal, C.D.; de la Hoz, D.M.; Gentry, F.E.S. Lett. 266, 123-127, 1990  
A:Title: Complete amino acid sequence of fetal bovine serum acetylcholinesterase and  
A:Reference number: S10712; MUID:90306335  
A:Accession: S10712  
A:Molecule type: protein  
A:Residues: 1-583 <DOC>  
A:Experimental source: fetal serum  
R:Roberts, W.D.; Doctor, B.P.; Foster, J.D.; Rosenberry, T.L.  
J. Biol. Chem. 266, 7481-7487, 1991  
A:Title: Bovine brain acetylcholinesterase primary sequence involved in intersubunit  
A:Reference number: A39734; MUID:91210255  
A:Accession: A39734  
A:Molecule type: protein  
A:Residues: 1-15, R, 17-38; 225-235, X', 237-244; 248-264, X', 266-273; 365-380; 396-404, X'  
A:Experimental source: brain, erythrocyte  
A:Accession: B39734  
A:Molecule type: protein  
A:Residues: 1-38 <R02>  
A:Experimental source: fetal serum  
R:Bon, S.; Chang, J.Y.; Strosberg, A.D.  
FEBS Lett. 209, 206-212, 1986  
A:Title: Identical N-terminal peptide sequences of asymmetric forms and of low-salt-s  
inesterase.  
A:Reference number: A91370; MUID:87080761  
A:Accession: B25650  
A:Molecule type: protein  
A:Residues: 'XS', 3-12 <BON>  
A:Experimental source: caudate nucleus  
C:Superfamily: cholinesterase; cholinesterase homology  
C:Keywords: carboxylic ester hydrolase; glycoprotein  
F;32-538/Domain: cholinesterase homology <CHE>  
F;61,265,350,464,541/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;203/Active site: Ser #status predicted

Query Match 100.0%; Score 14; DB 2; Length 583;  
Best Local Similarity 100.0%; Pred. No. 8.9e-10;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSVMVHWK 14

Db 555 AEFHRWSSVMVHWK 568

RESULT 2

S48724  
acetylcholinesterase - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 07-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 14-Nov-1997  
C:Accession: S48724  
R:Jbilo, O.; L'Hernite, Y.; Talsesa, V.; Toutant, J.P.; Chatonnet, A.  
Eur. J. Biochem. 225, 115-124, 1994  
A:Title: Acetylcholinesterase and butyrylcholinesterase expression in adult rabbit tissue  
A:Reference number: S48724; MUID:95010096  
A:Accession: S48724  
A:Status: preliminary  
A:Superfamily: cholinesterase; cholinesterase homology  
A:Molecule type: mRNA  
A:Residues: 1-584 <JBIL>  
C:Superfamily: cholinesterase; cholinesterase homology  
C:Keywords: glycoprotein  
F:32-539/Domain: cholinesterase homology <CHE>

Query Match 100.0%; Score 14; DB 2; Length 584;  
Best Local Similarity 100.0%; Pred. No. 8.9e-10; Mismatches 0; Gaps 0;  
Matches 14; Conservative 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14  
|||||  
Db 556 AEFHRWSSYVHWK 569  
|||||

RESULT 3  
JH0811  
acetylcholinesterase (EC 3.1.1.7) catalytic chain precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 18-Jun-1999  
C:Accession: JH0811  
R:Legay, C.; Bon, S.; Vernier, P.; Coussen, F.; Massoulie, J.  
J. Neurochem. 60, 337-346, 1993  
A:Title: Cloning and expression of a rat acetylcholinesterase subunit: generation of mul  
A:Reference number: JH0811; MUID:93107932  
A:Accession: JH0811  
A:Molecule type: mRNA  
A:Residues: 1-614 <LEG>  
A:Cross-references: GB:S50879; NID:Q262092; PIDN:AAB24586.1; PID:Q262093  
A:Experimental source: striatum  
C:Comment: This protein is responsible for hydrolysis of acetylcholine at cholinergic sy  
C:Superfamily: cholinesterase; cholinesterase homology  
C:Keywords: carboxylic ester hydrolase; glycoprotein; membrane protein; muscle; nerve; n  
F:1-31/Domain: signal sequence #status predicted <SIG>  
F:32-614/Product: acetylcholinesterase catalytic chain #status predicted <MAT>  
F:53-569/Domain: cholinesterase homology <CHE>  
F:100-127,288-303,440-560/Disulfide bonds: #status predicted  
F:234,365,478/Active site: Ser, Glu, His #status predicted  
F:296,381,495/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 14; DB 2; Length 614;  
Best Local Similarity 100.0%; Pred. No. 9.2e-10;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14  
|||||  
Db 586 AEFHRWSSYVHWK 599  
|||||

RESULT 4  
A39256  
acetylcholinesterase (EC 3.1.1.7) precursor, brain splice form - human  
C:Species: Homo sapiens (man)  
C:Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 18-Jun-1999  
C:Accession: A39256; S03959  
R:Scorq, H.; Ben-Aziz, R.; Prody, C.A.; Seidman, S.; Gnatt, A.; Neville, L.; Lieman-Hurw  
Proc. Natl. Acad. Sci. U.S.A. 87, 9688-9692, 1990  
A:Title: Molecular cloning and construction of the coding region for human acetylcholine  
A:Reference number: A39256; MUID:91088577  
A:Accession: A39256

A:Molecule type: mRNA; DNA  
A:Residues: 1-614 <SOR>  
A:Cross-references: GB:M55040; NID:g177974; PIDN:AAA68151.1; PID:g177975  
A:Note: this sequence represents composite of clones including clone ABGACHE from adu  
nce should represent an authentic brain splice form  
R:Chhajlani, V.; Derr, D.; Earles, B.; Schmeil, E.; August, T.  
FEBS Lett. 247, 279-282, 1989  
A:Title: Purification and partial amino acid sequence analysis of human erythrocyte a  
A:Reference number: S03959; MUID:89232136  
A:Accession: S03959  
A:Molecule type: protein  
A:Residues: 256-266,'Y',268-273;306-308,'X',310-313,'X',315-316,'D',318-323,'D',325-3  
Y',532-551 <CHE>  
A:Experimental source: erythrocytes  
A:Note: this form was a disulfide-linked homodimer  
C:Genetics:  
A:Gene: GDB:ACHE; YT  
A:Cross-references: GDB:118746; OMIM:100740  
A:Map position: 7q22-7q22  
C:Superfamily: cholinesterase; cholinesterase homology  
C:Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein; phosphati  
F:63-569/Domain: cholinesterase homology <CHE>

Query Match 100.0%; Score 14; DB 2; Length 614;  
Best Local Similarity 100.0%; Pred. No. 9.2e-10;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14  
|||||  
Db 586 AEFHRWSSYVHWK 599  
|||||

RESULT 5  
JH0314  
acetylcholinesterase (EC 3.1.1.7) precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 18-Jun-1999  
C:Accession: JH0314  
R:Rachinsky, T.L.; Camp, S.; Li, Y.; Ekstroem, T.J.; Newton, M.; Taylor, P.  
Neuron 5, 317-327, 1990  
A:Title: Molecular cloning of mouse acetylcholinesterase: tissue distribution of alte  
A:Reference number: JH0314; MUID:90380429  
A:Accession: JH0314  
A:Molecule type: mRNA  
A:Residues: 1-614 <RAC>  
A:Cross-references: EMBL:X56518; NID:g49844; PIDN:CAA39867.1; PID:g49845  
A:Experimental source: brain  
C:Superfamily: cholinesterase; cholinesterase homology  
C:Keywords: carboxylic ester hydrolase; glycoprotein; membrane protein; muscle; nerve  
F:1-31/Domain: signal sequence #status predicted <SIG>  
F:32-614/Product: acetylcholinesterase #status predicted <MAT>  
F:63-569/Domain: cholinesterase homology <CHE>  
F:100-127,288-303,440-560/Disulfide bonds: #status predicted  
F:234/Active site: Ser #status predicted  
F:296,381,495/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 14; DB 2; Length 614;  
Best Local Similarity 100.0%; Pred. No. 9.2e-10;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14  
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Db 586 AEFHRWSSYVHWK 599  
|||||

RESULT 6  
ACRYE  
acetylcholinesterase (EC 3.1.1.7) precursor, 11S form - Pacific electric ray  
N:Alternate names: acetylcholinesterase, asymmetric form  
C:Species: Torpedo californica (Pacific electric ray)  
C:Date: 17-Mar-1987 #sequence\_revision 08-Nov-1996 #text\_change 26-Feb-1999

C;Accession: A00773; A60820; A31962; B31962; A23902; B41117; S15677  
 R;Schumacher, M.; Camp, S.; Maulet, Y.; Newton, M.; MacPhee-Quigley, K.; Taylor, S.S.; F  
 Nature 319, 407-409, 1986  
 A;Title: Primary structure of Torpedo californica acetylcholinesterase deduced from its  
 A;Reference number: A00773; MUID:86118676  
 A;Accession: A00773  
 A;Molecule type: mRNA  
 A;Residues: 557-596 <SCH>  
 A;Cross-references: GB:X03439; NID:g64389  
 A;Experimental source: Electric organ  
 A;Note: parts of this sequence, including the amino and carboxyl ends of the mature protein  
 R;Schumacher, M.; Camp, S.; Maulet, Y.; Newton, M.; MacPhee-Quigley, K.; Taylor, S.S.; F  
 Fed. Proc. 45, 2976-2981, 1986  
 A;Title: Primary structure of acetylcholinesterase: implications for regulation and function  
 A;Reference number: A60820; MUID:87054662  
 A;Accession: A60820  
 A;Status: nucleic acid sequence not shown  
 A;Molecule type: mRNA  
 A;Residues: 22-596 <SC2>  
 R;Schumacher, M.; Maulet, Y.; Camp, S.; Taylor, P.  
 J. Biol. Chem. 263, 18979-18987, 1988  
 A;Title: Multiple messenger RNA species give rise to the structural diversity in acetylcholinesterase  
 A;Reference number: A92701; MUID:89066695  
 A;Accession: A31962  
 A;Molecule type: mRNA  
 A;Residues: 1-23 <SC3>  
 A;Cross-references: EMBL:X03439; NID:g64389  
 A;Experimental source: clones Ache-11 and Ache-18  
 A;Note: revision to sequence A00773  
 A;Accession: B31962  
 A;Molecule type: DNA; mRNA  
 A;Residues: 499-565 <SC4>  
 A;Cross-references: GB:X03439; NID:g64389  
 A;Experimental source: clone Ache-1  
 R;MacPhee-Quigley, K.; Taylor, P.; Taylor, S.  
 J. Biol. Chem. 260, 12185-12189, 1985  
 A;Title: Primary structures of the catalytic subunits from two molecular forms of acetylcholinesterase  
 A;Reference number: A23902; MUID:86008285  
 A;Accession: A23902  
 A;Molecule type: protein  
 A;Residues: 22, B, 24-45; 214-237 <MAC>  
 A;Note: active site Ser identification  
 R;Kreienkamp, H.J.; Weiss, C.; Raba, R.; Aaviksaar, A.; Hucho, F.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 6117-6121, 1991  
 A;Title: Anionic subsites of the catalytic center of acetylcholinesterase from Torpedo a  
 A;Reference number: A4117; MUID:91296772  
 A;Accession: B4117  
 A;Molecule type: protein  
 A;Residues: 100-108 <KRE>  
 A;Note: substrate binding site  
 R;Maulet, Y.; Camp, S.; Gibney, G.; Rachinsky, T.L.; Ekstroem, T.J.; Taylor, P.  
 Neuron 4, 289-301, 1990  
 A;Title: Single gene encodes glycopospholipid-anchored and asymmetric acetylcholinesterase  
 A;Reference number: P50113; MUID:90166618  
 A;Accession: S15677  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 557-596 <MAU>  
 A;Cross-references: EMBL:X55516  
 R;MacPhee-Quigley, K.; Vedvick, T.S.; Taylor, P.; Taylor, S.S.  
 J. Biol. Chem. 261, 13565-13570, 1986  
 A;Title: Profile of the disulfide bonds in acetylcholinesterase.  
 A;Reference number: A43059; MUID:87008586  
 A;Contents: annotation; disulfide bonds  
 R;Sussman, J.L.; Harel, M.; Silman, I.  
 submitted to the Brookhaven Protein Data Bank, October 1991  
 A;Reference number: A50061; PDB:1ACE  
 A;Contents: annotation: X-ray crystallography, 2.8 angstroms, residues 26-481, 511-555 of  
 R;Sussman, J.L.; Harel, M.; Frolow, F.; Oefner, C.; Goldman, A.; Tokar, L.; Silman, I.  
 Science 253, 872-879, 1991  
 A;Title: Atomic structure of acetylcholinesterase from Torpedo californica: a prototypic  
 A;Reference number: A43098; MUID:91343928  
 A;Contents: annotation; X-ray crystallography, 2.8 angstroms, residues 26-481, 511-555 of

C;Comment: Synapses usually contain this 11S (asymmetric) form of cholinesterase with  
 hollinesterase occurs on the outer surfaces of cell membranes, including those of eryt  
 C;Complex: 11S form is disulfide linked homodimer; 18S form is homotetramer, a dimer  
 C;Function:  
 A;Description: hydrolyzes acetylcholine to choline and acetate  
 A;Pathway: neurotransmitter degradation  
 C;Superfamily: cholinesterase; cholinesterase homology  
 C;Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein; membrane  
 F:1-21/Domain: signal sequence #status predicted <SIG>  
 F:22-596/Product: acetylcholinesterase, 11S form #status experimental <MAT>  
 F:51-555/Domain: cholinesterase homology <CHE>  
 F:80,478,554/Binding site: carbohydate (Asn) (covalent) #status predicted  
 F:88-115,275-286,423-542/Disulfide bonds: #status experimental  
 F:105/Binding site: substrate (Trp) #status experimental  
 F:221/Active site: Ser #status experimental  
 F:348,461/Active site: Glu, His #status predicted  
 F:437/Binding site: carbohydate (Asn) (covalent) #status experimental  
 F:593/Disulfide bonds: interchain #status experimental  
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 Best Local Similarity 100.0%; Pred. No. 0.00098;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2 EFHRWSSYM 10  
 Db 569 EFHRWSSYM 577  
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 A38868  
 acetylcholinesterase (EC 3.1.1.7) precursor - marbled electric ray  
 C;Species: Torpedo marmorata (marbled electric ray)  
 C;Date: 23-Apr-1993 #sequence.Revision 15-Nov-1996 #text\_change 11-Jun-1999  
 C;Accession: A38868; A29682; S15696; A25650  
 R;Massoulié, J.; Bon, S.  
 submitted to the EMBL Data Library, June 1992  
 A;Reference number: A38868  
 A;Accession: A38868  
 A;Molecule type: mRNA  
 A;Residues: 1-599 <MAS>  
 A;Cross-references: EMBL:X05497; NID:g64414; PIDN:CAA29047.1; PID:g64415  
 R;Sikorav, J.L.; Krejci, E.; Massoulié, J.  
 EMBO J. 6, 1865-1873, 1987  
 A;Title: cDNA sequences of Torpedo marmorata acetylcholinesterase: primary structure  
 A;Reference number: A29682; MUID:88004392  
 A;Accession: A29682  
 A;Molecule type: mRNA  
 A;Residues: 1-40, 'G', 42-226, 'G', 228-272, 'G', 274-284, 'E', 286-420, 'N', 422-599 <SIK>  
 A;Cross-references: EMBL:X05497  
 R;Sikorav, J.L.; Duval, N.; Anselmet, A.; Bon, S.; Krejci, E.; Legay, C.; Osterlund,  
 EMBO J. 7, 2983-2993, 1988  
 A;Title: Complex alternative splicing of acetylcholinesterase transcripts in Torpedo  
 A;Reference number: S01293; MUID:89030590  
 A;Accession: S15696  
 A;Molecule type: mRNA  
 A;Residues: 526-599 <SI2>  
 A;Cross-references: EMBL:X13172; NID:g64416; PIDN:CAA31570.1; PID:g64417  
 A;Experimental source: clone pACHE2  
 R;Bon, S.; Chang, J.X.; Strosberg, A.D.  
 FEBS Lett. 209, 206-212, 1986  
 A;Title: Identical N-terminal peptide sequences of asymmetric forms and of low-salt-s  
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 A;Reference number: A91370; MUID:87080761  
 A;Accession: A25650  
 A;Molecule type: protein  
 A;Residues: 25-40, 'G', 42-47 <BON>  
 C;Genetics:  
 A;Gene: Ache  
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 A;Description: hydrolyzes acetylcholine to choline and acetate  
 A;Pathway: neurotransmitter degradation  
 C;Superfamily: cholinesterase; cholinesterase homology

C:Keywords: alternative splicing: carboxylic ester hydrolase; glycoprotein; neurotransmitter  
 F:1-24/Domain: signal sequence #status predicted <SIG>  
 F:25-599/Product: acetylcholinesterase #status predicted <WAT>  
 F:54-554/Domain: cholinesterase homology <CHE>  
 F:83,440,481,557/Binding site: carboxylate (Asn) (covalent) #status predicted  
 F:91-118,278-289,426-545/Disulfide bonds: #status predicted  
 F:224,351,464/Active site: Ser, Glu, His #status predicted  
 F:596/Disulfide bonds: interchain #status predicted

Query Match 64.3%; Score 9; DB 1; Length 599;  
 Best Local Similarity 100.0%; Pred. No. 0.00099;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EPHRWSSYM 10  
 Db 572 EPHRWSSYM 580

RESULT 8  
 S47639  
 Acetylcholinesterase (EC 3.1.1.7) - chicken  
 C:Species: Gallus gallus (chicken)  
 C:Date: 25-Dec-1994 #sequence\_revision 10-Nov-1995 #text\_change 17-Mar-2000  
 C:Accession: S47639  
 R:Randall, W.R.; Rimer, M.; Gough, N.R.  
 Biochim. Biophys. Acta 1218, 453-456, 1994  
 A:Title: Cloning and analysis of chicken acetylcholinesterase transcripts from muscle and brain  
 A:Reference number: S47639; MUID:94325359  
 A:Accession: S47639  
 A:Molecule type: mRNA  
 A:Residues: 1-767 <RAN>  
 A:Cross-references: EMBL:U03472; NID:G623031; PID:G424115  
 C:Superfamily: cholinesterase; cholinesterase homology  
 C:Keywords: carboxylic ester hydrolase

Query Match 64.3%; Score 9; DB 2; Length 767;  
 Best Local Similarity 100.0%; Pred. No. 0.0012;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EPHRWSSYM 10  
 Db 740 EPHRWSSYM 748

RESULT 9  
 S53990  
 DNA methyltransferase pmt1 - fission yeast (Schizosaccharomyces pombe)  
 C:Species: Schizosaccharomyces pombe  
 C:Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 17-Mar-2000  
 C:Accession: S53990; T39793  
 R:Wilkinson, C.R.M.; Bartlett, R.; Nurse, P.; Bird, A.P.  
 Nucleic Acids Res. 23, 203-210, 1995  
 A:Title: The fission yeast gene pmt1(+) encodes a DNA methyltransferase homologue.  
 A:Reference number: S53990; MUID:95166638  
 A:Accession: S53990  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-330 <WIL>  
 A:Cross-references: EMBL:X82444; NID:G563910; PIDN:CAA57824.1; PID:G563911  
 R:McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.  
 Submitted to the EMBL Data Library, July 1999  
 A:Reference number: Z21880  
 A:Accession: T39793  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-330 <MCD>  
 A:Cross-references: EMBL:AL109731; PIDN:CAB52029.1; GSPDB:GN000067; SPDB:SPBIC19C2.02  
 A:Experimental source: strain 972h-; cosmid c19C2  
 C:Genetics:  
 A:Gene: SPBIC19C2.02  
 A:Map position: 2

A: Introns: 56/3  
 C: Superfamily: site-specific methyltransferase (cytosine-specific) EcoRII

Query Match 42.9%; Score 6; DB 2; Length 330;  
 Best Local Similarity 100.0%; Pred. No. 2.7;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WSSYMW 11  
 Db 208 WSSYMW 213

RESULT 10  
 S74825  
 probable Rieske iron-sulfur protein sir1747 - Synechocystis sp. (strain PCC 6803)  
 C:Species: Synechocystis sp.  
 A:Variety: PCC 6803  
 C:Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 08-Oct-1999  
 C:Accession: S74825  
 R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, O.; K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas  
 DNA Res. 3, 109-136, 1996  
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis

A:Reference number: S74322; MUID:97061201  
 A:Accession: S74825  
 A>Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-469 <KAN>  
 A:Cross-references: EMBL:D90909; GB:AB001339; NID:G1652844; PIDN:BAAL7786.1; PID:di01  
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996  
 C:Superfamily: Rieske [2Fe-2S] homology  
 C:Keywords: 2Fe-2S; metalloprotein; Rieske iron-sulfur protein  
 F:56-114/Domain: Rieske [2Fe-2S] homology <RSK>  
 F:76,78,96,99/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent) #status pr

Query Match 42.9%; Score 6; DB 2; Length 469;  
 Best Local Similarity 100.0%; Pred. No. 3.5;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRW 6  
 Db 349 AEFHRW 354

RESULT 11  
 H81442  
 hypothetical protein Cj0249 [imported] - Campylobacter jejuni (strain NCTC 11168)  
 C:Species: Campylobacter jejuni  
 C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 31-Mar-2000  
 C:Accession: H81442  
 R:Parkhill, J.; Wren, B.W.; Muncall, K.; Kettle, J.M.; Churcher, C.; Basham, D.; Chil  
 C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Ba  
 Nature 403, 665-668, 2000  
 A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals  
 A:Reference number: H81250; MUID:20150912  
 A:Accession: H81442  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-159 <PAR>  
 A:Cross-references: GB:AL139074; GB:AL111168; NID:G967505; PIDN:CAB7217.1; PID:G9696  
 C:Experimental source: serotype O2, strain NCTC 11168  
 C:Genetics:  
 A:Gene: Cj0249

Query Match 35.7%; Score 5; DB 2; Length 159;  
 Best Local Similarity 100.0%; Pred. No. 27;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHR 5



```
Db 20 AEFHR 24
|||||
RESULT 12
F81124
conserved hypothetical protein NMB1075 [imported] - Neisseria meningitidis (group B strain F81124)
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 31-Mar-2000
C:Accession: F81124
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.;
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moron, E.R.; Rappuoli, R.; V
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain Mc58.
A:Reference number: A81000; MUID:20175755
A:Accession: F81124
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-222 <TEXT>
A:Cross-references: GB:AE002458; GB:AE002098; NID:g7226311; PIDN:AAF41470.1; PID:g722631
A:Experimental source: serogroup B, strain MMD58
C:Genetics:
A:Gene: NMB1075

Query Match 35.7%; Score 5; DB 2; Length 222;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHR 5
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Db 75 AEFHR 79

RESULT 13
S09256
homeotic protein Hox D4 - chicken
N:Alternate names: homeotic protein Chox-4.2; homeotic protein Chox-a
C:Species: Gallus gallus (chicken)
C:Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 24-Jul-1997
C:Accession: S09256
R:Sasaki, H.; Yokoyama, E.; Kuroiwa, A.
Nucleic Acids Res. 18, 1739-1747, 1990
A:Title: Specific DNA binding of the two chicken deformed family homeodomain proteins,
A:Reference number: S09256; MUID:90245562
A:Accession: S09256
A:Molecule type: mRNA
A:Residues: 1-236 <SAS>
A:Cross-references: EMBL:X52671; EMBL:X52672
C:Genetics:
A:Gene: hoxd-4
C:Function:
A:Description: control of embryonic development by tissue- and stage-specific regulation
C:Superfamily: homeotic protein Hox D4; homeobox homology
C:Keywords: DNA binding; embryo; homeobox; nucleus; transcription regulation
F:146-202/Domain: homeobox homology <Hox>

Query Match 35.7%; Score 5; DB 1; Length 236;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SSMV 11
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Db 4 SSMV 8

RESULT 14
A36170
homeotic protein Hox D4 - mouse
N:Alternate names: homeotic protein Hox 4.2; homeotic protein Hox 5.1
C:Species: Mus musculus (house mouse)
C:Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 24-Jul-1997
C:Accession: A36170
R:Featherstone, M.S.; Baron, A.; Gaunt, S.J.; Mattei, M.G.; Duboule, D.
Proc. Natl. Acad. Sci. U.S.A. 85, 4760-4764, 1988
A:Title: Hox-5.1 defines a homeobox-containing gene locus on mouse chromosome 2.
A:Reference number: A36170; MUID:88263027
A:Accession: A36170
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-250 <FEA>
A:Cross-references: GB:J03770
C:Genetics:
A:Gene: Hoxd-4
A:Map position: 2
C:Function:
A:Description: control of embryonic development by tissue- and stage-specific regulat
C:Superfamily: homeotic protein Hox D4; homeobox homology
C:Keywords: DNA binding; embryo; homeobox; nucleus; transcription regulation
F:153-209/Domain: homeobox homology <Hox>

Query Match 35.7%; Score 5; DB 1; Length 250;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SSMV 11
|||||
Db 4 SSMV 8

RESULT 15
WJHU4B
homeotic protein Hox D4 - human
N:Alternate names: homeotic protein c13; homeotic protein Hox 4B; homeotic protein Ho
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 22-Jun-1999
C:Accession: S10985; A38787; A25238; S15546
R:Cianetti, L.; di Cristofaro, A.; Zappavigna, V.; Bottero, L.; Boccoli, G.; Testa, U
Nucleic Acids Res. 18, 4361-4368, 1990
A:Title: Molecular mechanisms underlying the expression of the human HOX-5.1 gene.
A:Reference number: S10985; MUID:90356367
A:Accession: S10985
A:Molecule type: DNA
A:Residues: 1-255 <CIA>
A:Cross-references: EMBL:X17360; NID:g32394; PIDN:CAA35237.1; PID:g296652
A:Accession: A38787
A:Molecule type: mRNA
A:Residues: 1-122, 'S', 124-255 <CIA2>
R:Mavilio, F.; Simeone, A.; Giampaolo, A.; Faiella, A.; Zappavigna, V.; Acampora, D.;
Nature 324, 664-668, 1986
A:Title: Differential and stage-related expression in embryonic tissues of a new huma
A:Reference number: A25238; MUID:87090377
A:Accession: A25238
A:Molecule type: mRNA
A:Residues: 1-122, 'S', 124-141, 'A', 143-255 <MAV>
A:Cross-references: EMBL:X04706; NID:g32366; PIDN:CAA28411.1; PID:g32367
R:Bocchini, E.; Acampora, D.; Pannese, M.; d'Esposito, M.; Somma, R.; Gaudino, G.;
Genome 31, 745-756, 1989
A:Title: Organization of human class I homeobox genes.
A:Reference number: S15036; MUID:90215256
A:Accession: S15036
A:Molecule type: DNA
A:Residues: 154-219 <BON>
C:Genetics:
A:Gene: GDB:HOXD4
A:Cross-references: GDB:120677; OMIM:142981
A:Map position: 2q31-2q31
A:Introns: 145/1
C:Function:
A:Description: control of embryonic development by tissue- and stage-specific regulat
C:Superfamily: homeotic protein Hox D4; homeobox homology
C:Keywords: DNA binding; embryo; homeobox; nucleus; transcription regulation
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Wed Sep 13 08:11:28 2000

F:155-211/Domain: homeobox homology <HOX>

Query Match 35.7%; Score 5; DB 1; Length 255;  
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 SSYMW 11  
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Db 4 SSYMW 8

Search completed: September 13, 2000, 02:25:55  
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 About: Results were produced by the GenCore software, version 4.5,  
 Copyright (c) 1993-2000 CompuGen Ltd.

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gb_om:BTACHE4	+	14.00	305.02	140	AF061816 Bos taurus acetylcholinesterase
gb_pr3:HUMACHE04	+	14.00	296.89	147	L22562 Human acetylcholinesterase
gb_om:OCU05036	+	14.00	287.51	1947	U05036 Oryctolagus cuniculus acetylcholinesterase
gb_ro:S50879	+	14.00	287.11	2066	S50879 Mouse mRNA for acetylcholinesterase
gb_ro:HMACHE	+	14.00	287.04	2089	X56518 Human acetylcholinesterase
gb_pr2:HUMACHE	+	14.00	286.64	2218	M5040 Human acetylcholinesterase
gb_pat:AR070205	+	14.00	286.53	2216	AR070205 Sequence 5 from patent
gb_pat:AR070207	+	14.00	284.60	3016	AR070207 Sequence 7 from patent
gb_pat:AR070206	+	14.00	284.42	3096	AR070206 Sequence 6 from patent
gb_om:AF053485	+	14.00	282.79	3958	AF053485 Felis catus acetylcholinesterase
gb_pr3:HUMACHEB	+	14.00	282.42	4195	L42812 Homo sapiens acetylcholinesterase
gb_pr3:HSFA002993	+	14.00	268.31	34221	AF002993 Homo sapiens cosmid
gb_htg29:AC011895	-	14.00	257.58	175155	AC011895 Homo sapiens chromosome
gb_ov:AF030422	+	10.00	196.67	0.0074	AF030422 Electrophorus electricus
gb_ov:TMACHE2	+	9.00	188.65	0.0207	X13172 Torpedo marmorata mRNA
gb_ov:TCACHE3A	+	9.00	180.34	0.0600	X56516 Torpedo californica acetylcholinesterase
gb_ov:TMACHE	+	9.00	179.60	0.0659	X05497 Torpedo marmorata mRNA
gb_ov:TCACER	+	9.00	179.24	0.0691	X03439 Torpedo californica mRNA
gb_ov:GGU03472	+	9.00	175.25	0.1153	U03472 Gallus gallus acetylcholinesterase
gb_pl3:AEF20204	-	7.00	136.90	15.77	AF20204 Malus domestica unkn
gb_in2:CEUK04F1	-	7.00	109.14	185.08	AF106575 Caenorhabditis elegans
gb_htg13:AC021287	+	7.00	107.70	554.92	AC021287 Homo sapiens clone
gb_htg18:AC024535	+	7.00	108.96	567.39	AC024535 Homo sapiens chromosome
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gb_htg18:AC024043	+	7.00	108.45	606.21	AC024043 Homo sapiens chromosome
gb_htg23:AC021842	+	7.00	107.83	656.32	AC021842 Homo sapiens chromosome
gb_vil:MLMTGA	+	6.00	137.41	14.76	M12274 Moloney murine leukemia virus
gb_pr2:HS285900	+	6.00	130.65	35.14	285900 H.sapiens BF2p3-Kg3-B08
gb_pr2:S65199	+	6.00	130.26	36.96	S65199 Ig kappa V3 [human, chrd
gb_vil:FIVSEQ	+	6.00	127.05	55.79	L16939 Feline immunodeficiency
gb_sts:G23571	-	6.00	126.68	58.48	G23571 human STS WI-14862, sequ
gb_in1:AF033946	+	6.00	125.10	71.63	AF033946 Bactrocera quadrisetosa
gb_sts:CSN01HKO	+	6.00	125.04	72.17	U145455 Anopheles gambiae STS
gb_pr3:HS079588	+	6.00	125.02	72.39	AL15387 Human clone OR immunoglobulin
gb_sts:CSN01OR9	-	6.00	123.99	82.59	AL15387 Anopheles gambiae STS
gb_pl2:CSN01ASJ	-	6.00	123.51	87.82	AL12511 Botrytis cinerea STS
gb_htg30:AC063337	+	6.00	123.24	90.94	AC063337 Giardia intestinalis
gb_htg31:AC066684	-	6.00	123.00	93.72	AC066684 Giardia intestinalis
gb_htg30:AC064060	+	6.00	122.41	101.08	AC064060 Giardia intestinalis

gb\_ro:AF139769 + 6.00 122.36 101.79 856 AF139769 Mus musculus type 1  
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 gb\_pl2:AU035826 - 6.00 121.32 116.33 1001 U35826 Arabidopsis thaliana  
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 gb\_in1:DME271414 - 6.00 120.89 122.93 1068 AJ271414 Drosophila melanogaster

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seq\_documentation\_block:  
 LOCUS BTACHE4 140 bp DNA 16-OCT-1998  
 DEFINITION Bos taurus acetylcholinesterase T-subunit precursor (Ache) gene,  
 exon 6 and partial cds.

ACCESSION AF061816  
 VERSION AF061816.1 GI:3746574

KEYWORDS

SEGMENT 4 of 4

SOURCE Bos taurus.

ORGANISM Bos taurus.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovinae; Bos.

REFERENCE 1 (bases 1 to 140)

AUTHORS Mendelson, I., Kronman, C., Ariel, N., Shafferman, A. and Velan, B.

TITLE Bovine acetylcholinesterase: cloning, expression and

characterization

JOURNAL Biochem. J. 334 (Pt 1), 251-259 (1998)

MEDLINE 98359754

REFERENCE 2 (bases 1 to 140)

AUTHORS Mendelson, I., Kronman, C., Ariel, N., Shafferman, A. and Velan, B.

TITLE Direct Submission

JOURNAL Submitted (28-APR-1998) Biochemistry and Molecular Genetics, Israel  
 Institute for Biological Research, PO Box 19, Ness Ziona 70450,  
 Israel

## FEATURES

Location/Qualifiers

1..140

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gene

exon

mRNA

CDS

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/gene="Ache"

/function="cholinesterase"

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ORIGIN

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US-09-155-076-1 x BTACHE4

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seq\_documentation\_block:  
LOCUS HUMACHE04 475 bp DNA PRI 14-JUN-1995  
DEFINITION Human acetylcholinesterase (ACHE) gene, exon 6.  
ACCESSION L22562  
VERSION L22562.1 GI:862302  
KEYWORDS acetylcholinesterase.  
SEGMENT 4 of 4  
SOURCE Homo sapiens DNA.  
ORGANISM Homo sapiens  
REFERENCE 1 (sites)  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Homidae; Homo.  
TITLE Molecular cloning and construction of the coding region for human  
acetylcholinesterase reveals a G + C-rich attenuating structure  
Proc. Natl. Acad. Sci. U.S.A. 87 (24), 9688-9692 (1990)  
91088577  
REFERENCE 2 (sites)  
AUTHORS Li.Y., Camp.S., Rachinsky.T.L., Getman.D. and Taylor.P.  
TITLE Gene structure of mammalian acetylcholinesterase. Alternative exons  
dictate tissue-specific expression  
J. Biol. Chem. 266 (34), 23083-23090 (1991)  
92078174  
REFERENCE 3 (bases 1 to 475)  
AUTHORS Bartels.C.F., Zelinski.T. and Lockridge.O.  
TITLE Mutation at codon 322 in the human acetylcholinesterase (ACHE) gene  
accounts for YF blood group polymorphism  
Am. J. Hum. Genet. 52 (5), 928-936 (1993)  
93256075  
COMMENT On Jun 15, 1995 this sequence version replaced gi:857448.  
\*\*Reference [1] reports bases 142-480;  
Reference [J. Biol. Chem. 266, 23083-23090 (1991)] reports bases  
132-141.  
Reference [3] reports bases 1-131\*\*.

FEATURES  
source

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Percent Similarity: 100.000 Percent Identity: 100.000

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1 AlaGluPheHisArgTrpSerTyrMetValHisTrpLys 14  
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169 GCGAGTTCACCGCTGGAGCTCCTACATGCTGCTGGAAG 210

seq\_name: gb\_om:OCU05036

seq\_documentation\_block:  
LOCUS OCU05036 1947 bp mRNA MAM 28-NOV-1994  
DEFINITION Oryctolagus cuniculus acetylcholinesterase mRNA, partial cds.  
ACCESSION U05036  
VERSION U05036.1 GI:576446  
KEYWORDS  
SOURCE Oryctolagus cuniculus.  
ORGANISM Oryctolagus cuniculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
REFERENCE 1 (bases 1 to 1947)  
AUTHORS Jbilo.O., Lhermitte.Y., Toutant.J. and Chatonnet.A.  
TITLE Acetylcholinesterase and Butyrylcholinesterase expression in adult  
rabbit tissues and during development  
Eur. J. Biochem. 225, 115-124 (1994)  
95010096  
REFERENCE 2 (bases 1 to 1947)  
AUTHORS Chatonnet.A.  
TITLE Direct Submission  
JOURNAL Submitted (13-JAN-1994) Arnaud Chatonnet, Physiologie Animale,  
Institut National de la Recherche Agronomique, Place Viala,  
Montpellier, 34060 France  
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SRGLFRAVLQSGAPGWATVGVGARRATLLARLVCPGAGGNDTELVLART  
RPAQDLVDHEWRVLPQESIFRFSFVVDGDFLSDTPEALINAGDFQGLVGVVKD  
ECYFLVYGAPGSKONESIFSAQFLAGVGVGQVQASDLAAFAVLHYTDLHPEDP  
ARLADALSDVGVHNVCPVAQAGLAAQAGARVAYVFEHRASTLSWFLMGVPHGY  
EIEFIFGLPLEPSLNTTEERIFAQLRMRYWANFARTGDPNEPRDAPQWPPYTAG  
QQVYSLNRLPELVRRGLRAQACAFWRFLPKLLSATDTLDEAFERQWKAEFHRWSSYMW  
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polyA\_signal  
polyA\_site 1933. .1938  
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ORIGIN

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alignment\_block:

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1666 GCGAGTTCACCGCTGGAGCTCCTACATGCTGCTGGAAG 1707

seq\_name: gb\_ro:S50879

seq\_documentation\_block:

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LOCUS       S50879             2066 bp      mRNA           ROD      08-MAY-1993
DEFINITION   acetylcholinesterase T subunit [rats, mRNA Partial, 2066 nt].
ACCESSION    S50879
VERSION      S50879.1  GI:262092
KEYWORDS     Rattus sp.
SOURCE       Rattus sp.
ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
              Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE    1 (bases 1 to 2066)
AUTHORS      Legay,C., Bon,S., Vernier,P., Coussen,F. and Massoulié,J.
TITLE        Cloning and expression of a rat acetylcholinesterase subunit:
              generation of multiple molecular forms and complementarity with a
              Torpedo collagenic subunit
JOURNAL      J. Neurochem. 60 (1), 337-346 (1993)
MEDLINE      93107932
REMARK       GenBank staff at the National Library of Medicine created this
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              This sequence comes from Fig. 1.
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                1..1845
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                LDVIDGRFLAQVEGAVLVSMNYRVGTGFLALPGSREAPGVNGLDQLRALQWQENI
                AAFGDPMSVTLFGESAGAAVGMHILSLPSRSLFRAVLQSGTPNGPWATVSAGEAR
                RRATLLARLVGPPGGAGNDTEILSCLTRPAQDLVDHEHVLFPQESIFRFSFPVY
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              seq_name: gb_ro:MMACHE
              seq_documentation_block:
                LOCUS       MMACHE             2089 bp      mRNA           ROD      20-JUL-1995
                DEFINITION   Mouse mRNA for acetylcholinesterase.
                ACCESSION    X56518
                VERSION      X56518.1  GI:49844
                KEYWORDS     acetylcholinesterase.
                SOURCE       house mouse.
                ORGANISM     Mus musculus
                Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
                Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              alignment_scores:
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                Ratio: 1.000      Gaps: 0
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                1 AlaGluPheHisArgTirpSerTyrMetValHisTriplys 14
                |||||
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              seq_name: gb_pr2:HUMACHE
              seq_documentation_block:
                LOCUS       HUMACHE             2218 bp      mRNA           PRI      09-JUN-1995
                DEFINITION   Human acetylcholinesterase (ACHE) mRNA, complete cds.
                ACCESSION    M55040
                VERSION      M55040.1  GI:177974
                KEYWORDS     acetylcholinesterase.
                SOURCE       Human 21-week old fetus DNA, and cDNA to mRNA.
                ORGANISM     Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                Eutheria; Primates; Catarrhini; Hominidae; Homo.
                REFERENCE    1 (bases 1 to 2218)
                AUTHORS      Soreq,H.E., Ben-Aziz,R., Prody,C.A., Seidman,S., Gnatt,A.,

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**Abstract**

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SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 3096)
AUTHORS      Soreq,H., Zakut,H. and Eckstein,F.
TITLE        Synthetic antisense oligodeoxynucleotides and pharmaceutical
              compositions containing them
JOURNAL      Patent: US 5891725-A 6 06-APR-1999;
FEATURES     Location/Qualifiers
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1 AlaGlupHeHisArgTrpSerTyrMetValHisTriPlys 14
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2755 GCGAGTTCACCGCTGAGCTCCTACATGGTGCACTGGAAG 2796

seq_name: gb_om:AF053485
seq_documentation_block:
LOCUS      AF053485      3958 bp      DNA      MAM      01-APR-1998
DEFINITION Felis catus acetylcholinesterase glycopospholipid-anchored form
            precursor (ACHE) and acetylcholinesterase collagen-tailed or
            globular form precursor (ACHE) genes, complete cds.
ACCESSION   AF053485
VERSION     AF053485.1 GI:3003019
KEYWORDS    cat.
SOURCE      Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Carnivora; Fissipedia; Felidae; Felis.
REFERENCE   1 (bases 1 to 3958)
AUTHORS     Bartels,C.F., Xie,W.-H., Miller-Lindholm,A.K. and Lockridge,O.
TITLE       Sequence and characterization of domestic cat acetylcholinesterase
            and butyrylcholinesterase
JOURNAL     Unpublished
AUTHORS     Bartels,C.F., Xie,W.-H., Miller-Lindholm,A.K. and Lockridge,O.
TITLE       Direct Submission
JOURNAL     Submitted (12-MAR-1998) Eppley Institute, University of Nebraska
            Medical Center, 600 S. 42nd St., Omaha, NE 68198-6805, USA
FEATURES    Location/Qualifiers
            1..3958
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GGDPMSTLFGESAGAAVGMHLLSPSRGLFRAVLQSGAPNGPMTATVGVGARARRA
TLARLVGCPGGAGGNDTELARTRPAQDLVDHEWHVLPQESVFRFVPVVDGD
FLSDTPALINAGDFHGLQVLGVKDEGSYFLVYGAPGSKNESLISRAQFLAGVR
VGYPQASDLAAEAVVLYHTDNLNPDPEARLRMSDVGVGHNVCYPAQLAGRLAAG
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VGYPQASDLAAEAVVLYHTDNLNPDPEARLRMSDVGVGHNVCYPAQLAGRLAAG
ARVAYLFEHRASTLSWPLMWPHGYEIEIFGLPLEPSLNTYAEERIFAQRLMRW
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BASE COUNT 723 a 1256 c 1205 g 772 t 2 others
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1 AlaGlupHeHisArgTrpSerTyrMetValHisTriPlys 14
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3817 GCAGAGTTCACCGCTGAGCTCCTACATGGTGCACTGGAAG 3858

seq_name: gb_pr3:HUMACHEB
seq_documentation_block:
LOCUS      HUMACHEB      4185 bp      DNA      PRI      23-JUN-1995
DEFINITION Homo sapiens acetylcholinesterase (ACHE) gene, exons 2-6.
ACCESSION   L42812
VERSION     L42812.1 GI:854682
KEYWORDS    acetylcholinesterase.
SOURCE      Homo sapiens DNA.
            ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (sites)
AUTHORS     Bartels,C.F., Zelinski,T. and Lockridge,O.
TITLE       Mutation at codon 322 in the human acetylcholinesterase (ACHE) gene
            accounts for YF blood group polymorphism
JOURNAL     Am. J. Hum. Genet. 52 (5), 928-936 (1993)
FEATURES    93256075
            2 (bases 1 to 4185)
            Bartels,C.F., Morlearty,P.L., Becker,R.E., Robbs,R.S.,
            Sorenson,R.C., Mountjoy,C.P. and Lockridge,O.
            Polymorphic sites in the acetylcholinesterase gene of patients with
            Alzheimer's disease

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JOURNAL Unpublished (1995)
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    /note="G00-118-746"
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    /note="G00-118-746"
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    1871
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seq\_name: gb\_pr3:HSAF002993

seq documentation\_block:  
LOCUS HSAF002993 34921 bp DNA PRI 01-JAN-1998  
DEFINITION Homo sapiens cosmid from 7q22, complete sequence.  
ACCESSION AF002993  
VERSION AF002993.1 GI:2735699  
KEYWORDS HTG.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 34921)  
Drescher,B., Rosenthal,A., Hinzmann,B. and Korner,M.  
Genomic sequencing in 7q22 revealed a novel arsenite resistance  
gene  
JOURNAL Unpublished (1997)  
REFERENCE  
2 (bases 1 to 34921)  
Drescher,B., Rosenthal,A., Hinzmann,B. and Korner,M.  
Direct Submission  
TITLE Submitted (07-MAY-1997) Genome Analysis, Institute of Molecular  
Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany  
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Location/Qualifiers  
1..34921  
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841..1011  
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Percent Similarity: 100.000 Percent Identity: 100.000

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6975 GCCGAGTTCACCGCTGAGCTCTACATGCTGCTGGAAG 6934

seq\_name: gb\_htg29:AC011895

## seq\_documentation\_block:

LOCUS AC011895 175155 bp DNA HTG 21-APR-2000  
DEFINITION Homo sapiens chromosome 7 clone RP11-126L15, WORKING DRAFT  
SEQUENCE, 3 unordered pieces.

ACCESSION AC011895

VERSION AC011895.3 GI:7630854

KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.

SOURCE human.

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 175155)

AUTHORS Waterston,R.H.

TITLE The sequence of Homo sapiens clone

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 175155)

AUTHORS Waterston,R.H.

TITLE Direct Submission

JOURNAL Submitted (15-OCT-1999) Genome Sequencing Center, Washington

University School of Medicine, 4444 Forest Park Parkway, St. Louis,

MO 63108, USA

COMMENT On Apr 21, 2000 this sequence version replaced gi:6136444.

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Ratio: 1.000 Gaps: 0  
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US-09-155-076-1 x AC011895/rev

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seq\_name: gb\_ov:AF030422

## seq\_documentation\_block:

LOCUS AF030422 4472 bp DNA VRT 20-NOV-1997  
DEFINITION Electrophorus electricus acetylcholinesterase catalytic subunit  
precursor gene, complete cds.

ACCESSION AF030422

VERSION AF030422.1 GI:2613035

KEYWORDS electric eel.

SOURCE

ORGANISM

Electrophorus electricus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;  
Neopterygii; Teleostei; Euteleostei; Ostariophysi; Gymnotiformes;  
Gymnotoidei; Electrophoridae; Electrophorus.

REFERENCE 1 (bases 1 to 4472)

AUTHORS Simon,S. and Massoulié,J.

TITLE Cloning and expression of acetylcholinesterase from Electrophorus

JOURNAL J. Biol. Chem. (1997) In press

REFERENCE 2 (bases 1 to 4472)

AUTHORS Simon,S. and Massoulié,J.

TITLE Direct Submission

JOURNAL Submitted (15-OCT-1997) Neurobiology, Ecole Normale Supérieure, 46

Rue d'Ulm, Paris 75005, France

## FEATURES

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/note="type T catalytic subunit"

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/product="acetylcholinesterase catalytic subunit

precursor"

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/db\_xref="GI:2613036"

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SKQERCTNL"

-mRNA  
Join(118..1525,1694..1886,2052..2230,3582..3703);

/product="acetylcholinesterase catalytic subunit

precursor"

Join(187..1525,1694..1886,2052..2230,3582..3700)

/note="acetylcholinesterase catalytic subunit"

## mat\_peptide

## FEATURES

Source

1..175155

/organism="Homo sapiens"

/db\_xref="taxon:9606"

\* NOTE: This is a 'working draft' sequence. It currently

\* consists of 3 contigs. The true order of the pieces

\* is not known and their order in this sequence record is

\* arbitrary. Gaps between the contigs are represented as

\* runs of N, but the exact sizes of the gaps are unknown.

\* This record will be updated with the finished sequence

\* as soon as it is available and the accession number will

\* be preserved.

\* 1 28804: contig of 28804 bp in length

\* 28805 28904: gap of unknown length

\* 28905 93340: contig of 64436 bp in length

\* 93341 93440: gap of unknown length

\* 93441 175155: contig of 81715 bp in length.

BASE COUNT 1234 a 904 c 983 g 1351 t  
ORIGIN

## alignment\_scores:

Quality: 10.00 Length: 10  
Ratio: 1.000 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

## alignment\_block:

US-09-155-076-1 x AF030422 ..

Align seg 1/1 to: AF030422 from: 1 to: 4472

1 AlaGlupHeHisArgTrpSerSerTyrMet 10

|||||  
3614 GCAGAGTTCACCGAGTGCATG 3643

seq\_name: gb\_ov:TMACHE2

seq documentation block:

LOCUS TMACHE2 605 bp mRNA VRT 14-JUL-1995  
DEFINITION Torpedo marmorata mRNA fragment for acetylcholinesterase C-term.  
(pACHE2).

ACCESSION X13172

VERSION X13172.1 GI:64416

KEYWORDS acetylcholinesterase; alternative splicing.

SOURCE marbled electric ray.

ORGANISM

Torpedo marmorata

Eukaryota; Metazoa; Chordata; Vertebrata; Chondrichthyes;

Elasmobranchii; Rajiformes; Torpedinoidei; Torpedinidae; Torpedo.

1 (bases 1 to 605)

REFERENCE

AUTHORS Sikorav, J.L., Duval, N., Anselmet, A., Bon, S., Krejci, E., Legay, C.,

Osterlund, M., Reimund, B. and Massoulie, J.

Torpedo alternative splicing of acetylcholinesterase transcripts in

Torpedo electric organ; primary structure of the precursor of the

glycolipid-anchored dimeric form

EMBO J. 7 (10), 2983-2993 (1988)

JOURNAL 89030590

MEDLINE

COMMENT See also X13173, X13174 and X05497

DATA kindly reviewed (24-May-1989) by Massoulie J.

FEATURES

Source

1..605

/organism="Torpedo marmorata"

/db\_xref="taxon:7788"

/tissue\_type="electric organ."

/clone="pACHE2"

<1..103

/note="common mRNA sequence"

<1..225

/codon\_start=1

/product="acetylcholinesterase (74 AA)"

/protein\_id="CAA31370.1"

/db\_xref="GI:64417"

/db\_xref="SWISS-PROT:P07692"

/translation="FIDLNTEPIKQRLVQMCVFVNOFLPKLNATETIDEAERQW

KTEFHWSYMMHWKQFDQYSRHENCAEL"

104..>605

/note="unique mRNA sequence of pACHE2"

127 a 228 c 117 g 133 t

BASE COUNT

ORIGIN

alignment\_scores:

Quality: 9.00 Length: 9

Ratio: 1.000 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-155-076-1 x TMACHE2 ..

Align seg 1/1 to: TMACHE2 from: 1 to: 605

2 GlupHeHisArgTrpSerSerTyrMet 10  
|||||  
139 GAGTTTCATCGGTGGAGTTCCTACATG 165

---

OM of: US-09-155-076-1 to: N\_Geneseq\_36:\* out\_format : pfs

Date: Sep 13, 2000 3:50 AM

About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

-MODEL=framet.p2n.model -DEV=xlp  
-O=/cnp2\_1/USPTO\_spool/US09155076/runat\_29082000\_092539\_16943/app\_query.fasta\_1.144  
-DB=N\_Geneseq\_36 -QFMT=fastcap -SUFFIX=ring -GAPOP=4.500  
-GAPEXT=0.050 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000  
-GAPOP=4.500 -GAPEXT=0.050 -XGAPOP=60.000 -XGAPEXT=60.000  
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=60.000 -YGAPEXT=60.000  
-DELOP=6.000 -DELEX=7.000 -START=1 -MATRIX=oligo  
-TRANS=human40.cdi -LISP=45 -DOCALIGN=200 -THR\_SCORE=quality  
-THR\_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM-ext -MINLEN=0  
-MAXLEN=100000 -USER=US09155076.ecgnl\_1\_75 -NCPU=6 -ICPU=3  
-LONGLOG -NO\_XLPXY -WAIT -THREADS=1

Search information block:

Query: US-09-155-076-1

Query length: 14

Database: N\_Geneseq\_36:\*

Database sequences: 311585

Database length: 125096042

Search time (sec): 75.910000

WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPOP=XGAPOP=60.000

WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=XGAPEXT=60.000

score\_list:

Sequence	Strd	Orig	ZScore	EScore	Len	Documentation
N_Geneseq_36:Q05999	+	14.00	275.66	9.4e-08	1800	Sequence encoding foetal human
N_Geneseq_36:Q05998	+	14.00	274.13	1.1e-07	2256	Sequence encoding human acetyl
N_Geneseq_36:Q05997	+	14.00	274.14	1.1e-07	2256	Human acetylcholinesterase (AC
N_Geneseq_36:Q05996	+	6.00	116.61	67.94	1237	Feline immunodeficiency virus
N_Geneseq_36:Q05995	+	6.00	116.01	73.38	1353	FIV gag gene, Recombinant rac
N_Geneseq_36:Q05994	+	6.00	116.01	73.38	1353	Feline immunodeficiency virus
N_Geneseq_36:Q05993	+	6.00	115.69	76.40	1418	gag gene of NCSU1 strain of fe
N_Geneseq_36:Q05992	+	6.00	114.45	89.61	1707	Human secreted protein gene 19
N_Geneseq_36:Q05991	+	6.00	109.06	178.86	3815	DNA encoding one known and fou
N_Geneseq_36:Q05990	+	6.00	109.06	178.86	3815	DNA encoding a Staphylococcus
N_Geneseq_36:Q05989	+	6.00	100.81	515.01	13059	Staphylococcus aureus contig
N_Geneseq_36:Q05988	+	6.00	100.81	515.01	13059	Continuation (5 of 6) of V3
N_Geneseq_36:Q05987	+	6.00	86.53	3.2e+03	110000	Continuation (5 of 6) of V3
N_Geneseq_36:Q05986	+	5.00	124.05	26.15	20	Sequence of PCR primer for HBV S
N_Geneseq_36:Q05985	+	5.00	122.83	30.59	24	Rat hexokinase I gene PCR primer
N_Geneseq_36:Q05984	+	5.00	122.83	30.59	24	Hexokinase PCR primer SEQ ID NO:
N_Geneseq_36:Q05983	+	5.00	122.83	30.59	24	Hexokinase PCR primer SEQ ID NO:
N_Geneseq_36:Q05982	+	5.00	122.83	30.59	24	Primer 2 used in an assay for ta
N_Geneseq_36:Q05981	+	5.00	121.12	38.11	31	Cellular apoptosis susceptibility
N_Geneseq_36:Q05980	+	5.00	118.62	52.50	45	Oligonucleotide L4 for monellin
N_Geneseq_36:Q05979	+	5.00	118.62	52.50	45	Oligonucleotide U3 for monellin
N_Geneseq_36:Q05978	+	5.00	116.36	70.10	63	Human CP2 PCR primer CME 00399.
N_Geneseq_36:Q05977	+	5.00	113.94	100.68	96	Platelet derived growth factor A
N_Geneseq_36:Q05976	+	5.00	111.59	122.84	121	Friedreich's ataxia STM7 gene
N_Geneseq_36:Q05975	+	5.00	111.99	122.84	121	EST clone CW771. New polynucle
N_Geneseq_36:Q05974	+	5.00	107.77	210.95	227	Methods for diagnosing Friedrei
N_Geneseq_36:Q05973	+	5.00	106.94	234.70	257	Human gene signature HUMG07376
N_Geneseq_36:Q05972	+	5.00	106.46	249.54	276	Human gene signature HUMG08288
N_Geneseq_36:Q05971	+	5.00	106.44	250.31	277	Human brain Expressed Sequence
N_Geneseq_36:Q05970	+	5.00	106.32	254.19	282	ORF 9 from MYM complementary s
N_Geneseq_36:Q05969	+	5.00	106.32	254.19	282	EST clone EN271. New polynucle
N_Geneseq_36:Q05968	+	5.00	106.25	256.51	285	Sequence encoding single chain
N_Geneseq_36:Q05967	+	5.00	106.25	256.51	285	Monellin single-chain analogue.
N_Geneseq_36:Q05966	+	5.00	106.25	256.51	285	Single chain form monellin anal
N_Geneseq_36:Q05965	+	5.00	106.25	256.51	285	Single-chain monellin syntheti
N_Geneseq_36:Q05964	+	5.00	106.25	256.51	285	DNA encoding single-chain form
N_Geneseq_36:Q05963	+	5.00	106.25	256.51	285	Synthetic gene encoding single
N_Geneseq_36:Q05962	+	5.00	106.25	256.51	285	Single chain monellin protein a
N_Geneseq_36:Q05961	+	5.00	106.09	261.92	292	"Fused monellin" gene. New recd

N\_Geneseq\_36:Q021454 - 5.00 106.00 265.00 296 ! Sequence of a synthetic gene  
N\_Geneseq\_36:V77456 + 5.00 105.86 289.61 302 ! Staphylococcus aureus contig  
N\_Geneseq\_36:Q061097 + 5.00 105.25 291.71 331 ! Human brain Expressed Sequence  
N\_Geneseq\_36:V27413 + 5.00 105.19 293.99 334 ! Streptococcus pneumoniae sp-  
N\_Geneseq\_36:V78736 - 5.00 105.07 298.52 340 ! Staphylococcus aureus contig  
N\_Geneseq\_36:V20283 - 5.00 104.83 307.55 352 ! Probe (184) for microbial ge

seq\_name: N\_Geneseq\_36:Q05999

seq\_documentation\_block:

ID Q05999 standard; DNA; 1800 BP.

AC Q05999;

DT 16-JAN-1991 (first entry)

DE Sequence encoding foetal human acetylcholinesterase (hACHE).

KW Organophosphorous poisoning; OP; cancer; leukaemia;

OS megakaryocytopoiesis; ovarian cancer; ds.

FN Homo sapiens.

FT cds

FT 1..1500

FT 3'utr

FT 1501..1800

FT /\*tag= a

FT /\*tag= b

PN EP-388906-A.

PD 26-SEP-1990.

PE 20-MAR-1990; 105274.

PR 21-MAR-1989; IL-089703.

PA (YISS ) YISSUM RES DEV CO.

PI Soreq H, Zakut H;

DR WPI; 90-291865/39.

DR P-PSDB; R06990.

PT Human acetylcholinesterase DNA and prodn. of recombinant hACHE -

PT for treatment of organo-phosphorous poisoning and diagnosis of haemo-

PS cytoposic disorders and ovarian carcinomas.

CC hACHE is useful as an active pharmacological component for the

CC prophylaxis and treatment of organophosphorous poisoning, and

CC post-surgical apnea due to succinylcholine administration.

CC CDNA probe to the sequence may be used in diagnosis of various

CC leukaemias, abnormal megakaryocytopoiesis and ovarian carcinomas.

CC Bases given as N are obscured in the patent specification

SQ Sequence 1800 BP; 330 A; 602 C; 539 G; 326 T;

alignment\_scores:

Quality: 14.00 Length: 14

Ratio: 1.000 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-155-076-1 x Q05999 ..

Align seg 1/1 to: Q05999 from: 1 to: 1800

1 AlaGluPHisHArgTrpSerSerTyrMetValHisTrpLys 14  
|||||  
1414 GCCGAGTTCACCGCTGGAGCTCCTACATGTCACATGGAG 1455

seq\_name: N\_Geneseq\_36:Q05998

seq\_documentation\_block:

ID Q05998 standard; DNA; 2253 BP.

AC Q05998;

DT 16-JAN-1991 (first entry)

DE Sequence encoding human acetylcholinesterase (hACHE).

KW Organophosphorous poisoning; OP; cancer; leukaemia;

OS megakaryocytopoiesis; ovarian cancer; ds.

FN Homo sapiens.

FT EP-388906-A.

PD 26-SEP-1990.

PE 20-MAR-1990; 105274.

PR 21-MAR-1989; IL-089703.

PA (YISS ) YISSUM RES DEV CO.

PI Soreq H, Zakut H;

DR WPI; 90-291865/39.

DR P-PSDB; R06989.  
PT Human acetylcholinesterase DNA and prodn. of recombinant hAChE -  
PT for treatment of organo-phosphorous poisoning and diagnosis of haemo-  
PT cytopoietic disorders and ovarian carcinomas.  
PS Claim 5; Page 25; 47pp; English.  
CC Gene product is useful as an active pharmacological component for the  
CC prophylaxis and treatment of organophosphorous poisoning, and post-  
CC surgical apnea due to succinylcholine administration.  
CC cDNA probe to the sequence may be used in diagnosis of various  
CC leukemias, abnormal megakaryocytopoiesis and ovarian carcinomas.  
SQ Sequence 2253 BP; 390 A; 740 C; 594 G; 429 T;

alignment\_scores:  
Quality: 14.00 Length: 14  
Ratio: 1.000 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-155-076-1 x Q05998

Align seg 1/1 to: Q05998 from: 1 to: 2253

1 AlaCluPheHisArgTrpSerSerTyrMetValHisTrpLys 14  
|||||  
1912 GCCGAGTTCACCGCTGGAGCTCTACATGGTGCCTGGAAG 1953

seq\_name: N\_Geneseq\_36:Q99002

seq\_documentation\_block:

ID Q99002 standard; DNA; 2256 BP.

AC Q99002;

DE 31-MAR-1996 (first entry)

DT Human acetylcholinesterase (ACHE) gene.

KW Acetylcholinesterase; acetyl cholinesterase; EC-3.1.1.7;

KW chromosome-7q22; acetylcholine-hydrolyzing enzyme; ss.

OS Homo sapiens.

FT Key Location/Qualifiers

FT cds 160..2206

FT /\*tag= a

PN W09523158-AL.

PD 31-AUG-1995.

PF 28-FEB-1995; U02806.

PR 28-FEB-1994; US-202755.

PR 09-JAN-1995; US-370156.

PA (YISS) YISSUM RES & DEV CO.

PI Shani M, Soreq H, Zakut H;

PI WPI; 95-311499/40.

DR P-PSDB; R80726.

DR Alternative forms of human acetyl cholinesterase (ChE) gene -

PT expressed in transgenic animal assay system for evaluating anti-ChE

PT activity of organo:phosphate(s), etc. or as model of ChE imbalance

PS Claim 3; Fig.1A; 55pp; English.

CC This DNA sequence encoding human acetylcholinesterase is useful

CC for producing transgenic animals which express AChE. The

CC transgenic animals are in turn useful as an assay system for

CC determining the anti-ChE activity of organophosphates, carbamates,

CC anti-ChE drugs, plant glycoalkaloids and snake venoms. This gene

CC contains a promoter region, 6 exons (E1 to E6) and 4 introns (I1-

CC I4).

SQ Sequence 2256 BP; 390 A; 757 C; 680 G; 429 T;

alignment\_scores:

Quality: 14.00 Length: 14  
Ratio: 1.000 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-155-076-1 x Q99002

Align seg 1/1 to: Q99002 from: 1 to: 2256

1 AlaCluPheHisArgTrpSerSerTyrMetValHisTrpLys 14  
|||||  
1915 GCCGAGTTCACCGCTGGAGCTCTACATGGTGCCTGGAAG 1956

seq\_name: N\_Geneseq\_36:T74084

seq\_documentation\_block:

ID T74084 standard; DNA; 1237 BP.

AC T74084;

DT 24-SEP-1997 (first entry)

DE Feline immunodeficiency virus p10 encoding DNA with deletion.

KW FIV p10; nucleocapsid; virion; vaccine; cat; ss.

OS Feline immunodeficiency virus

FT Key Location/Qualifiers

FT cds 1..1237

FT /\*tag= a

FT /product= FIV\_p10

FT /note= "With a deleted section that encodes the

FT nucleocapsid (p10) protein"

FT PN W09640953-AL.

PD 19-DEC-1996.

PF 03-JUN-1996; U08639.

PR 07-JUN-1995; US-479703.

PA (AMHP ) AMERICAN HOME PROD CORP.

PI Chavez LG, Huang C, Wasmoen T;

PI WPI; 97-065191/06.

DR P-PSDB; W23543.

DR Plasmid encoding feline immunodeficiency virus with incomplete

PT nucleocapsid p10 protein - for production of virion(s) lacking

PT packaged RNA useful in FIV vaccines

PS Claim 1; Page -; 36pp; English.

CC The present sequence encodes the feline immunodeficiency virus

CC (FIV) p10 genome, in which nucleotides encoding at least part of the

CC nucleocapsid (p10) protein have been deleted from the gag gene.

CC FIV virions which lack nucleocapsid protein p10 are used in vaccines

CC to prevent or reduce disease caused by FIV in cats. Protein p10 is

CC responsible for packaging RNA into virions, deletion of part of the

CC nucleocapsid protein will result in empty, and therefore, non-

CC infectious FIV virions.

CC N.B. The present sequence does not appear in the specification but

CC has been derived from the sequence in figure 2.

CC Sequence 1237 BP; 433 A; 216 C; 298 G; 290 T;

alignment\_scores:

Quality: 6.00 Length: 6  
Ratio: 1.000 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-155-076-1 x T74084/rev

Align seg 1/1 to reverse of: T74084 from: 1 to: 1237

3 PheHisArgTrpSerSer 8

|||||

366 TTTCATAGTGGTCTAGT 349

seq\_name: N\_Geneseq\_36:T747239

seq\_documentation\_block:

ID T47239 standard; DNA; 1353 BP.

AC T47239;

DT 06-APR-1997 (first entry)

DE FIV gag gene.

KW FIV; gag gene; env gene; racoon poxvirus; recombinant vaccine; ds.

OS Feline immunodeficiency virus strain NCSU-1.

FT Key Location/Qualifiers

FT primer\_bind complement (857..880)

FT /\*tag= a

FT /note= "5' primer binding region"

FT

```

FT primer_bind 1513..1535
FT /*tag= b
FT /note= "3' primer binding region"
PN W09640268-A1.
PD 19-DEC-1996.
PF 03-JUN-1996; U08508.
PR 07-JUN-1995; US-482090.
PA (AMHP ) AMERICAN HOME PROD CORP.
PI Chavez LG, Chu H, Wasmoen T;
DR WPI; 97-051908/05.
DR P-PSDB; W07847.
PT Recombinant raccoon poxvirus - with at least 1 internal gene
PT encoding feline immunodeficiency virus env or gag protein, useful in
PS vaccine for prophylaxis of disease
PS Claim 11; Fig 5A-C; 50pp; English.
CC The FIV gag gene (T47238) encoding the FIV gag protein (W07847) can
CC be included in recombinant raccoon poxviruses (RRPV) to provide
CC recombinant vaccines that protect felines from FIV infection. The
CC gag gene was obtd. by PCR amplification (see also T47246-47) and
CC cloned into pS11190. Vero cells were infected with wild-type RPV
CC (ATCC VR-838) and then transfected with pS111-FIV gag to obtain
CC the RRPV. Other RRPVs may include DNA sequences encoding FIV
CC env (see also T47238), envAB or immunogenic fragments of FIV env
CC and gag.
SQ Sequence 1353 BP; 480 A; 230 C; 325 G; 318 T;

alignment_scores:
Quality: 6.00 Length: 6
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-1 x T47239/rev ..
Align seg 1/1 to reverse of: T47239 from: 1 to: 1353

3 PheHisArgTrpSerSer 8
|||||
366 TTTCATAGATGGCTAGT 349

seq_name: N_Geneseq_36:T49076

seq_documentation_block:
ID T49076 standard; DNA; 1353 BP.
AC T49076;
DE 24-SEP-1997 (first entry)
DE Feline immunodeficiency virus gag gene encoding DNA.
KW FIV p10; nucleocapsid; virion; vaccine; cat; ss.
OS Feline immunodeficiency virus.
FH key Location/Qualifiers
FT cds 1..1353
FT /*tag= a
FT misc_feature 1126..1241
FT /*tag= b
FT /note= "Can delete this segment of nucleotides
FT encoding the nucleocapsid (p10) protein"
PN W09640953-A1.
PD 19-DEC-1996.
PF 03-JUN-1996; U08639.
PR 07-JUN-1995; US-479703.
PA (AMHP ) AMERICAN HOME PROD CORP.
PI Chavez LG, Huang C, Wasmoen T;
DR WPI; 97-065191/06.
DR P-PSDB; W08435.
PT Plasmid encoding feline immunodeficiency virus with incomplete
PT nucleocapsid p10 protein - for production of virion(s) lacking
PT packaged RNA useful in FIV vaccines
PS Claim 2; Fig 2; 36pp; English.
CC The present sequence encodes the feline immunodeficiency virus
CC (FIV) gag gene, which contains the nucleotides encoding the whole
CC nucleocapsid (p10) protein. In a preferred example of the FIV

```

```

CC nucleotide sequence the nucleotides encoding the nucleocapsid (p10)
CC protein (or a portion of them) are deleted from the gag gene, see
CC features table. FIV virions which lack nucleocapsid protein p10 are
CC used in vaccines to prevent or reduce disease caused by FIV in cats.
CC Protein p10 is responsible for packaging RNA into virions, deletion
CC of part of the nucleocapsid protein will result in empty, and
CC therefore, non-infectious FIV virions.
SQ Sequence 1353 BP; 479 A; 229 C; 327 G; 318 T;

alignment_scores:
Quality: 6.00 Length: 6
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-1 x T49076/rev ..
Align seg 1/1 to reverse of: T49076 from: 1 to: 1353

3 PheHisArgTrpSerSer 8
|||||
366 TTTCATAGATGGCTAGT 349

seq_name: N_Geneseq_36:Q85885

seq_documentation_block:
ID Q85885 standard; cDNA; 1418 BP.
AC Q85885;
DE 24-OCT-1995 (first entry)
DE gag gene of NCSU1 strain of feline immunodeficiency virus.
KW Feline immunodeficiency virus; FIV; CD8; antigen; vaccine;
KW diagnosis; primer; probe; acquired immune deficiency syndrome; AIDS;
KW model system; screening; long terminal repeat; LTR; ss.
OS Feline immunodeficiency virus (NCSU1 strain).
FH key Location/Qualifiers
FT cds 23..1375
FT /*tag= a
FT /product= NCSU1 FIV gag gene product.
PN W09505450-A.
PD 23-FEB-1995.
PF 25-JUL-1994; U08364.
PR 03-SEP-1991; US-752424.
PR 12-AUG-1993; US-105710.
PA (UNNC-) UNIV NORTH CAROLINA STATE.
PI Tompkins MB, Tompkins WAF;
DR WPI; 95-098760/13.
DR P-PSDB; R71479.
PT New isolate of feline immunodeficiency virus - and infected host
PT cells, DNA, vectors and infected cats, useful in vaccines and as
PT models for human AIDS
PS Example 12; Page 38-40; 50pp; English.
CC The NCSU1 strain (ATCC VR2333) of the feline immunodeficiency virus
CC (FIV) is highly infectious in vivo and causes a rapid inversion of
CC the CD4+CD8+ ratio in infected animals. Antigenic fragments of the
CC virus can be used in vaccines. Fragments of the DNA can also be used
CC diagnostically as probes and primers and for expressing viral
CC antigens. Cats infected with the virus are useful as model systems
CC for studying AIDS and for screening therapeutic drugs. Two primers
CC (Q85883, Q85884) were used to amplify the gag gene of the NCSU1
CC strain of FIV for its subcloning and subsequent sequencing.
SQ Sequence 1418 BP; 506 A; 239 C; 341 G; 332 T;

alignment_scores:
Quality: 6.00 Length: 6
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-1 x Q85885/rev ..
Align seg 1/1 to reverse of: Q85885 from: 1 to: 1418

```

wed sep 13 08:11:26 2000

us-09-155-076-1-1.rng

3 PheHisArgTrpSerSer 8  
|||||

388 TTTCATAGATGGTCTAGT 371

seq\_name: N\_Geneseq\_36.V84600

seq\_documentation\_block:

ID\_V84600 standard; DNA; 1707 BP.

AC V84600; 1999 (first entry)

DE Human secreted protein gene 190 clone HIASB53.  
KW Human; secreted protein; fusion protein; gene therapy; protein therapy;  
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;  
KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;  
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;  
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;  
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;  
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;  
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.  
OS Homo sapiens.  
PN W09854963-A2.  
PD 10-DEC-1998

PF 04-JUN-1998; U11422

PR 18-DEC-1997; US-070923.

PR 06-JUN-1997; US-048877.

PR 06-JUN-1997; US-048881.

PR 06-JUN-1997; US-048884.

PR 06-JUN-1997; US-048893.

PR 06-JUN-1997; US-048896.

PR 06-JUN-1997; US-048899.

PR 06-JUN-1997; US-048915.

PR 06-JUN-1997; US-048949.

PR 06-JUN-1997; US-048964.

PR 06-JUN-1997; US-048972.

PR 06-JUN-1997; US-049020.

PR 06-JUN-1997; US-049375.

PR 05-SEP-1997; US-057628.

PR 05-SEP-1997; US-057635.

PR 05-SEP-1997; US-057644.

PR 05-SEP-1997; US-057647.

PR 05-SEP-1997; US-057650.

PR 05-SEP-1997; US-057661.

PR 05-SEP-1997; US-057667.

PR 05-SEP-1997; US-057761.

PR 05-SEP-1997; US-057764.

PR 05-SEP-1997; US-057770.

PR 05-SEP-1997; US-057775.

PR 05-SEP-1997; US-057778.

PR 06-JUN-1997; US-048875.

PR 06-JUN-1997; US-048878.

PR 06-JUN-1997; US-048882.

PR 06-JUN-1997; US-048885.

PR 06-JUN-1997; US-048894.

PR 06-JUN-1997; US-048897.

PR 06-JUN-1997; US-048900.

PR 06-JUN-1997; US-048916.

PR 06-JUN-1997; US-048962.

PR 06-JUN-1997; US-048970.

PR 06-JUN-1997; US-048974.

PR 06-JUN-1997; US-049373.

PR 05-SEP-1997; US-057584.

PR 05-SEP-1997; US-057629.

PR 05-SEP-1997; US-057642.

PR 05-SEP-1997; US-057645.

PR 05-SEP-1997; US-057648.

PR 05-SEP-1997; US-057651.

PR 05-SEP-1997; US-057662.

PR 05-SEP-1997; US-057666.

PR 05-SEP-1997; US-057662.

PR 05-SEP-1997; US-057765.

PR 05-SEP-1997; US-057771.

PR 05-SEP-1997; US-057776.

06-JUN-1997; US-048876.  
06-JUN-1997; US-048880.  
06-JUN-1997; US-048883.  
06-JUN-1997; US-048892.  
06-JUN-1997; US-048895.  
06-JUN-1997; US-048898.  
06-JUN-1997; US-048901.  
06-JUN-1997; US-048917.  
06-JUN-1997; US-048963.  
06-JUN-1997; US-048971.  
06-JUN-1997; US-049019.  
06-JUN-1997; US-049374.  
05-SEP-1997; US-057627.  
05-SEP-1997; US-057634.  
05-SEP-1997; US-057643.  
05-SEP-1997; US-057646.  
05-SEP-1997; US-057649.  
05-SEP-1997; US-057654.  
05-SEP-1997; US-057656.  
05-SEP-1997; US-057760.  
05-SEP-1997; US-057763.  
05-SEP-1997; US-057769.  
05-SEP-1997; US-057774.  
05-SEP-1997; US-057777.  
(HUMA-) HUMAN GENOME SCI INC.  
PI Brewer LA, Carter KC, Dillon PJ, Ebner R, Endress GA,  
PI Fan P, Feng P, Ferrie AM, Fischer CL, Florence C,  
PI Florence K, Greene JM, Hu J, Kyaw H, Lafleur DW,  
PI Li Y, Moore PA, Ni J, Olsen HS, Rosen CA, Ruben SM,  
PI Shi Y, Soppet DR, Wei Y, Young P, Yu G, Zeng Z;  
DR WPI: 99-059865/05.  
DR P-PSDB; W88723, W89065, W89066, W89067, W89068, W89069, W89070, W89071,  
DR W89072.  
DR New isolated human genes and the secreted polypeptides they encode -  
PT useful for diagnosis and treatment of e.g. cancers, neurological  
PT disorders, immune diseases, inflammation or blood disorders  
PS Claim 4; Page 452-453; 772pp; English.  
CC The invention relates to nucleic acid sequences (V84411 to V84633)  
CC encoding human secreted proteins (W88534 to W88756). The secreted protein  
CC gene sequences are deposited with the ATCC under deposit numbers ATCC  
CC 97979, 97974, 97975, 97976, 97977, 209007, 209008, 209009, 209010,  
CC 209011, 209080, 209081, 209082, 209083, 209084, 209085, 209511. Host  
CC cells comprising recombinant vectors containing the nucleic acid  
CC sequences are used for the recombinant production of the secreted  
CC proteins. The polynucleotide and amino acid sequences are useful for are  
CC useful for preventing, treating or ameliorating medical conditions e.g.  
CC by protein or gene therapy. Pathological conditions can be also diagnosed  
CC by determining the amount of the new polypeptides in a sample or by  
CC determining the presence of mutations in the new polynucleotides.  
CC Specific uses are described for each of the polynucleotides, based on  
CC which tissues they are most highly expressed in, and include developing  
CC products for the diagnosis or treatment of cancer, neurodegenerative  
CC disorders, developmental abnormalities and foetal deficiencies, blood  
CC disorders, tumours, leukemias, diseases of the immune system, autoimmune  
CC diseases, hepatic and renal disease, lymphomas, inflammation, allergies,  
CC ischemic shock, Alzheimer's and cognitive disorders, schizophrenia,  
CC restenosis, prostate diseases, obesity, disorders involving osteoclasts  
CC such as osteoporosis, arthritis or malignancies, diseases of testes, lung  
CC or thymus, digestive/endocrine disorders, infections and AIDS. The  
CC polypeptides are also useful for identifying their binding partners.  
CC The present sequence represents a gene encoding a human secreted protein  
CC (see descriptor line for gene number and clone identification).  
SQ Sequence 1707 BP; 469 A; 316 C; 368 G; 552 T;

alignment\_scores:

Quality: 6.00

Ratio: 1.000

Percent Similarity: 100.000

Percent Identity: 100.000

Length: 6

Gaps: 0

alignment\_block:

US-09-155-076-1 x W84600/rev



Align seg 1/1 to reverse of: V84600 from: 1 to: 1707

6 TrpSerSerTyrMetVal 11  
 |||||  
 750 TGGTCTCTTATATGGTT 733

seq\_name: N\_Geneseq\_36.T84154

seq\_documentation\_block:  
 ID T84154 standard; DNA; 3815 BP.

AC T84154;  
 DT 07-SEP-1998 (first entry)  
 DE DNA encoding one known and four unknown Staphylococcus aureus proteins.  
 KW Staphylococcus aureus protein; ribozyme; antisense sequence; control;  
 KW Staphylococcal gene; regulatory element; bacterial gene expression;  
 KW vaccine; Staphylococcal infection; food poisoning; scaled skin syndrome;  
 KW toxic shock syndrome; ss.  
 OS Staphylococcus aureus.  
 FH Key Location/Qualifiers  
 CDS 257..934

FT /\*tag= a  
 FT /product= "Preprotein translocase SECY subunit"  
 FT 945..1280

FT CDS  
 FT /\*tag= b  
 FT /product= "Encodes protein W28243"  
 FT 1610..2362

FT CDS  
 FT /\*tag= c  
 FT /product= "Encodes protein W28244"  
 FT 3173..3364

FT CDS  
 FT /\*tag= d  
 FT /product= "Encodes protein W28245"  
 FT 3380..3559

FT CDS  
 FT /\*tag= e  
 FT /product= "Encodes protein W28246"  
 FT 3573..3764

FT WO9730070-A1.

PN 21-AUG-1997.

PD 19-FEB-1997; U02318.

PF 20-FEB-1996; US-011888.

PR (SMIK ) SMITHKLINE BEECHAM CORP.

PI Black MT, Burnham MK, Hodgson JE, Knowles DJC, Nicholas RO,

PI Pratt JM, Reichard RW, Rosenberg M, Ward JM;

PI WPI; 97-424969/39.

DR P-PSDB; W28243, W28244, W28245, W28246.

DR P-PSDB; W28242, W28243, W28244, W28245, W28246.

PT Novel polypeptide(s) from Staphylococcus aureus strain WCWU29 - used

PT to isolate antimicrobial compounds, and in vaccines against S.

PT aureus infection

PS Claim 9; Pages 915-916; 989pp; English.

CC The present sequence encodes four Staphylococcus aureus proteins of  
 CC unknown function. The sequence also encodes a Staphylococcus aureus  
 CC protein, that, based on homology with a Bacillus subtilis protein,  
 CC is believed to be a preprotein translocase SECY subunit. The present  
 CC sequence was obtained from a library of clones of S. aureus WCWU 29  
 CC in Escherichia coli. The DNA sequence can be used in the construction  
 CC of ribosomes and antisense sequences to control the expression of  
 CC Staphylococcal genes. The DNA sequence is also useful as a source of  
 CC regulatory elements for the control of bacterial gene expression. The  
 CC encoded protein may be used to produce vaccines to enable a host to  
 CC produce specific antibodies with antibacterial action. These vaccines  
 CC and antibodies would protect a host against invasion by S. aureus, and  
 CC conditions relating to Staphylococcal infection, e.g. Staphylococcal  
 CC food poisoning, scaled skin syndrome, and toxic shock syndrome.  
 SQ Sequence 3815 BP; 1267 A; 562 C; 750 G; 1199 T;

alignment\_scores:  
 Quality: 6.00 Length: 6  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-155-076-1 x T84154/rev ...

Align seg 1/1 to reverse of: T84154 from: 1 to: 3815

4 HisArgTrpSerSerTyr 9  
 |||||  
 985 CATCGTTGGTCATCGTAC 968

seq\_name: N\_Geneseq\_36.V53496

seq\_documentation\_block:

ID V53496 standard; DNA; 3815 BP.

AC V53496;  
 DT 30-OCT-1998 (first entry)

DE DNA encoding a Staphylococcus aureus protein of unknown function.  
 KW Staphylococcus aureus protein; immune response induction; eye infection;  
 KW antibody production; T-cell immune response; gastrointestinal infection;  
 KW respiratory infection; inhibitor; bacterial infection; cardiac infection;  
 KW central nervous system; kidney infection; urinary tract infection;  
 KW antimicrobial compound identification; broad spectrum antibiotic;  
 KW therapy; ss.

OS Staphylococcus aureus.

PN EP-841394-A2.

PD 13-MAY-1998.

PF 24-SEP-1997; 307485.

PR 24-SEP-1996; US-027032.

PA (SMIK ) SMITHKLINE BEECHAM CORP.

PI Black MT, Burnham MK, Hodgson JE, Knowles DJC,

PI Lonetto MA, Nicholas RO, Pratt JM, Reichard RW, Rosenberg M,

PI Ward JM;

PI WPI; 98-252940/23.

DR P-PSDB; W77704.

PT New nucleic acid sequences from Staphylococcus aureus WCWU29 -  
 PT useful in vaccines and for treatment of bacterial infections of e.g.

PT respiratory tract and central nervous system

PS Claim 1; Page 160-162; 390pp; English.

CC This sequence encodes a Staphylococcus aureus protein of unknown

CC function, and represents a DNA sequence of the invention.

CC The DNA sequences were isolated from Staphylococcus aureus WCWU29

CC (NCIMB 40771). Host cells containing the DNA sequences are used to

CC produce polypeptides or fragments. The proteins are used in the treatment

CC of disease, for inducing an immune response by administering them, to

CC produce antibody and/or T-cell immune response. Antagonists of the

CC proteins are used for the inhibition of bacterial polypeptides.

CC Conditions which may be treated include bacterial infections, especially

CC respiratory, cardiac, gastrointestinal, central nervous, eye, kidney,

CC urinary tract, skin, bones and joints. The proteins can also be used to

CC identify antimicrobial compounds which are broad spectrum antibiotics,

CC especially useful in the treatment of H. pylori infection.

SQ Sequence 3815 BP; 1267 A; 562 C; 750 G; 1199 T;

alignment\_scores:

Quality: 6.00 Length: 6  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-155-076-1 x V53496/rev ..

Align seg 1/1 to reverse of: V53496 from: 1 to: 3815

4 HisArgTrpSerSerTyr 9  
 |||||  
 985 CATCGTTGGTCATCGTAC 968

seq\_name: N\_Geneseq\_36.V74531

seq\_documentation\_block:

ID V74531 standard; DNA; 13059 BP.

AC V74531;

DT 16-MAR-1999 (first entry)

DE Staphylococcus aureus contig SEQ ID #220.

KW Computer readable medium; vaccine; S.aureus infection; immunodetection;

KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;

skin infection; surgical wound infection; scalded skin syndrome;  
toxic shock syndrome; ds.

OS Staphylococcus aureus;  
FH Location/Qualifiers  
FT misc\_feature 301..360

FT /\*tag= a  
FT /note= "these bases represent a line of missing text in  
FT the sequence listing in the specification. They  
FT are included to maintain the nucleotide numbering  
FT given in the specification for this DNA sequence"  
FT misc\_feature 2101..2160

FT /\*tag= b  
FT /note= "these bases represent a line of missing text in  
FT the sequence listing in the specification. They  
FT are included to maintain the nucleotide numbering  
FT given in the specification for this DNA sequence"  
FT misc\_feature 3901..3960

FT /\*tag= c  
FT /note= "these bases represent a line of missing text in  
FT the sequence listing in the specification. They  
FT are included to maintain the nucleotide numbering  
FT given in the specification for this DNA sequence"  
FT misc\_feature 5701..5760

FT /\*tag= d  
FT /note= "these bases represent a line of missing text in  
FT the sequence listing in the specification. They  
FT are included to maintain the nucleotide numbering  
FT given in the specification for this DNA sequence"  
FT misc\_feature 7501..7560

FT /\*tag= e  
FT /note= "these bases represent a line of missing text in  
FT the sequence listing in the specification. They  
FT are included to maintain the nucleotide numbering  
FT given in the specification for this DNA sequence"  
FT misc\_feature 9301..9360

FT /\*tag= f  
FT /note= "these bases represent a line of missing text in  
FT the sequence listing in the specification. They  
FT are included to maintain the nucleotide numbering  
FT given in the specification for this DNA sequence"  
FT misc\_feature 11101..11160

FT /\*tag= g  
FT /note= "these bases represent a line of missing text in  
FT the sequence listing in the specification. They  
FT are included to maintain the nucleotide numbering  
FT given in the specification for this DNA sequence"  
FT misc\_feature 12901..12960

FT /\*tag= h  
FT /note= "these bases represent a line of missing text in  
FT the sequence listing in the specification. They  
FT are included to maintain the nucleotide numbering  
FT given in the specification for this DNA sequence"

EP-786519-A2.

PD 30-JUL-1997.

PF 07-JAN-1997; 100117.

PR 05-JAN-1996; US-009861.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA,

PI Rosen CA;

DR WPI; 97-374922/35.

PT Polynucleotide(s) and proteins derived from Staphylococcus aureus  
PT stored on computer readable medium and used in the production of

PT anti-S aureus vaccines

PS Claim 1; Page 972-980; 3271pp; English.

CC This sequence represents one of 5191 Staphylococcus aureus DNA sequences  
CC of the invention. The DNA sequences are recorded on a computer readable  
CC medium, preferably selected from a floppy or hard disk, random access  
CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using  
CC the S aureus DNA sequences allows putative functions to be assigned so  
CC that protein-encoding or regulatory regions of commercial, therapeutic or  
CC industrial importance can be obtained. Specifically, sequences which are  
CC likely to encode antigens have been identified and these polypeptides can  
CC be used in a vaccine composition against S.aureus infection. The

CC polypeptides can also be used in a kit for the immunodetection of  
CC S.aureus in a sample. S.aureus is implicated in numerous human diseases,  
CC including cellulitis, eyelid infections, food poisoning, osteomyelitis,  
CC skin and surgical wound infections, scalded skin syndrome, toxic shock  
CC syndrome, etc. Organisms transformed with the DNA sequences can be used  
CC for recombinant production of the polypeptides. The new DNA sequences  
CC (and their fragments) are useful as primers or probes for isolating  
CC homologues of any of the S.aureus DNA sequences contained on the  
CC computer readable medium.  
SQ Sequence 13059 BP; 3881 A; 2438 C; 1860 G; 4390 T;

alignment\_scores:  
Quality: 6.00 Length: 6  
Ratio: 1.000 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
US-09-155-076-1 x V74531 ..

Align seg 1/1 to: V74531 from: 1 to: 13059

4 HisArgTrpSerSerTyr 9

|||||||

10149 CATGTTGGTCATCGTAC 10166

seq\_name: N\_Geneseq\_36:V30458\_4

seq\_documentation\_block:

Continuation (5 of 6) of V30458 from base 400001 (Rhizobium species plasmid PNGR334a.  
WP sequence split into 6 fragments LOCUS V30458 Accession V30458

WP	Fragment Name	Begin	End
WP	V30458_0	1	110000
WP	V30458_1	100001	210000
WP	V30458_2	200001	310000
WP	V30458_3	300001	410000
WP	V30458_4	400001	510000
WP	V30458_5	500001	534720

alignment\_scores:  
Quality: 6.00 Length: 6  
Ratio: 1.000 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
US-09-155-076-1 x V30458\_4/rev ..

Align seg 1/1 to reverse of: V30458\_4 from: 1 to: 110000

3 PheHisArgTrpSerSer 8

|||||||

73348 TTTCACAGGIGGCCCT 73331

seq\_name: N\_Geneseq\_36:V30459\_4

seq\_documentation\_block:

Continuation (5 of 6) of V30459 from base 400001 (Rhizobium species symbiotic plasmid  
WP sequence split into 6 fragments LOCUS V30459 Accession V30459

WP	Fragment Name	Begin	End
WP	V30459_0	1	110000
WP	V30459_1	100001	210000
WP	V30459_2	200001	310000
WP	V30459_3	300001	410000
WP	V30459_4	400001	510000
WP	V30459_5	500001	536165

alignment\_scores:  
Quality: 6.00 Length: 6  
Ratio: 1.000 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

## alignment\_block:

US-09-155-076-1 x V30459\_4/rev ..

Align seg 1/1 to reverse of: V30459\_4 from: 1 to: 110000

3 PheHisArgTyrSerSer 8

|||||

73348 TTTCACAGGTGGTCTCT 73331

seq\_name: N\_Geneseq\_36:Q67988

## seq\_documentation\_block:

ID Q67988 standard; DNA; 20 BP.

AC Q67988; 1995 (first entry)

DE Sequence of PCR primer for HBV S-region.

KW Core antigen; recombinant replicable vaccinia virus; hepatitis;

KW prevention; therapy; epitope; hepatitis B virus; PCR primer; ss.

OS Synthetic.

PN W09412617-A.

PD 09-JUN-1994.

PF 24-NOV-1993; U11474.

PR 25-NOV-1992; US-982211.

PA (TBI-) INT BIO TECHNOLOGY LAB INC.

PI Bernstein EG, Lewis T, Okeefe RW, Souw PTS;

DR WFI; 94-200247/24.

PT Prevention and treatment of hepatitis - using recombinant

PT replicable vaccinia viruses contg. hepatitis B virus surface and

PT core antigen nucleotide sequences

PS Example; Page 76; 252pp; English.

CC A construct was made consisting from the amino terminus of

CC AA residues 1-144 of core, a 1 AA spacer (D), AAS 107-163

CC of the S antigen, and a 7 AA tail (NSGLLVK). This fusion

CC polypeptide is referred to a core-S\* because only a small

CC portion of the S antigen is present. A 197 bp piece of the S

CC region containing the immunogenic regions was generated by PCR

CC of pLEH-04 using primer Q67987 which hybridises from bases

CC +304 to +323 of the S region and is designed to introduce

CC a BspBI site. A second primer was Q67988 which hybridises to the

CC opposite strand from bps +500 to +481 of the S region and is designed to

CC create an EcoRI site upon amplification. The sequences of the

CC core-S\* fusion in the resulting plasmid, pHTL-28, are given in

CC Q67971 and R55288.

SQ Sequence 20 BP; 5 A; 4 C; 6 G; 5 T;

## alignment\_scores:

Quality:	5.00	Length:	5
Ratio:	1.000	Gaps:	0
Percent Similarity:	100.000	Percent Identity:	100.000

## alignment\_block:

US-09-155-076-1 x Q67988 ..

Align seg 1/1 to: Q67988 from: 1 to: 20

1 AlaGluPheHisArg 5

|||||

5 GCCGAATTCATAGG 19

seq\_name: N\_Geneseq\_36:T75042

## seq\_documentation\_block:

ID T75042 standard; DNA; 24 BP.

AC T75042;

DE 02-FEB-1998 (first entry)

DE Rat hexokinase I gene PCR primer.

KW Recombinant protein; expression; secretory cell line; RIN;

KW insulinoma; hexokinase I; insulin; diabetes; gene therapy; primer;

KW PCR; polymerase chain reaction; rat; ss.

OS Synthetic.

OS Rattus sp.

PN W09726321-A2.

PD 24-JUL-1997. U00761.

PF 17-JAN-1997; US-028427.

PR 15-OCT-1996; US-589028.

PR 19-JAN-1996; US-589028.

PA (BETA-) BETAGENE INC.

PA (TEXA ) UNIV TEXAS SYSTEM.

PI Clark SA, Halban PA, Kruse F, McGarry D, Newgard CB;

PI Northington KD, Quaade C, Thigpen AE;

DR WFI; 97-385326/35.

PT Recombinant cell engineered to provide amylin to a mammal - useful

PT to treat e.g. angiogenesis, anorexia, obesity, hypertension,

PT osteoporosis etc.

PS Example 1; Page 132; 336pp; English.

CC This primer is located in the rat hexokinase I (HKI) gene

CC downstream of a putative recombination site. It was used with a

CC primer (see T75041) located upstream of the recombination site

CC in a control PCR to detect homologous and random integrants of a

CC HKI gene replacement vector following electroporation of rat RIN

CC insulinoma cells. Interference with HKI function reduces the

CC growth rate of cells and may allow the development of engineered

CC cells that exhibit glucose-regulatable insulin secretion. The

CC invention provides methods for production of heterologous

CC polypeptides, e.g. amylin, using recombinantly engineered cell

CC lines. Also described are methods of engineering cells for high

CC level expression, methods of large-scale heterologous protein

CC production, methods for treatment of disease in vivo using viral

CC delivery systems and recombinant cell lines, and methods for

CC isolating novel amylin receptors.

SQ Sequence 24 BP; 4 A; 6 C; 6 G; 8 T;

## alignment\_scores:

Quality:	5.00	Length:	5
Ratio:	1.000	Gaps:	0
Percent Similarity:	100.000	Percent Identity:	100.000

## alignment\_block:

US-09-155-076-1 x T75042 ..

Align seg 1/1 to: T75042 from: 1 to: 24

7 SerSerTyrMetVal 11

|||||

5 AGCTCTTACATGGTG 19





```
;
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTICHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reising, Ethington, Barnard & Perry
; STREET: P.O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: US
; ZIP: 48099
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/370,156
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: P-307 (Mulford)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 689-3500
; TELEFAX: (810) 689-4071
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1215 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..78
;
US-08-370-156-26

alignment_scores:
    Quality: 14.00      Length: 14
    Ratio: 1.000        Gaps: 0
    Percent Similarity: 100.000    Percent Identity: 100.000

alignment_block:
US-09-155-076-1 x US-08-370-156-26 ..

Align seg 1/1 to: US-08-370-156-26 from: 1 to: 1215

1 AlaGlupHeHisArgTrpSerSeryrMetValHisTrpLys 14
|||||
874 GCCGAGTTCACCGTGGAGCTCTACATGTTGCTGCACTGGAAG 915

seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-07-732-962A-1

seq_documentation_block:
; Sequence 1, Application US/07732962A
; Patent No. 5248604
; GENERAL INFORMATION:
; APPLICANT: Fischer, Meir
; TITLE OF INVENTION: EXPRESSION OF ENZYMATICALLY ACTIVE
; TITLE OF INVENTION: RECOMBINANT HUMAN ACETYLCHOLINESTERASE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White, Esq.
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06106
; FILING DATE: 19920722
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 39304-B-PCT/JPW/EAB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
```

```
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/732,962A
; FILING DATE: 19910722
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 39304/JPW/LSW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1845 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1842
;
US-07-732-962A-1

alignment_scores:
    Quality: 14.00      Length: 14
    Ratio: 1.000        Gaps: 0
    Percent Similarity: 100.000    Percent Identity: 100.000

alignment_block:
US-09-155-076-1 x US-07-732-962A-1 ..

Align seg 1/1 to: US-07-732-962A-1 from: 1 to: 1845

1 AlaGlupHeHisArgTrpSerSeryrMetValHisTrpLys 14
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1756 GCCGAGTTCACCGTGGAGCTCTACATGTTGCTGCACTGGAAG 1797

seq_name: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US92-06106-1

seq_documentation_block:
; Sequence 1, Application PC/TUS9206106
; GENERAL INFORMATION:
; APPLICANT: Fischer, Meir
; TITLE OF INVENTION: ENZYMATICALLY ACTIVE RECOMBINANT HUMAN
; TITLE OF INVENTION: ACETYLCHOLINESTERASE AND USES THEREOF
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White, Esq.
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06106
; FILING DATE: 19920722
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 39304-B-PCT/JPW/EAB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
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; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1845 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1842
;
PCT-US92-06106-1

alignment_scores:
  Quality: 14.00 Length: 14
  Ratio: 1.000 Gaps: 0
  Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-1 x PCT-US92-06106-1 ..
Align seg 1/1 to: PCT-US92-06106-1 from: 1 to: 1845

1 AlaGluPheHisArgTrpSerSerTyrMetValHisTrpLys 14
1756 GCCGAGTTCACCGCTGGAGCTCTACATGTCGACTGGAAG 1797

seq_name: /cgn2_6/ptodata/2/ina/5C_COMB.seq:US-08-318-826A-5

seq_documentation_block:
; Sequence 5, Application US/08318826A
; Patent No. 5891725
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Eckstein, Fritz
; TITLE OF INVENTION: Synthetic Antisense
; TITLE OF INVENTION: Oligodeoxynucleotides and Pharmaceutical Compositions
; TITLE OF INVENTION: Containing Them
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kohn & Associates
; STREET: 30500 No. 5891725thwestern Hwy., Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: US
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,826A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: 2391.00001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2256 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
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; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: /note= "Splice variant: Exons 1, 2,
; OTHER INFORMATION: 3, 4 and 6"
;
US-08-318-826A-5

alignment_scores:
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  Ratio: 1.000 Gaps: 0
  Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-1 x US-08-318-826A-5 ..
Align seg 1/1 to: US-08-318-826A-5 from: 1 to: 2256

1 AlaGluPheHisArgTrpSerSerTyrMetValHisTrpLys 14
1915 GCCGAGTTCACCGCTGGAGCTCTACATGTCGACTGGAAG 1956

seq_name: /cgn2_6/ptodata/2/ina/5D_COMB.seq:US-08-370-156-1

seq_documentation_block:
; Sequence 1, Application US/08370156
; Patent No. 5932780
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTICHLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reising, Ethington, Barnard & Perry
; STREET: P.O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: US
; ZIP: 48099
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/370,156
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: P-307 (Mulford)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 689-3500
; TELEFAX: (810) 689-4071
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2256 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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US-08-370-156-1

alignment_scores:
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  Ratio: 1.000 Gaps: 0
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alignment_block:
US-09-155-076-1 x US-08-370-156-1 ..
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Align seg 1/1 to: US-08-370-156-1 from: 1 to: 2256
1 AlaGluPheHisArgTrpSerSertyrMetValHisTrpLys 14
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seq_name: /cgn2_6/ptodata/2/ina/6_COMB.seq:US-08-814-095-1

seq_documentation_block:
; Sequence 1, Application US/08814095
; Patent No. 6025183
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Eckstein, Fritz
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KOHN & ASSOCIATES
; STREET: 30500 No. 6025183thwestern Highway, Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: U.S.
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/814,095
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Montgomery, Ilene N.
; REGISTRATION NUMBER: 38,972
; REFERENCE/DOCKET NUMBER: 2391.00066
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2256 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "ACHE gene comprising exons
; DESCRIPTION: 2, 3, 4 and 6"
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-814-095-1

alignment_scores:
Quality: 14.00 Length: 14
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-1 x US-08-814-095-1 ..
Align seg 1/1 to: US-08-814-095-1 from: 1 to: 2256
1 AlaGluPheHisArgTrpSerSertyrMetValHisTrpLys 14
|||||
1915 GCCGAGTTCACCGCTGGAGCTCTACATGGTGCACTGGAAG 1956
seq_name: /cgn2_6/ptodata/2/ina/5C_COMB.seq:US-08-318-826A-7
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seq_documentation_block:
; Sequence 7, Application US/08318826A
; Patent No. 5891725
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Eckstein, Fritz
; TITLE OF INVENTION: Synthetic Antisense
; TITLE OF INVENTION: Oligodeoxynucleotides and Pharmaceutical Compositions
; TITLE OF INVENTION: Containing Them
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kohn & Associates
; STREET: 30500 No. 5891725thwestern Hwy., Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: US
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,826A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: 2391.00001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3016 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 160..2010
; OTHER INFORMATION: /note= "Splice Variant: Exons 1, 2,
; OTHER INFORMATION: 3, 4, 5 and 6"
; US-08-318-826A-7

alignment_scores:
Quality: 14.00 Length: 14
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-1 x US-08-318-826A-7 ..
Align seg 1/1 to: US-08-318-826A-7 from: 1 to: 3016
1 AlaGluPheHisArgTrpSerSertyrMetValHisTrpLys 14
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2675 GCCGAGTTCACCGCTGGAGCTCTACATGGTGCACTGGAAG 2716
seq_name: /cgn2_6/ptodata/2/ina/5D_COMB.seq:US-08-370-156-5

seq_documentation_block:
; Sequence 5, Application US/08370156
; Patent No. 5932780
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; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTICHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reising, Ethington, Barnard & Perry
; STREET: P.O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: US
; ZIP: 48099
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/370,156
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: P-307 (Mulford)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 689-3500
; TELEFAX: (810) 689-4071
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3016 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 160..2010
;
US-08-370-156-5

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  Ratio: 1.000      Gaps: 0
  Percent Similarity: 100.000      Percent Identity: 100.000

alignment_block:
US-09-155-076-1 x US-08-370-156-5  ..
  Align seg 1/1 to: US-08-370-156-5 from: 1 to: 3016

1 AlaGluPheHisArgTrpSerSerTyrMetValHisTrpLys 14
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2675 GCCGAGTTCACCGCTGAGCTCTACATGTCGACTGGAAG 2716

seq_name: /cgn2_6/ptodata/2/ina/6_COMB.seq:US-08-814-095-5

seq_documentation_block:
; Sequence 5, Application US/08814095
; Patent No. 6025183
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KOHN & ASSOCIATES
; STREET: 30500 No. 6025183thwestern Highway, Suite 410
; CITY: Farmington Hills
; STATE: Michigan

```

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; COUNTRY: U.S.
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/814,095
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Montgomery, Ilene N.
; REGISTRATION NUMBER: 38,972
; REFERENCE/DOCKET NUMBER: 2391.00066
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3016 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Alternatively spliced Ache
; DESCRIPTION: comprising exons 2, 3, 4, 5 and 6"
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 160..2010
;
US-08-814-095-5

alignment_scores:
  Quality: 14.00      Length: 14
  Ratio: 1.000      Gaps: 0
  Percent Similarity: 100.000      Percent Identity: 100.000

alignment_block:
US-09-155-076-1 x US-08-814-095-5  ..
  Align seg 1/1 to: US-08-814-095-5 from: 1 to: 3016

1 AlaGluPheHisArgTrpSerSerTyrMetValHisTrpLys 14
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2675 GCCGAGTTCACCGCTGAGCTCTACATGTCGACTGGAAG 2716

seq_name: /cgn2_6/ptodata/2/ina/5C_COMB.seq:US-08-318-826A-6

seq_documentation_block:
; Sequence 6, Application US/08318826A
; Patent No. 5891725
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Eckstein, Fritz
; TITLE OF INVENTION: Synthetic Antisense
; TITLE OF INVENTION: Oligodeoxynucleotides and Pharmaceutical Compositions
; TITLE OF INVENTION: Containing Them
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kohn & Associates
; STREET: 30500 No. 5891725thwestern Hwy., Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: US
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/318.826A

## FILING DATE:

CLASSIFICATION: 514

## ATTORNEY/AGENT INFORMATION:

NAME: Kohn, Kenneth I.

REGISTRATION NUMBER: 30,955

REFERENCE/DOCKET NUMBER: 2391.00001

TELEPHONE: (248) 539-5050

TELEFAX: (248) 539-5055

INFORMATION FOR SEQ ID NO: 6:

## SEQUENCE CHARACTERISTICS:

LENGTH: 3096 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: 160..1959

OTHER INFORMATION: /note= "Splice variant: Exons 1, 2,

OTHER INFORMATION: 3, 4, 5 and the translated portion of Intron 4 (readthrough)"

US-08-318-826A-6

## alignment\_scores:

Quality: 14.00

Ratio: 1.000

Percent Similarity: 100.000

Length: 14

Gaps: 0

Percent Identity: 100.000

## alignment\_block:

US-09-155-076-1 x US-08-318-826A-6

Align seg 1/1 to: US-08-318-826A-6 from: 1 to: 3096

1 AlaGlupHeHisArgTrpSerTyrMetValHisTrpLys 14  
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2755 GCGGAGTTCACCGTGGAGCTCTACATGGTGCACTGGAAG 2796

seq\_name: /cgn2\_6/ptodata/2/ina/5D\_COMB.seq:US-08-370-156-3

## seq\_documentation\_block:

Sequence 3, Application US/08370156

Patent No. 5932780

## GENERAL INFORMATION:

APPLICANT: Soreq, Hermona

APPLICANT: Zakut, Haim

APPLICANT: Shani, Moshe

TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR

OPERATING SYSTEM: PC-DOS/MS-DOS

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: Reising, Ethington, Barnard &amp; Perry

STREET: P.O. Box 4390

CITY: Troy

STATE: Michigan

COUNTRY: US

ZIP: 48099

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/370,156

FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:  
NAME: Kohn, Kenneth I.  
REGISTRATION NUMBER: 30,955  
REFERENCE/DOCKET NUMBER: P-307 (Mulford)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (810) 689-3500  
TELEFAX: (810) 689-4071

INFORMATION FOR SEQ ID NO: 3:

## SEQUENCE CHARACTERISTICS:

LENGTH: 3096 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

NAME/KEY: CDS

LOCATION: 160..1959

US-08-370-156-3

## alignment\_scores:

Quality: 14.00

Ratio: 1.000

Percent Similarity: 100.000

Length: 14

Gaps: 0

Percent Identity: 100.000

## alignment\_block:

US-09-155-076-1 x US-08-370-156-3

Align seg 1/1 to: US-08-370-156-3 from: 1 to: 3096

1 AlaGlupHeHisArgTrpSerTyrMetValHisTrpLys 14  
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2755 GCGGAGTTCACCGTGGAGCTCTACATGGTGCACTGGAAG 2796

seq\_name: /cgn2\_6/ptodata/2/ina/6\_COMB.seq:US-08-814-095-3

## seq\_documentation\_block:

Sequence 3, Application US/08814095

Patent No. 6025183

## GENERAL INFORMATION:

APPLICANT: Soreq, Hermona

APPLICANT: Zakut, Haim

APPLICANT: Shani, Moshe

TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR

OPERATING SYSTEM: PC-DOS/MS-DOS

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: KOHN &amp; ASSOCIATES

STREET: 30500 No. 6025183thwestern Highway, Suite 410

CITY: Farmington Hills

STATE: Michigan

COUNTRY: U.S.

ZIP: 48334

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/814,095

FILING DATE:

CLASSIFICATION: 800

## ATTORNEY/AGENT INFORMATION:

NAME: Montgomery, Ilene N.

REGISTRATION NUMBER: 38,972

REFERENCE/DOCKET NUMBER: 2391.00066

TELECOMMUNICATION INFORMATION:

TELEPHONE: (248) 539-5050

TELEFAX: (248) 539-5055

INFORMATION FOR SEQ ID NO: 3:

## SEQUENCE CHARACTERISTICS:

LENGTH: 3096 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

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;; TOPOLOGY: linear
;; MOLECULE TYPE: other nucleic acid
;; DESCRIPTION: /desc = "Alternatively spliced Ache
;; DESCRIPTION: comprising exons 2, 3, 4 and 5 as well as the translated portion
;; DESCRIPTION: of Intron 4 (readthrough)"
;; ORIGINAL SOURCE:
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 160..1959
US-08-814-095-3

alignment_scores:
  Quality: 14.00 Length: 14
  Ratio: 1.000 Gaps: 0
  Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-1 x US-08-814-095-3 ..
Align seg 1/1 to: US-08-814-095-3 from: 1 to: 3096
1 AlaGluPheHisArgTrpSerSerTyrMetValHisIrrpLys 14
|||||
2755 GCCGAGTCCACCGCTGGAGCTCTACATGCTGCACGTGAAG 2796

seq_name: /cgn2_5/ptodata/2/lna/6_COMB.seq:US-08-814-095-7
seq_documentation_block:
; Sequence 7, Application US/08814095
; Patent No. 6025183
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KOHN & ASSOCIATES
; STREET: 30500 No. 6025183thwestern Highway, Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: U.S.
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/814,095
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Montgomery, Ilene N
; REGISTRATION NUMBER: 38,972
; REFERENCE/DOCKET NUMBER: 2391.00066
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35060 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
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; DESCRIPTION: promoter, Ache gene and Ars gene"
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

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; ORGANISM: Homo sapiens
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; CHROMOSOME/SEGMENT: 7q22
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; OTHER INFORMATION: /standard_name= "ACHE Promotor"
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; FEATURE:
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Gaps: 0
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; Sequence 13, Application US/08482090
; Patent No. 5820869
; GENERAL INFORMATION:
; APPLICANT: Wasmoen, Terri
; APPLICANT: Chu, Hsien-Jue
; APPLICANT: Chavez, Lloyd
; TITLE OF INVENTION: Recombinant Raccoon Pox Viruses and
; TITLE OF INVENTION: Their use as an Effective Vaccine Against Feline
; TITLE OF INVENTION: Immunodeficiency Virus Infection
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,090
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Schaffer, Robert
; REGISTRATION NUMBER: 31,194
; REFERENCE/DOCKET NUMBER: 0632/0B170
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)527-7700
; TELEFAX: (212)753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1353 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: feline immunodeficiency virus
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; MAP POSITION: 1-1353
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366 TTTCATAGATGGTCTAGT 349



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model  
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40.584 Million cell updates/sec

Title: US-09-155-076-1  
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Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 85661 seqs, 30989116 residues

Word size : 0

Total number of hits satisfying chosen parameters: 85661

Minimum DB seq length: 0  
Maximum DB seq length: 1000000

Post-processing: Listing first 45 summaries

Database : SwissProt\_38:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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2	14	100.0	584	1 ACES_RABIT	Q29499 oryctolagus
3	14	100.0	614	1 ACES_HUMAN	P22303 homo sapien
4	14	100.0	614	1 ACES_MOUSE	P21836 mus musculu
5	14	100.0	614	1 ACES_RAT	P37136 rattus norv
6	9	64.3	767	1 ACES_CHICK	P36196 gallus gall
7	6	42.9	330	1 PMTL_SCHPO	P40999 schizosacch
8	5	35.7	235	1 HXD4_CHICK	P17278 gallus gall
9	5	35.7	236	1 HXD4_BRARE	Q57374 brachydanio
10	5	35.7	250	1 HXD4_MOUSE	P10628 mus musculu
11	5	35.7	255	1 HXD4_HUMAN	P09016 homo sapien
12	5	35.7	282	1 YXJB_BACSV	P42313 bacillus su
13	5	35.7	408	1 YFNP_ECOLI	P46139 escherichia
14	5	35.7	427	1 PEPB_ECOLI	P37095 escherichia
15	5	35.7	444	1 NU4M_LOGMI	Q36424 locusta mig
16	5	35.7	444	1 YODT_BACSV	Q34662 bacillus su
17	5	35.7	486	1 PHOQ_ECOLI	P23837 escherichia
18	5	35.7	538	1 TPPL_MOUSE	Q89023 mus musculu
19	5	35.7	603	1 CHLE_MOUSE	Q03311 mus musculu
20	5	35.7	619	1 YAL6_CHLPN	Q26633 chlamydia p
21	5	35.7	919	1 AMY_STRLI	Q05884 streptomyce
22	5	35.7	1018	1 YKZ6_CAEEL	P34333 caenorhabdi
23	5	35.7	1886	1 GP21_RAT	P11654 rattus norv
24	4	28.6	21	1 RL5_HALME	P50557 halobacteri
25	4	28.6	58	1 RL30_HAEIN	P44366 haemophilus
26	4	28.6	59	1 RL30_ACYKS	P46184 acyrtosiph
27	4	28.6	82	1 YHYD_ANACY	P16420 anabaena cy
28	4	28.6	95	1 FER1_DUNSA	P00239 drosaliella
29	4	28.6	97	1 NHPI_BABBO	P40632 babesia bov
30	4	28.6	101	1 CYAY_HAEIN	P1358 haemophilus
31	4	28.6	101	1 Y53_BPT3	P20327 bacterioph
32	4	28.6	106	1 CYAY_ECOLI	P27838 escherichia
33	4	28.6	106	1 FER_MYCSM	P00215 mycobacteri

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AC P23795;  
DT 01-NOV-1991 (Rel. 20, Created)  
DT 01-NOV-1991 (Rel. 20, last sequence update)  
DT 01-OCT-1996 (Rel. 34, last annotation update)  
DE ACETYLCHOLINESTERASE (EC 3.1.1.7).  
GN ACHE.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
RN [1]  
RP SEQUENCE.  
RC TISSUE=FETAL SERUM;  
RX MEDLINE; 90306335.  
RA Doctor B.P., Chapman T.C., Christner C.E., Deal C.D., de la Hoz D.M.,  
RA Gentry M.K., Ogert R.A., Rush R.S., Smyth K.K., Wolfe A.D.;  
RA "Complete amino acid sequence of fetal bovine serum  
RT acetylcholinesterase and its comparison in various regions with other  
RT cholinesterases.";  
RL FEBS Lett. 266:123-127(1990).  
CC -!- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.  
CC -!- CATALYTIC ACTIVITY: ACETYLCHOLINE + H(2)O -> CHOLINE + ACETATE.  
CC -!- SUBUNIT: OLIGOMER COMPOSED OF DISULFIDE-LINKED HOMODIMERS.  
CC -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
DR PIR: S10712; S10712.  
DR PIR: P22303; 2CLJ.  
DR HSP; P22303; Coesterase; 1.  
DR PFAM; PF00135; CHOLNESTRASE.  
DR PRINTS; PR00878; CHOLNESTRASE.  
DR PROSITE; PS00122; CARBOXYLESTERASE\_B\_1; 1.  
DR PROSITE; PS00941; CARBOXYLESTERASE\_B\_2; 1.  
DR Hydrolase; Serine esterase; Synapse; Membrane; Nerve; Muscle;  
KW Neurotransmitter degradation; Glycoprotein.  
FT ACT\_SITE 203 203 BY SIMILARITY.  
FT ACT\_SITE 334 334 BY SIMILARITY.  
FT ACT\_SITE 447 447 BY SIMILARITY.  
FT DISULFID 69 96 BY SIMILARITY.  
FT DISULFID 257 272 BY SIMILARITY.  
FT DISULFID 409 529 BY SIMILARITY.  
FT DISULFID 580 580 INTERCHAIN (BY SIMILARITY).  
FT CARBOHYD 61 61 POTENTIAL.  
FT CARBOHYD 265 265 POTENTIAL.  
FT CARBOHYD 350 350 POTENTIAL.  
FT CARBOHYD 464 464 POTENTIAL.  
FT CARBOHYD 541 541 POTENTIAL.  
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P44266 haemophilus  
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P04945 mus musculu  
P41249 actinomycet  
P81116 trimeresuru  
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P15068 escherichia  
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Db 555 AEFHRSSYVHWK 568

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AC Q29499;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7) (FRAGMENT).
GN ACHE.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=MUSCLE;
RX MEDLINE; 95010096.
RA Jbilo O., Lhermite Y., Toutant J., Chatonnet A.;
RT "Acetylcholinesterase and butyrylcholinesterase expression in adult
RT rabbit tissues and during development.";
RL Eur. J. Biochem. 225:115-124(1994).
CC -|- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.
CC -|- CATALYTIC ACTIVITY: ACETYLCHOLINE + H(2)O = CHOLINE + ACETATE.
CC -|- SUBUNIT: OLIGOMER COMPOSED OF DISULFIDE-LINKED HOMODIMERS.
CC -|- MISCELLANEOUS: SYNAPSES USUALLY CONTAIN ASYMMETRIC MOLECULES OF
CC CHOLINESTERASE, WITH A COLLAGEN-LIKE PART DISULFIDE-BONDED TO THE
CC CATALYTIC PART. A DIFFERENT, GLOBULAR TYPE OF CHOLINESTERASE
CC OCCURS ON THE OUTER SURFACES OF CELL MEMBRANES, INCLUDING THOSE OF
CC ERYTHROCYTES.
CC -|- MISCELLANEOUS: THIS IS THE CATALYTIC SUBUNIT OF AN ASYMMETRIC OR
CC SOLUBLE FORM OF ACHE.
CC -|- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
CC EMBL; U05036; AAA53235.1; -.
CC HSP; P22303; 2CLT.
CC PFAM; PF00135; Coesterase; 1.
CC PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
CC PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
CC Hydrolase; Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal;
CC Neurotransmitter degradation; Glycoprotein.
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CC SIGNAL <1 1
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CC ACT_SITE 448 448
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CC CARBOHYD 351 351
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CC SEQUENCE 584 AA; 64630 MW; 2AE157F3063649FE CRC64;
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Db 556 AEFHRSSYVHWK 569
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AC P22303;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7).
GN ACHE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91088577.
RA Soreq H., Ben-Aziz R., Prody C.A., Seidman S., Ghatt A., Neville L.,
RA Lieman-Hurwitz J., Lev-Lehman E., Ginzberg D., Lipidot-Lifson Y.,
RA Zakut H.;
RT "Molecular cloning and construction of the coding region for human
RT acetylcholinesterase reveals a G + C-rich attenuating structure.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:9688-9692(1990).
RN [2]
RP PARTIAL SEQUENCE.
RC TISSUE=ERYTHROCYTE;
RX MEDLINE; 89232136.
RA Chhalani V., Derr D., Earles B., Schmell E., August T.;
RT "Purification and partial amino acid sequence analysis of human
RT erythrocyte acetylcholinesterase.";
RL FEBS Lett. 247:279-282(1989).
RN [3]
RP MUTAGENESIS OF CYS-611.
RX MEDLINE; 92084699.
RA Velan B., Grosfeld H., Kromman C., Leitner M., Gozes Y., Lazar A.,
RA Flashner Y., Marcus D., Cohen S., Shafferman A.;
RT "The effect of elimination of intersubunit disulfide bonds on the
RT activity, assembly, and secretion of recombinant human
RT acetylcholinesterase. Expression of acetylcholinesterase Cys-580-->Ala
RT mutant.";
RL J. Biol. Chem. 266:23977-23984(1991).
RN [4]
RP MUTAGENESIS OF ACTIVE SITE RESIDUES AND OF ASP-206 AND ASP-435.
RX MEDLINE; 92388112.
RA Shafferman A., Kromman C., Flashner Y., Leitner M., Grosfeld H.,
RA Ordentlich A., Gozes Y., Cohen S., Ariel N., Barak D.;
RT "Mutagenesis of human acetylcholinesterase. Identification of
RT residues involved in catalytic activity and in polypeptide folding.";
RL J. Biol. Chem. 267:17640-17648(1992).
RN [5]
RP VARIANT BLOOD GROUP YT(B).
RX MEDLINE; 93256075.
RA Bartels C.F., Zelinski T., Lockridge O.;
RT "Mutation at codon 322 in the human acetylcholinesterase (ACHE) gene
RT accounts for YT blood group polymorphism.";
RL Am. J. Hum. Genet. 52:928-936(1993).
CC -|- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.
CC -|- CATALYTIC ACTIVITY: ACETYLCHOLINE + H(2)O = CHOLINE + ACETATE.
CC -|- SUBUNIT: OLIGOMER COMPOSED OF DISULFIDE-LINKED HOMODIMERS.
CC -|- POLYMORPHISM: ACHE IS RESPONSIBLE FOR THE YT BLOOD GROUP SYSTEM.
CC THE MOLECULAR BASIS OF THE YT(A)-YT(B)/YT(B)-YT2 BLOOD GROUP
CC ANTIGENS IS A SINGLE VARIATION IN POSITION 353; HIS-353
CC CORRESPONDS TO YT(A) AND THE RARE VARIANT WITH ASN-353 TO YT(B).
CC -|- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
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DR EMBL; M55040; AAA68151.1; -.
DR PIR; S03959; S03959.
DR PIR; A39256; A39256.
DR PIR; 2CLJ; 04-MAR-98.
DR CARBBANK; CCSD:29374; -.
DR CARBBANK; CCSD:32958; -.
DR CARBBANK; CCSD:35085; -.
DR CARBBANK; CCSD:36427; -.
DR SWISS-2DPAGE; P22303; HUMAN.
DR MIM; 100740; -.
DR MIM; 112100; -.
DR PFAM; PF00135; Coesterase; 1.
DR PRINTS; PR00878; CHOLINESTRASE.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase; Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal;
KW Neurotransmitter degradation; Glycoprotein; Polymorphism;
KW Blood group antigen; Alternative splicing; 3D-structure.
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FT ACT_SITE 365 365
FT ACT_SITE 478 478
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FT DISULFID 288 303
FT DISULFID 440 560
FT DISULFID 611 611
FT CARBOHYD 296 296
FT CARBOHYD 381 381
FT CARBOHYD 495 495
FT VARIANT 353 353
FT MUTAGEN 234 234
FT MUTAGEN 365 365
FT MUTAGEN 478 478
FT MUTAGEN 206 206
FT MUTAGEN 435 435
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Query Match 100.0%; Score 14; DB 1; Length 614;
Best Local Similarity 100.0%; Pred. No. 9.4e-10;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEPHRSSSYMVHWK 14
Db 586 AEPHRSSSYMVHWK 599

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AC P21836;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7).
GN ACHE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE; 90380429.
RA Rachinsky T.L., Camp S., Li Y., Ekstroem T.J., Newton M., Taylor P.;
RT "Molecular cloning of mouse acetylcholinesterase: tissue distribution
of alternatively spliced mRNA species.";
RL Neuron 5:317-327(1990).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS) OF COMPLEX WITH FASCICULIN.
RX MEDLINE; 96067648.

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RA Bourne Y., Taylor P., Marchot P.;
RT "Acetylcholinesterase inhibition by fasciculin: crystal structure of
the complex.";
RL Cell 83:503-512(1995).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX MEDLINE; 99115643.
RA Bourne Y., Taylor P., Bougis P.E., Marchot P.;
RT "Crystal structure of mouse acetylcholinesterase. A peripheral site-
occluding loop in a tetrameric assembly.";
RL J. Biol. Chem. 274:2963-2970(1999).
CC -1- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.
CC -1- CATALYTIC ACTIVITY: ACETYLCHOLINE + H(2)O = CHOLINE + ACETATE.
CC -1- SUBUNIT: OLIGOMER COMPOSED OF DISULFIDE-LINKED HOMODIMERS.
CC -1- ALTERNATIVE PRODUCTS: THE DIFFERENT CATALYTIC SUBUNITS ARE ENCODED
BY ALTERNATIVELY SPLICED MENAS THAT ARISE FROM A SINGLE GENE.
CC THE T (ASYMMETRIC) FORM IS SHOWN HERE.
CC -1- TISSUE SPECIFICITY: PREDOMINATES IN MOST EXPRESSING TISSUES
EXCEPT ERYTHROCYTES WHERE A GLYCOPHOSPHOLIPID-ATTACHED FORM OF
ACHE PREDOMINATES.
CC -1- MISCELLANEOUS: SYNAPSES USUALLY CONTAIN ASYMMETRIC MOLECULES OF
CHOLINESTERASE, WITH A COLLAGEN-LIKE PART DISULFIDE-BONDED TO THE
CATALYTIC PART. A DIFFERENT, GLOBULAR TYPE OF CHOLINESTERASE
OCCURS ON THE OUTER SURFACES OF CELL MEMBRANES, INCLUDING THOSE OF
ERYTHROCYTES.
CC -1- MISCELLANEOUS: THIS IS THE CATALYTIC SUBUNIT OF AN ASYMMETRIC OR
SOLUBLE FORM OF ACHE.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
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CC EMBL; X56518; CAA39867.1; -.
DR PIR; JH0314; JH0314.
DR PDB; 1MAH; 03-APR-96.
DR PDB; 1MAA; 20-APR-99.
DR MGD; MGI:87876; ACHE.
DR PFAM; PF00135; Coesterase; 1.
DR PRINTS; PR00878; CHOLINESTRASE.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase; Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal;
KW Neurotransmitter degradation; Glycoprotein; Alternative splicing;
KW 3D-structure.
FT SIGNAL 1 31
FT CHAIN 32 614
FT ACT_SITE 234 234
FT ACT_SITE 365 365
FT ACT_SITE 478 478
FT DISULFID 100 127
FT DISULFID 288 303
FT DISULFID 440 560
FT DISULFID 611 611
FT CARBOHYD 296 296
FT CARBOHYD 381 381
FT CARBOHYD 495 495
FT SEQUENCE 614 AA; 68168 MW; 662512463C21172 CRC64;

Query Match 100.0%; Score 14; DB 1; Length 614;
Best Local Similarity 100.0%; Pred. No. 9.4e-10;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEPHRSSSYMVHWK 14
Db 586 AEPHRSSSYMVHWK 599

```

RESULT 5  
 ACES\_RAT ACES\_RAT STANDARD; PRT; 614 AA.  
 ID ACES\_RAT  
 AC P37136;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 15-FEB-2000 (Rel. 39, Last annotation update)  
 DE ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7).  
 GN ACH.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN [1]  
 RP SEQUENCE FROM N.A. (T FORM).  
 RX MEDLINE; 93107932.  
 RA Legay C., Bon S., Vernier P., Coussen F., Massoulié J.;  
 RT "Cloning and expression of a rat acetylcholinesterase subunit:  
 generation of multiple molecular forms and complementarity with a  
 Torpedo collagenic subunit.";  
 RL J. Neurochem. 60:337-346(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A. (H AND R FORMS).  
 RX MEDLINE; 93114454.  
 RA Legay C., Bon S., Massoulié J.;  
 RT "Expression of a cDNA encoding the glycolipid-anchored form of rat  
 acetylcholinesterase.";  
 RL FEBS Lett. 315:163-166(1993).  
 CC -1- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.  
 CC -1- CATALYTIC ACTIVITY: ACETYLCHOLINE + H(2)O = CHOLINE + ACETATE.  
 CC -1- SUBUNIT: OLIGOMER COMPOSED OF DISULFIDE-LINKED HOMODIMERS.  
 CC CATALYTIC FORMS H (GPI-ANCHOR DIMER) AND T (ASYMMETRIC COLLAGE-  
 TAILED), WHICH DIFFER IN THEIR C-TERMINUS, ACCOUNT FOR ALL TYPES  
 OF KNOWN ACH FORMS.  
 CC -1- ALTERNATIVE PRODUCTS: THE DIFFERENT CATALYTIC SUBUNITS ARE ENCODED  
 BY ALTERNATIVELY SPLICED MRNAS THAT ARISE FROM A SINGLE GENE.  
 CC IT IS NOT KNOWN WHETHER THE R FORM REPRESENTS A FUNCTIONAL  
 SPECIES. THE T (ASYMMETRIC) FORM IS SHOWN HERE.  
 CC -1- TISSUE SPECIFICITY: HAS BEEN FOUND IN CENTRAL NERVOUS SYSTEM AND  
 MUSCLE. FOUND IN EMBRYONIC LIVER AND SPLEEN BUT NOT IN ADULT  
 LIVER.  
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
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 EMBL; S50879; AAB24586.1; -;  
 EMBL; X70140; CAA49717.1; -;  
 EMBL; X70141; CAA49718.1; -;  
 PIR; JH0811; JH0811.  
 HSSP; P21836; IMAH.  
 PFM; PF00135; Coesterase; 1.  
 PRINTS; PR00878; CHOLNESTRASE.  
 PROSITE; PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 PROSITE; PS00941; CARBOXYLESTERASE\_B\_2; 1.  
 Hydrolyase; Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal;  
 Neurotransmitter degradation; Glycoprotein; Alternative splicing.  
 SIGNAL 1 31  
 CHAIN 31  
 ACT\_SITE 32 614  
 ACT\_SITE 234 234  
 ACT\_SITE 365 365  
 ACT\_SITE 478 478  
 DISULFID 100 127  
 DISULFID 288 303  
 DISULFID 440 560  
 DISULFID 611 611  
 CARBOHYD 296 296  
 CARBOHYD 381 381  
 CARBOHYD 495 495  
 FT ACT\_SITE 32 614  
 FT ACT\_SITE 234 234  
 FT ACT\_SITE 365 365  
 FT ACT\_SITE 478 478  
 FT DISULFID 100 127  
 FT DISULFID 288 303  
 FT DISULFID 440 560  
 FT DISULFID 611 611  
 FT CARBOHYD 296 296  
 FT CARBOHYD 381 381  
 FT CARBOHYD 495 495

FT VARSPLIC 570 614  
 FT CSDL -> LLSATDTLDEAERQWKAERHSSSYMVHWNKQFDHYSKOER  
 FT LFTFLHSLGLWL (IN ISOFORM H).  
 FT LLSATDTLDEAERQWKAERHSSSYMVHWNKQFDHYSKOER  
 FT CSDL -> LLSATGRRGVKGQGHKAARVGRYGERGGKRR  
 FT M (IN ISOFORM R).  
 SQ SEQUENCE 614 AA; 68196 MW; 2EDAE7D46282E7C0 CRC64;  
 Query Match 100.0%; Score 14; DB 1; Length 614;  
 Best Local Similarity 100.0%; Pred. No. 9.4e-10;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AEFHRSWSSYVHWK 14  
 | | | | | | | | | | | | | | | | | |  
 Db 586 AEFHRSWSSYVHWK 599  
 RESULT 6  
 ACES\_CHICK ACES\_CHICK STANDARD; PRT; 767 AA.  
 ID ACES\_CHICK  
 AC P36196;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7).  
 GN ACH.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 RN Gallus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=MUSCLE;  
 RX MEDLINE; 94325359.  
 RA Randall W.R., Rimer M., Gough N.R.;  
 RT "Cloning and analysis of chicken acetylcholinesterase transcripts  
 from muscle and brain.";  
 RL Biochim. Biophys. Acta 1218:453-456(1994).  
 CC -1- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.  
 CC -1- CATALYTIC ACTIVITY: ACETYLCHOLINE + H(2)O = CHOLINE + ACETATE.  
 CC -1- SUBUNIT: OLIGOMER COMPOSED OF DISULFIDE-LINKED HOMODIMERS.  
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
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 EMBL; U03472; AAA60456.1; -;  
 HSSP; P21836; IMAH.  
 PFM; PF00135; Coesterase; 2.  
 PRINTS; PR00878; CHOLNESTRASE.  
 PROSITE; PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 PROSITE; PS00941; CARBOXYLESTERASE\_B\_2; 1.  
 Hydrolyase; Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal;  
 Neurotransmitter degradation; Glycoprotein.  
 SIGNAL 1 19  
 CHAIN 20 767  
 ACT\_SITE 227 227  
 ACT\_SITE 520 520  
 ACT\_SITE 633 633  
 DISULFID 94 121  
 DISULFID 281 292  
 DISULFID 595 713  
 DISULFID 764 764  
 CARBOHYD 285 285  
 CARBOHYD 536 536  
 CARBOHYD 650 650  
 CARBOHYD 725 725  
 FT ACT\_SITE 227 227  
 FT ACT\_SITE 520 520  
 FT ACT\_SITE 633 633  
 FT DISULFID 94 121  
 FT DISULFID 281 292  
 FT DISULFID 595 713  
 FT DISULFID 764 764  
 FT CARBOHYD 285 285  
 FT CARBOHYD 536 536  
 FT CARBOHYD 650 650  
 FT CARBOHYD 725 725

SQ SEQUENCE 767 AA; 83020 MW; B1B3DF29C31F6062 CRC64;

Query Match 64.3%; Score 9; DB 1; Length 767;  
Best Local Similarity 100.0%; Pred. No. 0.00088;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EFRWSSYM 10  
| | | | | | | | | |  
Db 740 EFRWSSYM 748

RESULT 7  
PMT1\_SCHPO  
ID PMT1\_SCHPO STANDARD; PRT; 330 AA.  
AC P40959; 1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE DNA METHYLTRANSFERASE PMT1 (EC 2.1.1.-) (SPIM.SPOI) (M.SPOMI).  
PM1.  
OS Schizosaccharomyces pombe (Fission yeast).  
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales;  
OC Schizosaccharomycetaceae; Schizosaccharomycetes.  
RN [1]  
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
RC STRAIN-972;  
RX MEDLINE; 95166638.  
RA Wilkinson C.R.M., Bartlett R., Nurse P., Bird A.P.;  
RT "The fission yeast gene pmt1+ encodes a DNA methyltransferase  
RT homologue.";  
RL Nucleic Acids Res. 23:203-210(1995).  
RN [2]  
RP CHARACTERIZATION.  
RX MEDLINE; 96194447.  
RA Pinarbasi E., Elliott J., Hornby D.P.;  
RT "Activation of a yeast pseudo DNA methyltransferase by deletion of a  
RT single amino acid.";  
RL J. Mol. Biol. 257:804-813(1996).  
CC -1- FUNCTION: DOES NOT HAVE A CYTOSINE-5 METHYLTRANSFERASE ACTIVITY  
DUE TO THE INSERTION OF A SER RESIDUE BETWEEN THE PRO-CYS MOTIF  
CC FOUND AT THE ACTIVE SITE OF C5 MTASES. WHEN THIS SERINE IS DELETED  
CC IT BECOMES CATALYTICALLY ACTIVE AND RECOGNIZES AND METHYLATES THE  
CC SEQUENCE CC[AT]GG.  
CC -1- SIMILARITY: TO DNA (CYTOSINE-5)-METHYLTRANSFERASES (EC 2.1.1.37).  
CC  
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CC  
CC EMBL; X82444; CAA57824.1; -.  
CC REBASE; RB02888; M.Spomi.  
CC PFAM; PF00145; DNA\_methylase.2.  
KW Transferase; Methyltransferase.  
FT ACT\_SITE 81 81 BY SIMILARITY.  
SQ SEQUENCE 330 AA; 37976 MW; 50A7121FA7CF58A1 CRC64;

Query Match 42.9%; Score 6; DB 1; Length 330;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WSSYMW 11  
| | | | | | | | | |  
Db 208 WSSYMW 213

RESULT 8  
HXD4\_CHICK

ID HXD4\_CHICK STANDARD; PRT; 235 AA.  
AC P17278;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE HOMOBOX PROTEIN HOX-D4 (CHOX-A).  
GN HOXD4 OR HOXD-4 OR CHOX-A.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;  
OC Gallus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 90245562.  
RA Sasaki H., Yokoyama E., Kuroiwa A.;  
RT "Specific DNA binding of the two chicken Deformed family homeodomain  
RT proteins, Chox-1.4 and Chox-a.";  
RL Nucleic Acids Res. 18:1739-1747(1990).  
CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF  
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH  
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.  
CC -1- FUNCTION: BINDS TO SITES IN THE 5'-FLANKING SEQUENCE OF ITS CODING  
CC REGION WITH VARIOUS AFFINITIES. THE CONSENSUS SEQUENCES OF THE  
CC HIGH AND LOW AFFINITY BINDING SITES ARE TAATGA(C/G) AND CTAATTTT.  
CC -1- SUBCELLULAR LOCATION: NUCLEAR.  
CC -1- SIMILARITY: BELONGS TO THE ANTP FAMILY OF HOMOBOX PROTEINS.  
CC "DEFORMED" SUBFAMILY.  
CC  
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CC  
CC EMBL; X52671; CAA36897.1; -.  
CC EMBL; X52672; CAA36898.1; -.  
CC PIR; S09256; S09256.  
CC HSP; P02833; ISAN.  
CC TRANSFAC; T01753; -.  
CC PFAM; PF00046; homeobox; 1.  
CC PRINTS; PR00024; HOMOBOX.  
CC PRINTS; PR00025; ANTENNAPEDIA.  
CC PROSITE; PS00027; HOMOBOX\_1; 1.  
CC PROSITE; PS00071; HOMOBOX\_2; 1.  
CC PROSITE; PS00032; ANTENNAPEDIA; 1.  
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;  
FT DOMAIN 123 128 ANTP-TYPE HEXAPEPTIDE.  
FT DNA\_BIND 144 203 HOMOBOX.  
FT DOMAIN 212 217 SER-RICH.  
SQ SEQUENCE 235 AA; 26662 MW; B7115D434033E4B5 CRC64;

Query Match 35.7%; Score 5; DB 1; Length 235;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SSYMW 11  
| | | | | | | | | |  
Db 4 SSYMW 8

RESULT 9  
HXD4\_BRARE  
ID HXD4\_BRARE STANDARD; PRT; 236 AA.  
AC O57374;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE HOMOBOX PROTEIN HOX-D4;  
GN HOXD4.

OS Brachydanio rerio (Zebrafish) (Zebra danio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
OC Cypriniformes; Cyprinidae; Cyprinidae; Rasbora; Danio.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Prince V.E., Joly L., Ekker M., Ho R.K.;  
RT "Zebrafish box genes: genomic organization and modified colinear  
RT expression patterns in the trunk."  
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF  
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH  
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.  
CC -1- SUBCELLULAR LOCATION: NUCLEAR.  
CC -1- SIMILARITY: BELONGS TO THE ANTP FAMILY OF HOMEBOX PROTEINS.  
CC "DEFORMED" SUBFAMILY.  
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CC -----  
DR EMBL; Y14548; CAA74883.1; ALT\_INIT.  
DR ZFIN; ZDB-GENE-980526.214; HOXD4.  
DR PFAM; PF00046; homeobox; 1.  
DR PRINTS; PR00024; HOMEBOX.  
DR PROSITE; PS00027; HOMEBOX\_1; FALSE\_NEG.  
DR PROSITE; PS00071; HOMEBOX\_2; 1.  
DR PROSITE; PS00032; ANTENNAPEDIA; 1.  
DR Homeobox; DNA-binding; Developmental protein; Nuclear protein;  
KW Transcription regulation.  
FT DOMAIN 125 130 ANTP-TYPE HEXAPEPTIDE.  
FT DNA\_BIND 146 205 HOMEBOX.  
FT SEQUENCE 236 AA; 27132 MW; AAE8C7F34F17B5E CRC64;  
SQ  
  
Query Match 35.7%; Score 5; DB 1; Length 236;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 7 SSMYV 11  
Db 4 SSMYV 8  
|||||  
  
RESULT 10  
HXD4\_MOUSE STANDARD; PRT; 250 AA.  
AC P10628; P97451;  
DT 01-JUL-1989 (Rel. 11, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE HOMEBOX PROTEIN HOXD4 (HOXD-4.2) (HOXD-5.1).  
GN HOXD4 OR HOXD-4 OR HOXD-4.2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
RN [1]  
RP SEQUENCE FROM N.A.  
EX MEDLINE; 88263027.  
RA Featherstone M.S.; Baron A.; Gaunt S.J.; Mattei M.-G.; Duboule D.;  
RT "Hox-5.1 defines a homeobox-containing gene locus on mouse chromosome  
RT 2.";  
RL Proc. Natl. Acad. Sci. U.S.A. 85:4760-4764(1988).  
RN [2]  
RP REVISTONS.  
EX MEDLINE; 94173687.  
RA Rambaldi I.; Kovacs E.N.; Featherstone M.S.;  
RT "A proline-rich transcriptional activation domain in murine HOXD-4

RT (HOXD-4.2).";  
RL Nucleic Acids Res. 22:376-382(1994).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN-129/SV;  
RA Folberg A.; Featherstone M.S.;  
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE OF 175-198 FROM N.A.  
RX MEDLINE; 92212934.  
RA Nazari A.; Kim Y.; Nirenberg M.;  
RT "Hox-1.11 and Hox-4.9 homeobox genes.";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:2883-2887(1992).  
CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF  
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH  
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.  
CC -1- SUBCELLULAR LOCATION: NUCLEAR.  
CC -1- SIMILARITY: BELONGS TO THE ANTP FAMILY OF HOMEBOX PROTEINS.  
CC "DEFORMED" SUBFAMILY.  
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CC -----  
DR EMBL; J03770; AAA20072.1; ALT\_INIT.  
DR EMBL; M87804; AAA37851.1; -.  
DR EMBL; U77364; AAB41222.1; -.  
DR PIR; A36170; A36170.  
DR HSSP; P02833; 1SAN.  
DR TRANSFAC; T01752; -.  
DR MGD; MGI:96208; HOXD4.  
DR PFAM; PF00046; homeobox; 1.  
DR PRINTS; PR00024; HOMEBOX.  
DR PROSITE; PS00027; ANTENNAPEDIA.  
DR PROSITE; PS00027; HOMEBOX\_1; 1.  
DR PROSITE; PS00032; ANTENNAPEDIA; 1.  
DR PROSITE; PS00071; HOMEBOX\_2; 1.  
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;  
KW Transcription regulation.  
FT DOMAIN 131 136 ANTP-TYPE HEXAPEPTIDE.  
FT DNA\_BIND 152 211 HOMEBOX.  
FT DOMAIN 220 229 SER-RICH.  
FT CONFLICT 143 143 A -> V (IN REF. 3).  
FT SEQUENCE 250 AA; 27284 MW; 1057647C0A2665FF CRC64;  
SQ  
  
Query Match 35.7%; Score 5; DB 1; Length 250;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 7 SSMYV 11  
Db 4 SSMYV 8  
|||||  
  
RESULT 11  
HXD4\_HUMAN STANDARD; PRT; 255 AA.  
AC P09016;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-NOV-1990 (Rel. 15, Last sequence update)  
DT 01-JUN-1994 (Rel. 29, Last annotation update)  
DE HOMEBOX PROTEIN HOXD4 (HOXD-4B) (HOXD-5.1) (HMO.C13).  
GN HOXD4 OR HOXD4B.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
RN [1]  
RP SEQUENCE FROM N.A.

RX MEDLINE; 90356367.  
 RA Clanetti L., di Cristofaro A., Zappavigna V., Bottero L.,  
 RA Baccoli G., Testa U., Russo G., Boncinelli E., Peschle C.,  
 RT "Molecular mechanisms underlying the expression of the human HOX-5.1  
 RT gene.",  
 RL Nucleic Acids Res. 18:4361-4368(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 87090377.  
 RA Mavilio F., Simeone A., Giampaolo A., Faiella A., Zappavigna V.,  
 RA Acampora D., Polana G., Russo G., Peschle C., Boncinelli E.,  
 RT "Differential and stage-related expression in embryonic tissues of a  
 RT new human homeobox gene.",  
 RL Nature 324:664-668(1986).  
 RN [3]  
 RP SEQUENCE OF 154-219 FROM N.A.  
 RX MEDLINE; 90215236.  
 RA Boncinelli E., Acampora D., Pannese M., D'Esposito M., Somma R.,  
 RA Gaudino G., Stornaiuolo A., Cafiero M., Faiella A., Simeone A.,  
 RT "Organization of human class I homeobox genes.",  
 RL Genome 31:745-756(1989).  
 CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF  
 CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH  
 CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.  
 CC -1- SIMILARITY: BELONGS TO THE ANTP FAMILY OF HOMEBOX PROTEINS.  
 CC "DEFORMED" SUBFAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; X17360; CAA35237.1; -;  
 DR EMBL; X04706; CAA28411.1; -;  
 DR PIR; S10985; WJHU4B.  
 DR HSP; P02833; ISAN.  
 DR TRANSFAC; T00376; -;  
 DR MIM; 142981; -;  
 DR PFAM; PF00046; homeobox; 1.  
 DR PRINTS; PR00024; HOMEBOX.  
 DR PRINTS; PR00025; ANTENNAPEDIA.  
 DR PROSITE; PS00027; HOMEBOX\_1; 1.  
 DR PROSITE; PS00032; ANTENNAPEDIA; 1.  
 DR PROSITE; PS00071; HOMEBOX\_2; 1.  
 DR Homeobox; DNA-binding; Developmental protein; Nuclear protein;  
 KW Transcription regulation.  
 FT DOMAIN 133 138 ANTP-TYPE HEXAPEPTIDE.  
 FT DNA\_BIND 154 213 HOMEBOX.  
 FT DOMAIN 222 234 POLY-SER.  
 FT CONFLICT 123 123 P -> S (IN REF. 2).  
 FT CONFLICT 142 142 V -> A (IN REF. 2).  
 SQ SEQUENCE 255 AA; 27895 MW; 3920508CCCAF16FF CRC64;

Query Match 35.7%; Score 5; DB 1; Length 255;  
 Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SSMV 11  
 DB 4 SSMV 8  
 RESULT 12  
 YXJB\_BACSU  
 ID YXJB\_BACSU STANDARD; PRT; 282 AA.  
 AC P42313;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE HYPOTHETICAL 31.5 KDA PROTEIN IN KATB 3'REGION.  
 GN YXJB OR N151.  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
 OC Bacillus/Staphylococcus group; Bacillus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-168 / BGSC1A1;  
 RA Yoshida K.-I., Sano H., Seki S., Oda M., Fujimura M., Fujita Y.;  
 RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: TO E.COLI RMA AND M.GRISORUBIDA MYRA.  
 CC -----  
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 CC -----  
 DR EMBL; D83026; BAA11703.1; -;  
 DR EMBL; Z99123; CAB15927.1; -;  
 DR EMBL; Z99124; CAB15937.1; -;  
 DR SUBTILIST; EGI1151; YXJB.  
 KW Hypothetical protein.  
 SQ SEQUENCE 282 AA; 31473 MW; 35DE65D847D67E61 CRC64;

Query Match 35.7%; Score 5; DB 1; Length 282;  
 Best Local Similarity 100.0%; Pred. No. 22;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHR 5  
 DB 172 AEFHR 176

RESULT 13  
 YFIN\_ECOLI  
 ID YFIN\_ECOLI STANDARD; PRT; 408 AA.  
 AC P46139; P76598;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE HYPOTHETICAL 46.0 KDA PROTEIN IN AROF-RELS INTERGENIC REGION.  
 GN YFIN.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K12 / MG1655;  
 RX MEDLINE; 97426617.  
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 RA Riley M., Collado-Vides J., Glasner F.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA Mau B., Shao Y.;  
 RT "The complete genome sequence of Escherichia coli K-12.";  
 RL Science 277:1453-1474(1997).  
 RN [2]  
 RP SEQUENCE OF 330-408 FROM N.A.  
 RX MEDLINE; 84057772.  
 RA Bystrom A.S., Hjalmarsson K.J., Wikstrom P.M., Bjoerk G.R.;  
 RT "The nucleotide sequence of an Escherichia coli operon containing  
 RT genes for the tRNA(m<sup>6</sup>G)methyltransferase, the ribosomal proteins S16  
 RT and L19 and a 21-K polypeptide.";  
 RL EMBO J. 2:899-905(1983).  
 RN [3]  
 RP IDENTIFICATION  
 RX MEDLINE; 96032851.  
 RA Borodovsky M., McIninch J., Koonin E.V., Rudd K.E., Medigue C.,  
 RA Danchin A.;

RT "Detection of new genes in a bacterial genome using Markov models for  
 RT three gene classes";  
 RL Nucleic Acids Res. 23:3554-3562(1995).  
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).  
 CC -!- SIMILARITY: BELONGS TO THE YAIC / YFIN (E.COLI), YHCK (B.SUBTILIS)  
 CC FAMILY  
 CC -----  
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 CC -----  
 DR EMBL; AE000346; AAC75653.1; -;  
 DR EMBL; X01818; -; NOT\_ANNOTATED\_CDS.  
 DR EMBL; EG12880; YFIN.  
 DR PFAM; PF00990; DUF9; 1.  
 KW Hypothetical protein; Transmembrane.  
 FT TRANSMEM 25 45 POTENTIAL.  
 FT TRANSMEM 53 73 POTENTIAL.  
 FT TRANSMEM 113 133 POTENTIAL.  
 FT TRANSMEM 155 175 POTENTIAL.  
 SQ SEQUENCE 408 AA; 45989 MW; 720B6539EF43DB16 CRC64;

Query Match 35.7%; Score 5; DB 1; Length 408;  
 Best Local Similarity 100.0%; Pred. No. 29;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AEFHR 5  
 Db 215 AEFHR 219  
 |||||

RESULT 14  
 ID PEPR\_ECOLI STANDARD; PRT; 427 AA.  
 AC P37095; Q47131; P76580; P76989; P76991;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE PEPTIDASE B (EC 3...-...)  
 GN PEPR.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K12;  
 RA Suzuki H., Kim E., Yamamoto N., Hashimoto W., Yamamoto K., Kumagai H.;  
 RT "Mapping, cloning, and DNA sequencing of pepr gene which encodes  
 RT peptidase B of Escherichia coli K-12";  
 RL J. Ferment. Bioeng. 82:392-397(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K12 / MG1655;  
 RX MEDLINE; 97426617.  
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 RA Riley M., Collado-Vides J., Glasner F.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA Mau B., Shao Y.;  
 RT "The complete genome sequence of Escherichia coli K-12";  
 RL Science 277:1453-1474(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K12;  
 RA Alba H., Baba T., Fujita K., Hayashi K., Honjo A., Horiuchi T.,  
 RA Ikemoto K., Inada T., Isono S., Isono S., Itoh T., Kanai K.,  
 RA Kasai H., Kashimoto K., Kim S., Kimura S., Kitagawa M.,  
 RA Kitakawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H.,  
 RA Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,

RA Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C.,  
 RA Yamamoto Y., Yano M.;  
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 1-42 FROM N.A.  
 RC STRAIN-K12;  
 RX MEDLINE; 9411939.  
 RA Kawula T.H., Lelivelt M.J.;  
 RT "Mutations in a gene encoding a new Hsp70 suppress rapid DNA  
 RT inversion and bgl activation, but not proU derepression, in hns-1  
 RT mutant Escherichia coli";  
 RL J. Bacteriol. 176:610-619(1994).  
 CC -!- COFACTOR: ACTIVATED BY MANGANESE (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M17; ALSO KNOWN AS THE  
 CC CYTOSOL AMINOPEPTIDASE FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; D84499; BAA12689.1; -;  
 DR EMBL; AE000339; AAC75576.1; ALT\_INIT.  
 DR EMBL; D90882; CAB22347.1; -;  
 DR EMBL; D90883; CAB22357.1; -;  
 DR EMBL; U01827; -; NOT\_ANNOTATED\_CDS.  
 DR HSSP; P00727; ILAP.  
 DR EMBL; EG12310; PEPR.  
 DR PFAM; PF00883; Peptidase\_M17; 1.  
 DR PRINTS; PR00481; LAMNOPPTDASE..  
 DR PROSITE; PS00631; CYTOSOL\_AP; 1.  
 KW Hydrolase; Manganese.  
 FT METAL 195 195  
 FT METAL 200 200 MANGANESE (2) (BY SIMILARITY).  
 FT METAL 218 218 MANGANESE (1 AND 2) (BY SIMILARITY).  
 FT METAL 277 277 MANGANESE (2) (BY SIMILARITY).  
 FT METAL 279 279 MANGANESE (1) (BY SIMILARITY).  
 FT METAL 279 279 MANGANESE (1 AND 2) (BY SIMILARITY).  
 FT ACT\_SITE 207 207 POTENTIAL.  
 FT ACT\_SITE 281 281 POTENTIAL.  
 FT CONFLICT 155 155 Q -> P (IN REF. 1).  
 FT CONFLICT 375 426 STAAGFLSHVENYQQGLHIDCSATYRKAPQWSAGATG.  
 FT CONFLICT 375 426 LGVRTIANLT -> TERRASCRTLLRTISKACISTARRL  
 FT CONFLICT 41 41 TVKRLNSGLRALDVC (IN REF. 1).  
 FT CONFLICT 41 41 L -> P (IN REF. 3).  
 SQ SEQUENCE 427 AA; 46180 MW; 8299E7D440F5732E CRC64;

Query Match 35.7%; Score 5; DB 1; Length 427;  
 Best Local Similarity 100.0%; Pred. No. 30;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AEFHR 5  
 Db 348 AEFHR 352  
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 RESULT 15  
 ID NU4M\_LOCOMI  
 ID NU4M\_LOCOMI STANDARD; PRT; 444 AA.  
 AC Q36424;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 (EC 1.6.5.3).  
 GN NDA.  
 OS Locusta migratoria (Migratory locust).  
 OS Mitochondrion.  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Orthoptera; Orthopteroidea; Caelifera;  
 OC Acridomorpha; Acridoidea; Acrididae; Oedipodinae; Locusta.

```

RN  SEQUENCE FROM N.A.
RP  MEDLINE: 96139026.
RA  Flock P.K., Rowell C.H.F., Gellissen G.;
RT  "The sequence, organization, and evolution of the Locusta migratoria
RL  mitochondrial genome.";
RJ  J. Mol. Evol. 41:928-941(1995).
CC  -|- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
CC  -----
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CC  -----
DR  EMBL: X80245; CAA56534.1; -.
DR  PFAM: PF00361; oxidored_g1; 1.
DR  PFAM: PF01059; oxidored_g5_N; 1.
KW  Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SQ  SEQUENCE 444 AA; 51135 MW; B2D8DEC2584921BA CRC64;

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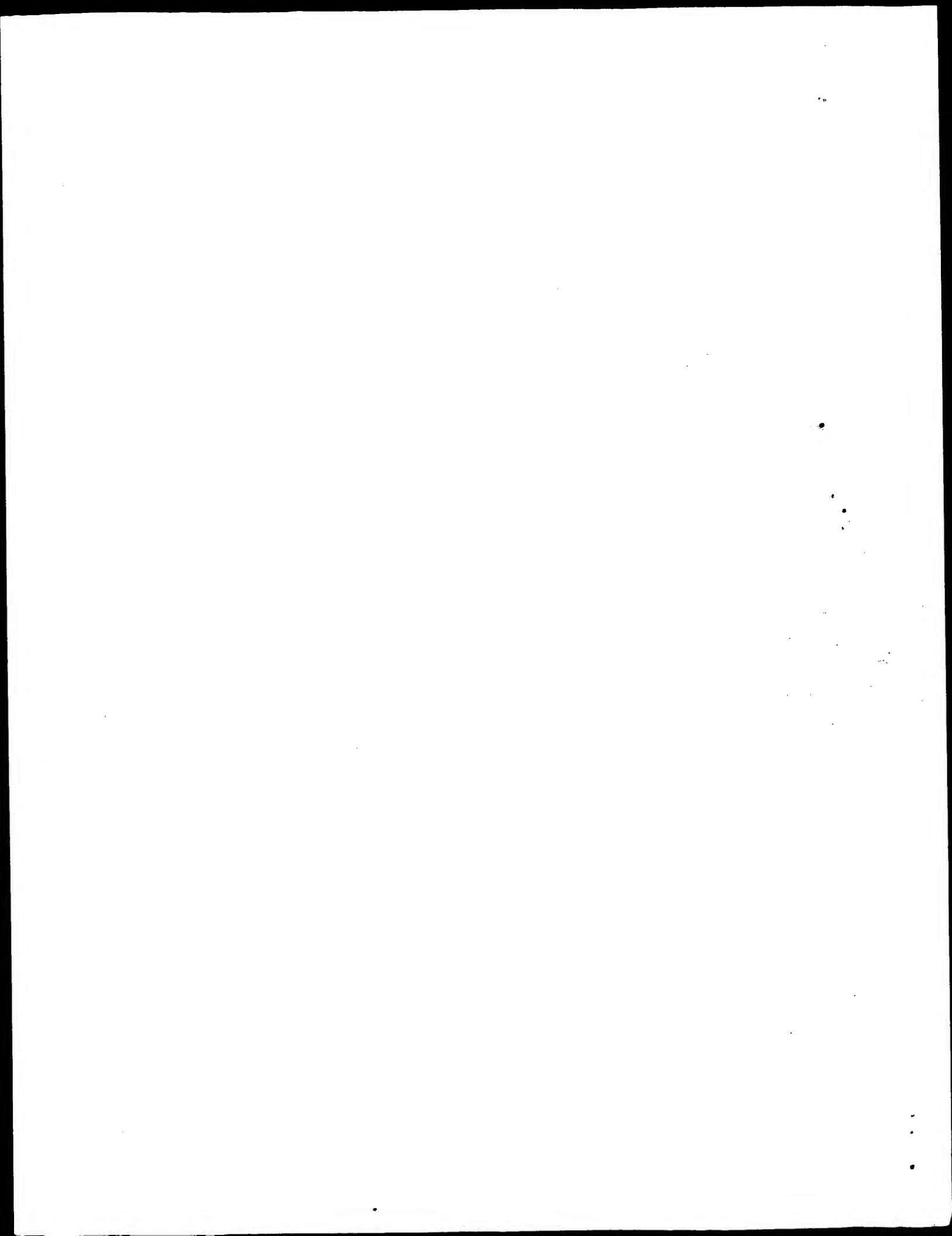
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Query Match      35.7%; Score 5; DB 1; Length 444;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  6 WSSYM 10
Db  376 WSSYM 380

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Search completed: September 13, 2000, 02:27:53  
Job time: 170 sec





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 13, 2000, 02:21:12 ; Search time 22.49 Seconds  
(without alignments)  
43.160 Million cell updates/sec

Title: US-09-155-076-1  
Perfect score: 87  
Sequence: 1 AEFHRWSSVMVHWK 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0  
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_12:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*

\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	87	100.0	611	6	062763 felis silve
2	84	96.6	633	13	042275 electrophor
3	80	92.0	95	13	09W6Y8 torpedo cal
4	70	80.5	95	13	073748 bungarus fa
5	56	64.4	602	6	062760 felis silve
6	56	64.4	602	6	062761 panchera ti
7	44	50.6	260	8	078318 arabidopsis
8	42	48.3	1788	4	060611 homo sapien
9	42	48.3	1788	4	060612 homo sapien
10	42	48.3	1792	6	046385 bos taurus
11	42	48.3	2214	4	095425 homo sapien
12	41	47.1	1323	11	062255 mus musculu
13	41	47.1	1687	10	09XGN9 oryza sativ
14	40.5	46.6	285	2	Q52970 rhizobium m
15	40.5	46.6	508	8	078332 perglularia
16	40.5	46.6	508	8	063177 plocosperma
17	40.5	46.6	511	8	078334 tylophora l
18	40.5	46.6	511	8	078335 vincetoxicu
19	40	46.0	183	2	Q57000 zymomonas m

20	40	46.0	351	12	072754
21	40	46.0	450	2	025000
22	40	46.0	517	8	09XPP6
23	40	46.0	1350	13	091929
24	39.5	45.4	469	2	073738
25	39.5	45.4	512	8	078333
26	39.5	45.4	542	10	064858
27	39.5	45.4	1057	3	09Y8H1
28	39	44.8	100	10	023949
29	39	44.8	226	12	037049
30	39	44.8	226	12	037351
31	39	44.8	226	12	07504
32	39	44.8	226	12	072839
33	39	44.8	259	8	078312
34	39	44.8	260	8	078311
35	39	44.8	260	8	078319
36	39	44.8	260	8	078320
37	39	44.8	262	12	010441
38	39	44.8	441	5	015814
39	39	44.8	524	10	049650
40	39	44.8	526	10	049652
41	38.5	44.3	287	10	09ZSU4
42	38.5	44.3	318	5	P91927
43	38.5	44.3	354	8	098848
44	38	43.7	65	13	098928
45	38	43.7	117	8	09XNM6

## ALIGNMENTS

RESULT 1  
062763 PRELIMINARY; PRT; 611 AA.  
AC 062763  
DT 01-AUG-1998 (TREMBLrel. 07, Created)  
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)  
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
DE ACETYLCHOLINESTERASE COLLAGEN-TAILED OR GLOBULAR FORM PRECURSOR.  
GN ACHE.  
OS Felis silvestris catus (Cat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA BARTLS C.F., XIE W.-H., MILLER-LINDHOLM A.K., LOCKRIDGE O.;  
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF053485; AAC08995.1; -  
DR HSSP; P22303; 2CLJ.  
DR PROSITE; PS00122; CARBOXYLESTERASE\_B\_1; 1.  
DR PROSITE; PS00941; CARBOXYLESTERASE\_B\_2; 1.  
DR PFAM; PF00135; Coesterase; 1.  
DR PRINTS; PR00878; CHOLINESTERASE.  
SQ SEQUENCE 611 AA; 67298 MW; 172DEB16 CRC32;

Query Match 100.0%; Score 87; DB 6; Length 611;  
Best Local Similarity 100.0%; Pred. No. 4.2e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSVMVHWK 14  
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DB 583 AEFHRWSSVMVHWK 596

RESULT 2  
042275 PRELIMINARY; PRT; 633 AA.  
ID 042275  
AC 042275;  
DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
DE ACETYLCHOLINESTERASE CATALYTIC SUBUNIT PRECURSOR (EC 3.1.1.7).

OS Electrophorus electricus (Electric eel).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;  
OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Gymnotiformes;  
OC Gymnotoidei; Electrophoridae; Electrophorus.  
[1]  
RP SEQUENCE FROM N.A.  
RA SIMON S., MASSOULIE J.;  
RL J. Biol. Chem. 0:0-0(1997).  
DR EMBL; AF030422; AAB86606.1; -.  
DR HSSP; P04058; IACL.  
DR PROSITE; PS00122; CARBOXYLESTERASE\_B\_1; 1.  
DR PROSITE; PS00941; CARBOXYLESTERASE\_B\_2; 1.  
DR PFAM; PF00135; Coesterase; 2.  
DR PRINTS; PR00878; CHOLNESTRASE.  
KW Signal; Hydrolase. 23 POTENTIAL.  
FT SIGNAL 1 23 POTENTIAL.  
FT CHAIN 24 633 POTENTIAL.  
SQ SEQUENCE 633 AA; 71814 MW; 6D50AB05 CRC32;

Query Match 96.6%; Score 84; DB 13; Length 633;  
Best Local Similarity 92.9%; Pred. No. 1.3e-05;  
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AEFHRSWSSVMVHWK 14  
| | | | | | | | | | | | | | | | | |  
DB 605 AEFHRSWSSVMVHWK 618

RESULT 3  
Q9W6Y8 PRELIMINARY; PRT; 95 AA.  
ID Q9W6Y8  
AC Q9W6Y8  
DT 01-NOV-1999 (TREMBlrel. 12, Created)  
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)  
DE ACETYLCOLINESTERASE (FRAGMENT).  
OS Torpedo californica (Pacific electric ray).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
OC Elasmobranchii; Rajiformes; Torpedinoidei; Torpedinidae; Torpedo.  
[1]  
RP SEQUENCE FROM N.A.  
RA MAULET Y., CAMP S., GIBNEY G., RACHINSKY T.L., EKSTROEM T.J.,  
RA TAYLOR P.;  
RL Submitted (OCT-1990) to the EMBL/GenBank/DBJ databases.  
DR EMBL; X56517; CAB37951.1; -.  
DR EMBL; X56516; CAB37951.1; JOINED.  
FT NON\_TER 1  
SQ SEQUENCE 95 AA; 11752 MW; F7387712 CRC32;

Query Match 92.0%; Score 80; DB 13; Length 95;  
Best Local Similarity 92.3%; Pred. No. 7.9e-06;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 2 EFRHRSWSSVMVHWK 14  
| | | | | | | | | | | | | | | | | |  
DB 68 EFRHRSWSSVMVHWK 80

RESULT 4  
O73748 PRELIMINARY; PRT; 95 AA.  
ID O73748  
AC O73748  
DT 01-AUG-1998 (TREMBlrel. 07, Created)  
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)  
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)  
DE ACETYLCOLINESTERASE (FRAGMENT).  
OS Bungarus fasciatus (Banded krait).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Lepidosauria;  
OC Squamata; Scleroglossa; Serpentes; Colubroidea; Elapidae; Bungarinae;  
OC Bungarus.  
[1]

RP SEQUENCE FROM N.A.  
RA COUSIN X., BON S., MASSOULIE J., BON C.;  
RL J. Biol. Chem. 0:0-0(1998).  
DR EMBL; AF045238; AAC16420.1; -.  
DR HSSP; P21836; IMAH.  
FT NON\_TER 1  
SQ SEQUENCE 95 AA; 11225 MW; 13280E02 CRC32;

Query Match 80.5%; Score 70; DB 13; Length 95;  
Best Local Similarity 76.9%; Pred. No. 0.00029;  
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 2 EFRHRSWSSVMVHWK 14  
| | | | | | | | | | | | | | | | | |  
DB 68 EFRHRSWSSVMVHWK 80

RESULT 5  
O62760 PRELIMINARY; PRT; 602 AA.  
ID O62760  
AC O62760  
DT 01-AUG-1998 (TREMBlrel. 07, Created)  
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)  
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)  
DE BUTYRYLCOLINESTERASE PRECURSOR.  
GN BCHE.  
OS Felis silvestris catus (Cat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
[1]  
RP SEQUENCE FROM N.A.  
RA BARTELS C.F., XIE W.-H., MILLER-LINDHOLM A.K., LOCKRIDGE O.;  
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF053483; AAC06261.1; -.  
DR HSSP; P21836; IMAH.  
DR PROSITE; PS00122; CARBOXYLESTERASE\_B\_1; 1.  
DR PROSITE; PS00941; CARBOXYLESTERASE\_B\_2; 1.  
DR PFAM; PF00135; Coesterase; 1.  
DR PRINTS; PR00878; CHOLNESTRASE.  
KW Signal.  
FT SIGNAL 1 28 POTENTIAL.  
FT CHAIN 29 602 BUTYRYLCOLINESTERASE.  
SQ SEQUENCE 602 AA; 68328 MW; 27B133D7 CRC32;

Query Match 64.4%; Score 56; DB 6; Length 602;  
Best Local Similarity 57.1%; Pred. No. 0.29;  
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
QY 1 AEFHRSWSSVMVHWK 14  
| | | | | | | | | | | | | | | | | |  
DB 573 AGFYRWNNYMDWK 586

RESULT 6  
O62761 PRELIMINARY; PRT; 602 AA.  
ID O62761  
AC O62761  
DT 01-AUG-1998 (TREMBlrel. 07, Created)  
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)  
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)  
DE BUTYRYLCOLINESTERASE PRECURSOR.  
GN BCHE.  
OS Panthera tigris tigris.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Carnivora; Fissipedia; Felidae; Panthera.  
[1]  
RP SEQUENCE FROM N.A.  
RA BARTELS C.F., XIE W.-H., MILLER-LINDHOLM A.K., LOCKRIDGE O.;  
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.

```

DR EMBL; AF053484; AAC06262.1; ..
DR HSSP; P21836; 1MAH.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
DR PFAM; PF00135; Coesterase; 1.
DR PRINTS; PR00878; CHOLNESTRASE.
KW Signal.
FT SIGNAL.
FT CHAIN
FT CHAIN 29 602 BUTYRYLCHOLINESTERASE.
SQ SEQUENCE 602 AA; 68290 MW; B019C09B CRC32;

Query Match
Best Local Similarity 64.4%; Score 56; DB 6; Length 602;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

* QY 1 AEFHRSSYMHVK 14
DB 573 AGFYRWNNYMDWK 586
| :|:|:|:|:|
| :|:|:|:|:|

RESULT 7
ID O78318 PRELIMINARY; PRT; 260 AA.
AC O78318;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE NADH DEHYDROGENASE SUBUNIT F (FRAGMENT).
GN NDHF.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC euryliophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
OC Arabidopsis.
RN [1]
RP SEQUENCE FROM N.A.
RA GALLOWAY G.L., MALMBERG R.L., PRICE R.A.;
RT "Phylogenetic utility of the nuclear gene arginine decarboxylase
RT within Brassicaceae".
RL Mol. Biol. Evol. 0:0-0(1998).
DR EMBL; AF064654; AAC68593.1; ..
DR MENDEL; 30386; Arath:ndhf; 30386.
DR PFAM; PF01010; oxidored_q1_C; 1.
KW Chloroplast.
FT NON_TER 1
FT NON_TER 260
SQ SEQUENCE 260 AA; 30565 MW; 916B2FFC CRC32;

Query Match
Best Local Similarity 50.6%; Score 44; DB 8; Length 260;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 FHRSSYMHVK 14
DB 192 FQKWSKRIHW 203
| :|:|:|:|
| :|:|:|:|

RESULT 8
ID O60611 PRELIMINARY; PRT; 1788 AA.
AC O60611;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE SUPERVILLIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.

```

```

RC TISSUE-CERVICAL CARCINOMA;
EX MEDLINE; 98044228.
RA PESTONJAMASP K.N., POPE R.K., WULFKUHLE J.D., LUNA E.J.;
RT "Supervillin (p205): A novel membrane-associated, F-actin-binding
RT protein in the villin/gelsolin superfamily.";
RL J. Cell Biol. 139:1255-1269(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-CERVICAL CARCINOMA;
RA POPE R.K., SMITH K.P., PESTONJAMASP K.N., WULFKUHLE J.D.,
RA LAWRENCE J.B., LUNA E.J.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF051850; AAC64695.1; ..
DR HSSP; P02640; IVII.
DR PFAM; PF00626; Gelsolin; 1.
SQ SEQUENCE 1788 AA; 200792 MW; 25862FCB CRC32;

Query Match
Best Local Similarity 48.3%; Score 42; DB 4; Length 1788;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 EFRWSSYMHVK 14
DB 1348 QFEGDAYVVKWK 1360
| :|:|:|:|
| :|:|:|:|

RESULT 9
ID O60612 PRELIMINARY; PRT; 1788 AA.
AC O60612;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE SUPERVILLIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA POPE R.K., SMITH K.P., PESTONJAMASP K.N., WULFKUHLE J.D.,
RA LAWRENCE J.B., LUNA E.J.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF051851; AAC64696.1; ..
DR HSSP; P02640; IVII.
DR PFAM; PF00626; Gelsolin; 1.
SQ SEQUENCE 1788 AA; 200820 MW; DEAE76B CRC32;

Query Match
Best Local Similarity 48.3%; Score 42; DB 4; Length 1788;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 EFRWSSYMHVK 14
DB 1348 QFEGDAYVVKWK 1360
| :|:|:|:|
| :|:|:|:|

RESULT 10
ID O46385 PRELIMINARY; PRT; 1792 AA.
AC O46385;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)

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01-NOV-1999 (TReMBLrel. 12, Last annotation update)  
DE SUPERVILLIN.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;  
OC Bovinae; Bos.  
[1]  
RN SEQUENCE FROM N.A.  
RX MEDLINE; 98044228.  
RA \*PESTONJANASP K.N., POPE R.K., WULFKUHL J.D., LUNA E.J.;  
RT "Supervillin (P05): A novel membrane-associated, F-actin-binding  
protein in the villin/gelsolin superfamily.";  
RL J. Cell Biol. 139:1255-1269(1997).  
DR EMBL; AF025996; AAC48783.1; -.  
DR HSSP; P02640; 1VII.  
DR PFAM; PF00626; Gelsolin; 1.  
SQ SEQUENCE 1792 AA; 200625 MW; 29AEB3CE CRC32;

Query Match 48.3%; Score 42; DB 6; Length 1792;  
Best Local Similarity 46.2%; Pred. No. 1.4e+02;  
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 EFRWSSYVHWK 14  
:|:|:|:|:|:|  
Db 1352 QFHGDYVVRWK 1364

RESULT 11  
Q95425 PRELIMINARY; PRT; 2214 AA.  
ID Q95425  
AC Q95425;  
DT 01-MAY-1999 (TReMBLrel. 10, Created)  
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)  
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)  
DE ARCHVILLIN.  
GN SVIL.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.  
[1]  
RN SEQUENCE FROM N.A.  
RX MEDLINE; 99058997.  
RA POPE R.K., PESTONJANASP K.N., SMITH K.P., WULFKUHL J.D.,  
RA STRASSEL C.P., LAWRENCE J.B., LUNA E.J.;  
RT "Cloning, characterization, and chromosomal localization of human  
supervillin (SVIL).";  
RL Genomics 52:342-351(1998).  
DR EMBL; AF109135; AAD14682.1; -.  
DR HSSP; P02640; 1VII.  
SQ SEQUENCE 2214 AA; 247704 MW; 020ADC99 CRC32;

Query Match 48.3%; Score 42; DB 4; Length 2214;  
Best Local Similarity 46.2%; Pred. No. 1.7e+02;  
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 EFRWSSYVHWK 14  
:|:|:|:|:|:|  
Db 1774 QFHGDYVVRWK 1786

RESULT 12  
Q62255 PRELIMINARY; PRT; 1323 AA.  
ID Q62255  
AC Q62255;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)  
DE SPALT HOMOLOGUE (SPALT PROTEIN) (FRAGMENT).  
GN SPALT OR NSAL.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

01-NOV-1999 (TReMBLrel. 12, Last annotation update)  
DE SUPERVILLIN.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;  
OC Bovinae; Bos.  
[1]  
RN SEQUENCE FROM N.A.  
RX MEDLINE; 98044228.  
RA \*PESTONJANASP K.N., POPE R.K., WULFKUHL J.D., LUNA E.J.;  
RT "Supervillin (P05): A novel membrane-associated, F-actin-binding  
protein in the villin/gelsolin superfamily.";  
RL J. Cell Biol. 139:1255-1269(1997).  
DR EMBL; AF025996; AAC48783.1; -.  
DR HSSP; P02640; 1VII.  
DR PFAM; PF00626; Gelsolin; 1.  
SQ SEQUENCE 1792 AA; 200625 MW; 29AEB3CE CRC32;

Query Match 48.3%; Score 42; DB 6; Length 1792;  
Best Local Similarity 46.2%; Pred. No. 1.4e+02;  
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 EFRWSSYVHWK 14  
:|:|:|:|:|:|  
Db 1352 QFHGDYVVRWK 1364

RESULT 11  
Q95425 PRELIMINARY; PRT; 2214 AA.  
ID Q95425  
AC Q95425;  
DT 01-MAY-1999 (TReMBLrel. 10, Created)  
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)  
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)  
DE ARCHVILLIN.  
GN SVIL.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.  
[1]  
RN SEQUENCE FROM N.A.  
RX MEDLINE; 99058997.  
RA POPE R.K., PESTONJANASP K.N., SMITH K.P., WULFKUHL J.D.,  
RA STRASSEL C.P., LAWRENCE J.B., LUNA E.J.;  
RT "Cloning, characterization, and chromosomal localization of human  
supervillin (SVIL).";  
RL Genomics 52:342-351(1998).  
DR EMBL; AF109135; AAD14682.1; -.  
DR HSSP; P02640; 1VII.  
SQ SEQUENCE 2214 AA; 247704 MW; 020ADC99 CRC32;

Query Match 48.3%; Score 42; DB 4; Length 2214;  
Best Local Similarity 46.2%; Pred. No. 1.7e+02;  
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 EFRWSSYVHWK 14  
:|:|:|:|:|:|  
Db 1774 QFHGDYVVRWK 1786

RESULT 12  
Q62255 PRELIMINARY; PRT; 1323 AA.  
ID Q62255  
AC Q62255;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)  
DE SPALT HOMOLOGUE (SPALT PROTEIN) (FRAGMENT).  
GN SPALT OR NSAL.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
[1]  
RN SEQUENCE FROM N.A.  
RX MEDLINE; 96391179.  
RA OTT T., KAESTNER K.H., MONAGHAN A.P., SCHUTZ G.;  
RT "The mouse homolog of the region specific homeotic gene spalt of  
Drosophila is expressed in the developing nervous system and in  
mesoderm-derived structures.";  
RL Mech. Dev. 56:117-128(1996).  
DR EMBL; X97581; CAA66196.1; -.  
DR HSSP; P07248; IARE.  
DR MGD; MGI:109295; Spalt.  
DR PROSITE; PS00028; ZINC\_FINGER\_C2H2; 9.  
DR PFAM; PF00096; zf-C2H2; 10.  
DR Zinc-finger; Metal-binding; DNA-binding.  
KW NON\_TER 1  
FT SEQUENCE 1323 AA; 139070 MW; DAD82AAD CRC32;

Query Match 47.1%; Score 41; DB 11; Length 1323;  
Best Local Similarity 42.9%; Pred. No. 1.4e+02;  
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14  
|||:|:|:|:|  
Db 29 AEFKWAQFLQHK 42

RESULT 13  
Q9XGN9 PRELIMINARY; PRT; 1687 AA.  
ID Q9XGN9  
AC Q9XGN9;  
DT 01-NOV-1999 (TReMBLrel. 12, Created)  
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)  
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)  
DE SIMILAR TO SEC7 PROTEIN.  
OS Oryza sativa (Rice).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;  
OC Poaceae; Oryza.  
[1]  
RN SEQUENCE FROM N.A.  
RC STRAIN-CV. NIPPONBARE;  
RA SASAKI T., MATSUMOTO T., YAMAMOTO K.;  
RT "Oryza sativa Nipponbare(GA3) genomic DNA, chromosome 2, PAC  
clone:PO437H03 (contig b).";  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF000367; BAA82387.1; -.  
DR HSSP; P060367; BAA82387.1; -.  
SQ SEQUENCE 1687 AA; 187179 MW; 5E0FDFF9 CRC32;

Query Match 47.1%; Score 41; DB 10; Length 1687;  
Best Local Similarity 63.6%; Pred. No. 1.8e+02;  
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 EFRWSSYVHWK 12  
|:|:|:|:|:|  
Db 1492 ETRWSEFYAEH 1502

RESULT 14  
Q52970 PRELIMINARY; PRT; 285 AA.  
ID Q52970  
AC Q52970;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)  
DE MODULATION GENES NOD8, NOD8 AND NODC.  
OS Rhizobium meliloti.  
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
OC Rhizobiaceae; Sinorhizobium.  
[1]  
RN SEQUENCE FROM N.A.  
RP

RX MEDLINE; 85087953.  
 RA TOEROEK I., KONDOROSI E., STEPROWSKI T., POSFAI J., KONDOROSI A.;  
 RT "Nucleotide sequence of Rhizobium meliloti nodulation genes."  
 RL Nucleic Acids Res. 12:9509-9524(1984).  
 DR EMBL; X01649; CAA25807.1; -.  
 SQ SEQUENCE 285 AA; 32342 MW; 157B9F20 CRC32;

Query Match 46.6%; Score 40.5; DB 2; Length 285;  
 Best Local Similarity 56.2%; Pred. No. 36;  
 Matches 9; Conservative 0; Mismatches 4; Indels 3; Gaps 1;

OY 2 EPHRWSSYM---VHWK 14  
 | | | | | | | | | |  
 Db 82 ETTWSSYMSLKVQWK 97

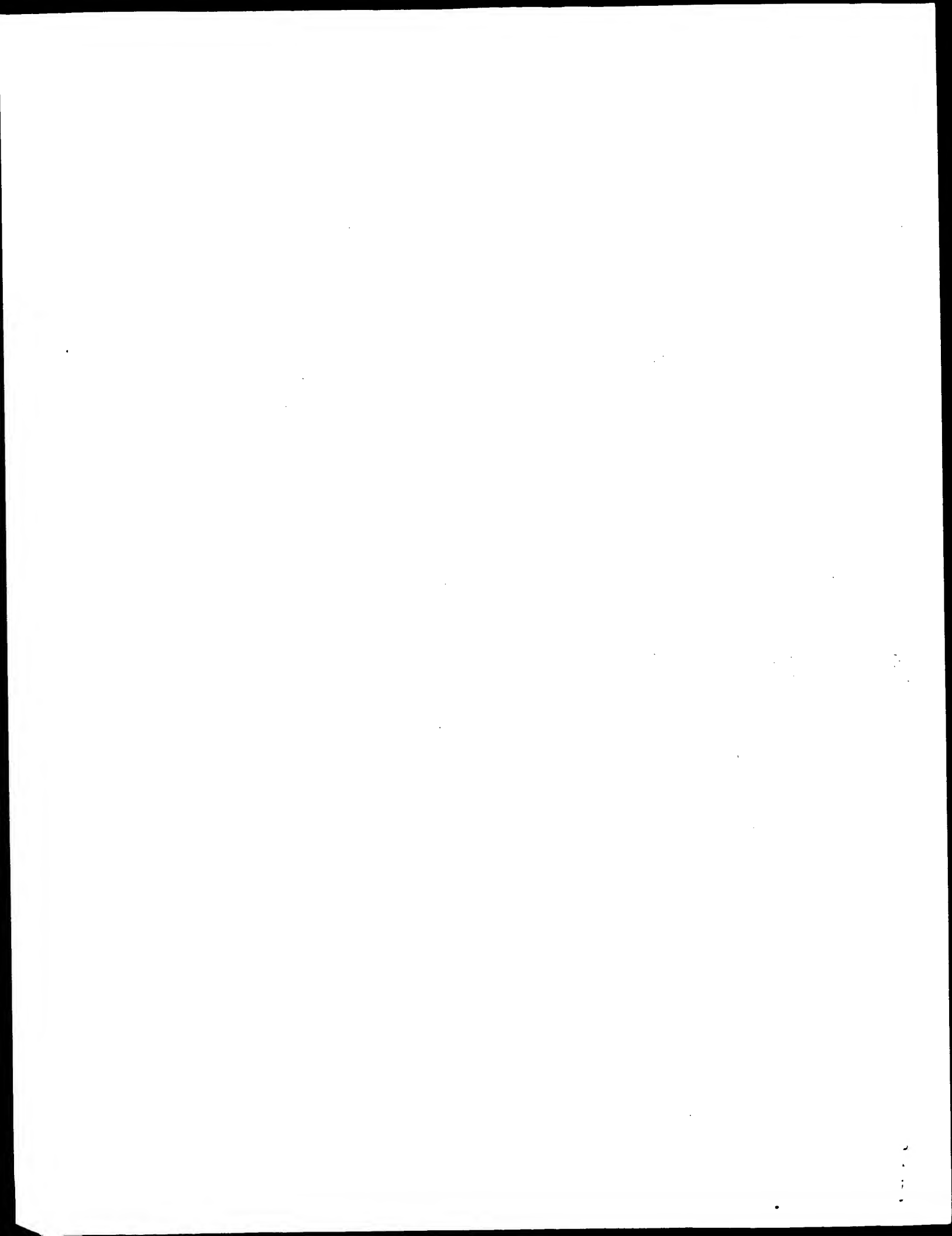
## RESULT 15

O78332 PRELIMINARY; PRT; 508 AA.  
 AC O78332;  
 DT 01-NOV-1998 (TREMELrel. 08, Created)  
 DT 01-MAY-1999 (TREMELrel. 10, Last sequence update)  
 DT 01-NOV-1999 (TREMELrel. 12, Last annotation update)  
 DE MATUREASE (FRAGMENT).  
 GN YCF14 OR MATK.  
 OS Pergularia daemia.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;  
 OC core eudicots; Asteridae; euasterids I; Gentianales; Asclepiadaceae;  
 OC Pergularia.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 98334575.  
 RA CIVEYREL L., LE THOMAS A., FERGUSON K., CHASE M.W.;  
 RT "Critical reexamination of palynological characters used to delimit  
 RT Asclepiadaceae in comparison to the molecular phylogeny obtained from  
 RT plastid matk sequences."  
 RL Mol. Phylogenet. Evol. 9:517-527(1998).  
 DR EMBL; 298191; CAB10879.2; -.  
 DR MENDEL; 30397; Perda:ycf14:30397.  
 DR PFAM; PF01348; Intron\_maturas2; 1.  
 KW Chloroplast.  
 FT NON\_TER 1  
 SQ SEQUENCE 508 AA; 60145 MW; EC02C198 CRC32;

Query Match 46.6%; Score 40.5; DB 8; Length 508;  
 Best Local Similarity 50.0%; Pred. No. 65;  
 Matches 6; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

OY 4 HRWSSYMYH-WK 14  
 : : | | | | |  
 Db 299 NKWKSYLHFWQ 310

Search completed: September 13, 2000, 02:24:09  
 Job time: 177 sec



OM of: US-09-155-076-1 to: EST.\* out\_format : pfs

Date: Sep 13, 2000 2:42 AM

About: Results were produced by the GenCore software, version 4.5,  
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Command line parameters:

-MODEL=framet p2n.model -DEV=xlp  
-O=/cn2\_1/USPTO\_spool/US09155076/runat\_20082000\_092504\_15735/app\_query.fasta\_1.144  
-DB=EST -CFMT=fastap -SUFFIX=first -GAPOP=12.000 -GAPEXT=4.000  
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -QGAPOP=4.500  
-GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000  
-FGAEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000  
-DELEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0  
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0  
-MAXLEN=100000 -USER=US09155076 -CGN1\_1\_1327 -NCPU=6 -ICPU=3  
-LONGLOG -NO\_XLPXY -WAIT -THREADS=1

Search information block:

Query: US-09-155-076-1

Query length: 14

Database: EST.\*

Database sequences: 5247842

Database length: -2090053206

Search time (sec): 875.890000

score\_list:

Sequence	Strd Orig	Zscore	Escore	Len	Documentation
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gb_est50:N90761	+	87.00	254.42	254	T28280 EST35080 Human Embryo HC
gb_est25:A1764103	+	87.00	251.16	378	A1764103 UR-R-YO-acy-h-04-0-UI-
gb_est48:F27586	+	87.00	250.76	378	F27586 HSPD15598 HM3 Homo sapie
gb_est14:AA933814	+	87.00	250.71	380	AA933814 0184b09.s1 NCI_CGAP_K1
gb_est44:AA612795	+	87.00	250.61	384	AA612795 hh33a07.x1 NCI_CGAP_Lu
gb_est14:AA998511	+	87.00	250.40	393	AA998511 UR-R-CO-le-h-11-0-UI-
gb_est25:A1766812	+	87.00	250.35	395	A1766812 w189a12.x1 NCI_CGAP_K1
gb_est26:A1847791	+	87.00	250.35	395	A1847791 UR-M-AK1-aev-f-02-0-UI-
gb_est19:A1360141	+	87.00	250.01	410	A1360141 Q983d10.x1 NCI_CGAP_Bu
gb_est24:A1890171	+	87.00	249.99	411	A1890171 tx33a02.x1 NCI_CGAP_Lu
gb_est7:AA401251	+	87.00	249.94	413	AA401251 zv66b01.s1 Soares tota
gb_est45:AA653940	+	87.00	248.15	496	AA653940 102878 MARC lBOV Bos t
gb_est1:AA030863	+	87.00	248.16	501	AA030863 m145c07.r1 Soares mous
gb_est2:AA118440	+	87.00	247.92	514	AA118440 mo34s07.r1 Life Tech m
gb_est38:AA141312	+	87.00	247.76	523	AA141312 EST291353 Normalized r
gb_est19:A1325377	+	87.00	247.57	534	A1325377 m145c07.y1 Soares mous
gb_est18:A1227851	+	87.00	247.47	540	A1227851 EST224546 Normalized r
gb_est19:A1323369	+	87.00	247.32	549	A1323369 m145c07.x1 Soares mous
gb_est23:A1651494	+	83.00	239.15	0.0002	A1651494 wb06d09.x1 NCI_CGAP_G
gb_est4:AA271549	+	82.00	235.94	0.0003	AA271549 vb74f09.r1 Soares mous
gb_est48:F34547	+	81.00	234.90	0.0003	F34547 HSPD29467 HM3 Homo sapie
gb_est53:W15259	+	74.00	211.03	0.0083	W15259 zb22e03.r1 Soares fetal
gb_est14:AA992576	+	71.00	196.46	0.0410	AA992576 ot97e06.s1 Soares tota
gb_est43:AA531512	+	65.00	183.13	0.2264	AA531512 UR-R-B01-aj1-h-01-0-UI-
gb_est26:A1837078	+	64.00	183.51	0.2156	A1837078 UR-M-AK0-ade-b-02-0-UI-
gb_est24:A1695880	+	62.00	172.63	0.8703	A1695880 tx94b01.x1 NCI_CGAP_G
gb_est7:AA443431	+	62.00	172.00	0.9440	AA443431 tx94b01.r1 Soares tota
gb_est9:AA555331	+	62.00	170.13	1.20	AA555331 hk79h09.s1 NCI_CGAP_B
gb_est13:AA885311	+	62.00	169.81	1.25	AA885311 al59g09.s1 Soares_NFL
gb_est13:AA1015613	+	62.00	169.77	1.26	AA1015613 ov29f06.x1 Soares test
gb_est25:A1829578	+	62.00	169.65	1.28	A1829578 wf28f01.x1 Soares_NFL
gb_est6:AA346027	+	57.00	163.19	2.92	AA346027 EST52141 Greater oment
gb_gss11:AO811907	+	56.00	156.71	6.71	AO811907 HS:5251.A2.C04.SP6E.RP
gb_gss7:AO506219	+	53.00	147.02	23.24	AO506219 RPCI-11-313B21.TU.RPC
gb_est23:A1575368	+	52.00	146.91	23.56	A1575368 wb9e05.x1 NCI_CGAP_PH
gb_gss19:AO724600	+	52.00	142.45	41.75	AO724600 HS-5387.A2.H01.T7A.RP
gb_gss9:AO633028	+	52.00	140.80	51.60	AO633028 RPCI-11-473N10.TV.RP
gb_gss18:CNS003MU	+	52.00	137.49	78.85	AL064706 Drosophila melanogaster
gb_gss18:CNS00CIS	+	52.00	137.33	80.49	AL059131 Drosophila melanogaster
gb_gss18:CNS00358	+	52.00	136.47	89.94	AL065901 Drosophila melanogaster

gb\_gss18:CNS00358 - 52.00 136.32 91.71 1101 ! AL064600 Drosophila melanogaster  
gb\_gss18:CNS00G7G - 52.00 136.32 91.71 1101 ! AL071732 Drosophila melanogaster  
gb\_gss18:CNS00LOD - 52.00 136.32 91.71 1101 ! AL068620 Drosophila melanogaster  
gb\_est5:AA318711 + 51.00 143.79 35.16 354 ! AA318711 EST20881 Adrenai ci

seq\_name: gb\_est50:N90761

seq\_documentation\_block:  
LOCUS N90761 248 bp mRNA 03-APR-1996  
DEFINITION zb22e03.s1 Soares fetal lung NBHL19W Homo sapiens cDNA clone  
IMAGE:302812 3' similar to gb:M55040 ACETYLCHOLINESTERASE PRECURSOR  
(HUMAN); mRNA sequence.

ACCESSION N90761  
VERSION N90761.1 GI:1444088  
KEYWORDS EST.  
SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 248)  
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Maria, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE The Washu-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT On Dec 30, 1997 this sequence version replaced gi:905921.

Contact: Wilson RK

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality

Possible reversed clone: polyT not found

Seq primer: EMPRimer

High quality sequence stop: 1.

Location/Qualifiers

1..248

/organism="Homo sapiens"

/db\_xref="GB:1247744"

/db\_xref="taxon:9606"

/clone="IMAGE:302812"

/clone\_lib="Soares fetal lung NBHL19W"

/dev\_stage="19 weeks"

/lab\_host="DH10B (ampicillin resistant)"

/note="Organ: lung; Vector: pT73D (Pharmacia) with a

modified polylinker; Site: 1: Not I; Site 2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo(dT) primer

[5'-GCTTACCAATGATGAGGAGCGCCGCAATTTTCTTTT-3']

double-stranded cDNA was size selected, ligated to Eco RI

adapters (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of a modified pT73 vector

(Pharmacia). Library went through one round of

normalization to a Cot = 5. Library constructed by Bento

Soares and M.Fatima Bonaldo. This library was constructed

from the same fetus as the fetal heart library, Soares

fetal heart NBHL19W."

BASE COUNT 47 a 89 c 57 g 47 t 8 others

ORIGIN

alignment\_scores:

Quality: 87.00 Length: 14

Ratio: 6.214 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-155-076-1 x N90761

Align seg 1/1 to: N90761 from: 1 to: 248

1 AlagluPheHisArgTrpSerSeryrMetValHisTrpLys 14  
 11 GCGAGTTCACCGCTGGAGCTCCTACATGGTGCACCTGGAAG 52

seq\_name: gb\_est52:T28280

seq\_documentation\_block: 254 bp mRNA EST 06-SEP-1995  
 LOCUS T28280 Human Embryo Homo sapiens cDNA 5' end similar to  
 DEFINITION acetylcholinesterase (HT:518), mRNA sequence.  
 ACCESSION T28280  
 VERSION T28280.1 GI:610378  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 254)  
 AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,  
 Bult,C.J., Lee,N., Kirtness,E.F., Weinstock,K.G., Gocayne,J.D.,  
 White,O., Sutton,G., Blake,J.A., Brandon,R.C., Chiu,M.-W.,  
 Clayton,R.A., Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,  
 Fitzgerald,L.M., FitzHugh,W.M., Fritchman,J.L., Geoghagen,N.S.M.,  
 Glodok,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkley,R.P.S.,  
 Kelley,J.M., Klimek,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M.,  
 Merrick,J.M., Moreno-Palancas,R.F., McDonald,L.A., Nguyen,D.T.,  
 Pellegrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L.,  
 Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R.,  
 Weidman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A.,  
 Coleman,T.A., Collins,E.-J., Dimke,D., Feng,P., Ferrie,A.,  
 Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,J.M.,  
 Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Ji,H., Li,H.,  
 Weisner,P.S., Olsen,H., Raymond,L., Wei,Y.-F., Wing,J., Xu,C.,  
 Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A.,  
 Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.  
 Initial Assessment of Human Gene Diversity and Expression Patterns  
 Based Upon 83 Million Basepairs of cDNA Sequence  
 NATURE 377, 3-174 (1995)  
 JOURNAL Nature 377, 3-174 (1995)  
 MEDLINE 96026280  
 COMMENT On May 10, 1995 this sequence version replaced gi:805490.  
 Other\_ESTs: TNC20776  
 Contact: Venter, JC  
 The Institute for Genomic Research  
 932 Clopper Rd, Gaithersburg, MD 20878  
 Tel: 3018699056  
 Fax: 3018699423  
 Email: tdbinfo@tdb.tigr.org  
 For clone availability, additional sequence and expression  
 information related to this EST, please contact the TIGR Database  
 (tdbinfo@tdb.tigr.org)  
 Insert Length: 1145 Std Error: 0.00  
 Seq primer: M13 Reverse  
 High quality sequence stop: 187.  
 Location/Qualifiers  
 1. 254  
 /organism="Homo sapiens"  
 /db\_xref="ATCC (inhost):101797"  
 /db\_xref="taxon:9606"  
 /clone\_lib="Human Embryo"  
 /tissue\_type="embryo"  
 45 a 89 c 78 g 41 t 1 others

alignment\_scores:  
 Quality: 87.00 Length: 14  
 Ratio: 6.214 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000  
 alignment\_block:  
 US-09-155-076-1 x T28280

Align seg 1/1 to: T28280 from: 1 to: 254

1 AlagluPheHisArgTrpSerSeryrMetValHisTrpLys 14  
 138 GCGAGTTCACCGCTGGAGCTCCTACATGGTGCACCTGGAAG 179

seq\_name: gb\_est25:AI764103

seq\_documentation\_block: 362 bp mRNA EST 25-JUN-1999  
 LOCUS AI764103  
 DEFINITION UI-R-YO-acy-h-04-0-UI-s1 UI-R-YO Rattus norvegicus cDNA clone  
 UI-R-YO-acy-h-04-0-UI 3', mRNA sequence.  
 ACCESSION AI764103  
 VERSION AI764103.1 GI:5210038  
 KEYWORDS EST.  
 SOURCE Norway rat.  
 ORGANISM Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 REFERENCE 1 (bases 1 to 362)  
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.  
 TITLE Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 JOURNAL Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE 97044477  
 COMMENT Contact: Soares, MB  
 Program for Rat Gene Discovery and Mapping  
 University of Iowa  
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: msoares@blue.weeg.uiowa.edu  
 The sequence contained an oligo-dt track that was present in the  
 oligonucleotide that was used to prime the synthesis of first  
 strand cDNA and therefore this may represent a bonafide poly A  
 tail. The sequence tag present in the cDNA between the NotI site  
 and the oligo-dt track served to verify it as a clone from the  
 normalized Eye library cDNA Library Preparation: M.B. Soares Lab  
 Clone distribution: clones will be available through Research  
 Genetics (www.resgen.com) The following repetitive elements were  
 found in this cDNA sequence: 1-30, >POLY\_A#simple\_repeat  
 Seq primer: M13 Forward  
 POLYR=Yes.  
 Location/Qualifiers  
 1. 362  
 /organism="Rattus norvegicus"  
 /strain="Sprague-Dawley"  
 /db\_xref="taxon:10116"  
 /clone="UI-R-YO-acy-h-04-0-UI"  
 /clone\_lib="UI-R-YO"  
 /dev\_stage="adult"  
 /lab\_host="DH10B (Life Technologies)"  
 /note="Vector: pT73D-Pac (Pharmacia) with a modified  
 polylinker; Site\_1: Not I; Site\_2: Eco RI; The UI-R-YO  
 library is a subtracted library derived from an  
 individually-tagged normalized whole-eye (minus the lens)  
 library. The driver for the subtraction consisted of a  
 pool of all previous libraries (UI-R-AO, UI-R-AI, UI-R-E0,  
 UI-R-EI, UI-R-CO, and UI-R-CI). The tag is a string of  
 3-5 nucleotides present between the Not I site and the  
 oligo-dt track which allows identification of the library  
 of origin of a clone within the mixture. The subtracted  
 library (UI-R-YO) was constructed as follows: PCR  
 amplified cDNA inserts from previous library clones from  
 which 3' ESTs had been derived were used as a driver in a  
 hybridization with the normalized whole-eye library in  
 the form of single-stranded circles. The remaining  
 single-stranded circles (subtracted library) was purified  
 by hydroxyapatite column chromatography, converted to  
 double-stranded circles and electroporated into DH10B  
 bacteria (Life Technologies) to generate the UI-R-YO

FEATURES  
 Source



library. This procedure has been previously described (Bonaldó, Lennon and Soares, Genome Research 8: 791-806, 1996); TAG\_LIB=UI-R-Y0; TAG\_TISSUE=EYE; TAG\_SEQ=CATTG

# BASE COUNT

71 a 87 c 116 g 88 t

## alignment\_scores:

Quality: 87.00 Length: 14  
Ratio: 6.214 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

## alignment\_block:

US-09-155-076-1 x AI764103/rev ..

Align seg 1/1 to reverse of: AI764103 from: 1 to: 362

1 AlaGlupPheHisArgTrpSerSerTyrMetValHisTrpLys 14

|||||  
340 GCCGAGTTCCACCGCTGGAGCTCTACATGGTGCACCTGGAAG 299

seq\_name: gb\_est48:F27586

## seq\_documentation\_block:

LOCUS F27586 378 bp mRNA EST 13-MAY-1999  
DEFINITION HSPD15598 HM3 Homo sapiens cDNA clone s4000002G06, mRNA sequence.  
ACCESSION F27586  
VERSION F27586.1 GI:4813212  
KEYWORDS EST.  
SOURCE human.

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 378)

## AUTHORS

Pandolfo, D., Topppo, S., Muraro, T., Caldara, F., Pacchioni, B., Pallavicini, A.,  
Identification of 4370 expressed sequence tags from a  
3'-end-specific cDNA library of human skeletal muscle by DNA  
sequencing and filter hybridization  
Genome Res. 6 (1), 35-42 (1996)

## JOURNAL

96276048

## MEDLINE

On Jul 7, 1999 this sequence version replaced gi:5410190.

## COMMENT

Contact: Valle G.  
CIRI Biotechnology Centre  
University of Padua  
Via Trieste 75, 35121 Padua, Italy  
ABI Chromatograms and other information are available on WWW at  
http://group.bio.unipd.it.

## FEATURES

### source

Location/Qualifiers  
1..378  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="s4000002G06"  
/clone\_lib="HM3"  
/sex="female"

/tissue\_type="pectoral muscle (after mastectomy)"  
/note="Vector: pcDNAII (Invitrogen); Site 1: BstXI;  
Site 2: NotI; The library was constructed by G.  
Lanfranchi. This library is not subtracted nor normalized.  
The first strand cDNA was primed with a biotinylated  
oligo-dT-NotI primer  
(5'-biotin-AACCCGCTCAGCGCCGCTTTTTTTTTTTTTTTT-3'). The  
ds cDNA was sonicated and size-selected in the range  
350-550 bp. The 3' specific fragments were selected by  
streptavidin coated magnetic beads, ligated to  
non-palindromic BstXI adapters, NotI digested and  
directionally cloned into BstXI-NotI cut pcDNAII vector."

# BASE COUNT

65 a 147 c 102 g 64 t

## ORIGIN

## alignment\_scores:

Quality: 87.00 Length: 14

Ratio: 6.214 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

## alignment\_block:

US-09-155-076-1 x F27586 ..

Align seg 1/1 to: F27586 from: 1 to: 378

1 AlaGlupPheHisArgTrpSerSerTyrMetValHisTrpLys 14

|||||  
115 GCCGAGTTCCACCGCTGGAGCTCTACATGGTGCACCTGGAAG 156

seq\_name: gb\_est14:AA933814

## seq\_documentation\_block:

LOCUS AA933814 380 bp mRNA EST 26-AUG-1998  
DEFINITION O184b09.s1 NCI-CGAP\_Kid5 Homo sapiens cDNA clone IMAGE:1536281 3',  
similar to gb:M55040 ACETYLCHOLINESTERASE PRECURSOR (HUMAN);, MRNA  
sequence.

## ACCESSION

AA933814

## VERSION

AA933814.1 GI:3090082

## KEYWORDS

EST.

## SOURCE

human.

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 380)

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

On Feb 11, 1998 this sequence version replaced gi:2873131.  
Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert\_Strausberg@nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/bbrp/image/image.html  
Insert length: 437 Std Error: 0.00  
Seq primer: -40ml3 fwd. RT from Amersham.

## FEATURES

### source

Location/Qualifiers  
1..380  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1536281"  
/clone\_lib="NCI-CGAP\_Kid5"  
/tissue\_type="2 pooled tumors (clear cell type)"  
/lab\_host="DH10B"

/note="Organ: kidney; Vector: p7T3D-Pac (Pharmacia) with  
a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(gt) primer [5',  
AAGTCGAGCAAGATCGCGCGCAATATTTTATTTTATTTT 3'],  
double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified p7T3 vector. Library  
went through one round of normalization. Library  
constructed by Bento Soares and M. Fatima Bonaldó."

BASE COUNT 65 a 150 c 101 g 64 t

## ORIGIN

## alignment\_scores:

Quality: 87.00 Length: 14  
Ratio: 6.214 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

## alignment\_block:

US-09-155-076-1 x AA933814 ..

Wed Sep 13 08:11:33 2000

Align seg 1/1 to: AA933814 from: 1 to: 380

1 AlagluPheHisArgTrpSerSerTyrMetValHisTrpLys 14  
 |||||  
 115 GCCGAGTTCACCGCTGGAGCTCTACATGTCGACTGGAAG 156

seq\_name: gb\_est44:AW612795

seq\_documentation\_block: 384 bp mRNA EST 23-MAR-2000  
 LOCUS AW612795 hh33a07.x1 NCI\_CGAP\_Lu24 Homo sapiens cDNA clone IMAGE:2958884 3'  
 DEFINITION similar to contains PTR5.t3 PTR5 repetitive element ;, mRNA  
 sequence.  
 ACCESSION AW612795  
 VERSION AW612795.1 GI:7317981  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 384)  
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Tel: (301) 496-1550  
 Email: Robert.Strausberg@nih.gov  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution Information can be  
 found through the I.M.A.G.E. Consortium/LINL at:  
 image.lnl.gov/image/html/iresources.shtml

Possible reversed clone: polyT not found  
 Seq primer: -400P from Gibco.  
 Location/Qualifiers  
 1..384  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2958884"  
 /clone\_lib="NCI\_CGAP\_Lu24"  
 /tissue\_type="carcinoid"  
 /lab\_host="DH10B"  
 /note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a  
 modified polylinker; Plasmid DNA from the normalized  
 library NCI\_CGAP\_Lu5 was prepared, and ss circles were  
 made in vitro. Following HAP purification, this DNA was  
 used as tracer in a subtractive hybridization reaction.  
 The driver was PCR-amplified cDNAs from a pool of 5,000  
 clones made from the same library (cloneIDs  
 1414920-1417991 and 1520904-1522439). Subtraction by Bento  
 Soares and M. Fatima Bonaldo.  
 66 a 154 c 96 g 68 t

BASE COUNT  
 ORIGIN

alignment\_scores:  
 Quality: 87.00 Length: 14  
 Ratio: 6.214 caps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
 US-09-155-076-1 x AW612795 ..

Align seg 1/1 to: AW612795 from: 1 to: 384

1 AlagluPheHisArgTrpSerSerTyrMetValHisTrpLys 14  
 |||||

88 GCCGAGTTCACCGCTGGAGCTCTACATGTCGACTGGAAG 129

seq\_name: gb\_est14:AA998511

seq\_documentation\_block: 393 bp mRNA EST 04-JUL-1999  
 LOCUS AA998511 UI-R-CO-ie-h-11-0-UI.s1 UI-R-CO Rattus norvegicus cDNA clone  
 DEFINITION UI-R-CO-ie-h-11-0-UI 3', mRNA sequence.  
 ACCESSION AA998511  
 VERSION AA998511.1 GI:4290364  
 KEYWORDS EST.  
 SOURCE Norway rat.  
 ORGANISM Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.

REFERENCE 1 (bases 1 to 393)  
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.  
 TITLE Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 JOURNAL Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE 9704477  
 COMMENT On Jun 5, 1998 this sequence version replaced gi:3189162.  
 Contact: Soares, MB  
 Program for Rat Gene Discovery and Mapping  
 University of Iowa  
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: mscoares@blue.weeg.uiowa.edu

The sequence tag present in the cDNA between the NotI site and the  
 oligo-dt track served to identify it as a clone from the normalized  
 adult Brain library. cDNA Library Preparation: M. Fatima Bonaldo,  
 Ph.D. Clone distribution: clones will be available through Research  
 Genetics This clone is also available through the I.M.A.G.E.  
 Consortium at LINL (info@image.lnl.gov). IMAGE ID=1774140  
 Seq primer: M13 Forward  
 POLYA=No.

Location/Qualifiers  
 1..393  
 /organism="Rattus norvegicus"  
 /strain="Sprague-Dawley"  
 /db\_xref="taxon:10116"  
 /clone="UI-R-CO-ie-h-11-0-UI"  
 /clone\_lib="UI-R-CO"  
 /dev\_stage="adult"  
 /lab\_host="DH10B (Life Technologies)"  
 /note="Vector: pT73D-Pac (Pharmacia) with a modified  
 polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-CO  
 library is a subtracted library derived from the UI-R-A1  
 and UI-R-E1 libraries. The UI-R-A1 library consisted of a  
 mixture of individually tagged normalized libraries  
 constructed from rat placenta, adult lung, brain, liver,  
 kidney, heart, spleen, ovary, and muscle. The UI-R-E1  
 library consisted of a mixture of individually tagged  
 normalized libraries constructed from 8, 12 and 18-day  
 embryo. The tag is a string of 3-5 nucleotides present  
 between the Not I site and the oligo-dt track which  
 allows identification of the library of origin of a clone  
 within the mixture. The subtracted library (UI-R-CO) was  
 constructed as follows: PCR amplified cDNA inserts from a  
 pool of UI-R-A1 and UI-R-E1 clones from which 3' ESTs had  
 been derived was used as a driver in a hybridization with  
 the pooled UI-R-A1 and UI-R-E1 library in the form of  
 single-stranded circles. The remaining single-stranded  
 circles (subtracted library) was purified by  
 hydroxyapatite column chromatography, converted to  
 double-stranded circles and electroporated into DH10B  
 bacteria (Life Technologies) to generate the UI-R-CO  
 library. This procedure has been previously described  
 (Bonaldo, Lennon and Soares, Genome Research 6: 791-806,  
 1996)"

BASE COUNT 80 a 92 c 130 g 91 t

## ORIGIN

alignment\_scores:  
 Quality: 87.00 Length: 14  
 Ratio: 6.214 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

## alignment\_block:

US-09-155-076-1 x AA998511/rev ..

Align seg 1/1 to reverse of: AA998511 from: 1 to: 393

1 AlaGluPheHisArgTrpSerTyrMetValHisTrpLys 14

327 GCCGAGTCCACCGCTCGAGCTCTACATGTCGACTGGAG 286

seq\_name: gb\_est25:AI766812

seq\_documentation\_block:  
 LOCUS AI766812 395 bp mRNA EST 21-DEC-1999  
 DEFINITION w189a12.x1 NCI CGAP Kid12 Homo sapiens cDNA clone IMAGE:2400478 3'  
 similar to gb:M55040 ACETYLCHOLINESTERASE PRECURSOR (HUMAN); mRNA  
 sequence.

ACCESSION AI766812  
 VERSION AI766812.1 GI:52333321  
 KEYWORDS EST.  
 SOURCE human.

## ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 395)

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

## TUMOR

## JOURNAL

## COMMENT

On Apr 7, 1998 this sequence version replaced gi:3034669.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Prepared by: M. Bento Soares, Ph.D.

DNA Sequencing by: Greg Lennon, Ph.D.

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.llnl.gov/dbrrp/image/image.html

Insert Length: 442 Std Error: 0.00

Seq primer: -40UP from Gibco.

## FEATURES

## source

1. .395  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2400478"  
 /clone\_lib="NCI CGAP Kid12"  
 /tissue\_type="2 pooled tumors (clear cell type)"  
 /lab\_host="DH10B"  
 /note="Organ: kidney; Vector: pT73D-Pac (Pharmacia) with  
 a modified polylinker; Site\_1: Not 1; Site\_2: Eco RI;  
 Plasmid DNA from the normalized library NCI CGAP Kid5 was  
 prepared, and ss circles were made in vitro. Following HAP  
 purification, this DNA was used as tracer in a subtractive  
 hybridization reaction. The driver was PCR-amplified cDNAs  
 from a pool of 5,000 clones made from the same library  
 (clones 1323912-1325831, 1471368-1472903 and  
 1492104-1493255). Subtraction by Bento Soares and M.  
 Fatima Bonaldo."

## BASE COUNT

## ORIGIN

64 a 155 c 107 g 69 t

## alignment\_scores:

Quality: 87.00 Length: 14  
 Ratio: 6.214 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

## alignment\_block:

US-09-155-076-1 x AI766812 ..

Align seg 1/1 to: AI766812 from: 1 to: 395

1 AlaGluPheHisArgTrpSerTyrMetValHisTrpLys 14

119 GCCGAGTCCACCGCTCGAGCTCTACATGTCGACTGGAG 160

seq\_name: gb\_est26:AI847791

seq\_documentation\_block:  
 LOCUS AI847791 395 bp mRNA EST 15-JUL-1999

DEFINITION UI-M-AK1-aev-f-02-0-UI.s1 NIH\_BMAP\_MHY.N Mus musculus cDNA clone  
 UI-M-AK1-aev-f-02-0-UI 3', mRNA sequence.

ACCESSION AI847791

VERSION AI847791.1 GI:5491697

KEYWORDS EST.

SOURCE house mouse.

## ORGANISM

Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## MEDLINE

## COMMENT

On Apr 7, 1998 this sequence version replaced gi:3035605.

Contact: Chin, H

National Institute of Mental Health

6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD

20892-9643, USA

Tel: 301 443 1706

Fax: 301 443 9890

Email: m5t@mail.nih.gov

The sequence contained an oligo-dT track that was present in the  
 oligonucleotide that was used to prime the synthesis of first  
 strand cDNA and therefore this may represent a bonafide poly A  
 tail. The sequence tag present in the cDNA between the NotI site  
 and the oligo-dT track served to verify it as a clone from the  
 normalized hypothalamus library cDNA Library Preparation: M.B.  
 Soares Lab Clone distribution: NIH BMAP cDNA clones will be made  
 available by the means that is soon to be determined. When NIH  
 determines the means for distribution of the BMAP cDNA clones, this  
 record will be updated accordingly when that means is determined.

Seq primer: M13 Forward

PolyA-Yes.

## FEATURES

## source

1. .395  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UI-M-AK1-aev-f-02-0-UI"  
 /clone\_lib="NIH\_BMAP\_MHY\_N"  
 /dev\_stage="27-32 days"  
 /lab\_host="DH10B (Life Technologies)"  
 /note="Vector: pT73D-Pac (Pharmacia) with a modified  
 polylinker; Site\_1: Not 1; Site\_2: Eco RI; The  
 NIH\_BMAP\_MHY\_N library is a normalized library constructed  
 from mouse hypothalamus. The tag is a string of 5  
 nucleotides present between the Not I site and the  
 oligo-dT track. The library was constructed as described  
 by Bonaldo, Lennon and Soares, Genome Research 6:  
 791-806, 1996. Tissue provided by Ms. Annie Novakovich,  
 Zivic-Miller Laboratories.; TAG\_LIB=NIH\_BMAP\_MHY\_N;  
 TAG\_TISSUE=Hypothalamus; TAG\_SEQ=CGTA"

78 a 91 c 137 g 89 t

## BASE COUNT

## ORIGIN

Quality: 87.00 Length: 14  
Ratio: 6.214 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_scores:

Quality: 87.00 Length: 14  
Ratio: 6.214 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-155-076-1 x AI847791/rev ..

Align seg 1/1 to reverse of: AI847791 from: 1 to: 395

1 AlaGlupHeHisArgTrpSerTyrMetValHisTrpLys 14

|||||  
119 GCGAGTTCACCGCTGGAGCTCTACATGTCACACTGGAAG 288

seq\_name: gb\_est19:AI360141

seq\_documentation\_block:

LOCUS AI360141 410 bp mRNA EST 16-FEB-1999  
DEFINITION QY83d10.x1 NCI-CGAP\_Brn25 Homo sapiens cDNA clone IMAGE:2018611 3'  
Similar to gb:M55040 ACETYLCHOLINESTERASE PRECURSOR  
(HUMAN); contains PTR5.b2 TAR1 repetitive element ;, mRNA sequence.

ACCESSION AI360141

VERSION AI360141.1

KEYWORDS AI360141.1 GI:4111762

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheraia; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 410)

NCI/NIHDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological

Disorders and Stroke, Brain Tumor Genome Anatomy Project

(CGAP/BTGP), Tumor Gene Index

Unpublished (1998)

On Jun 22, 1998 this sequence version replaced gi:3247207.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,

Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 440 Std Error: 0.00

Seq primer: -40UP from Gibco.

Location/Qualifiers

FEATURES

source

1..410

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:2018611"

/clone\_lib="NCI-CGAP\_Brn25"

/tissue\_type="anaplastic oligodendroglioma"

/lab\_host="DH10B"

/note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a

modified polylinker; Site:1: Not I; Site:2: Eco RI; lsc

strand cDNA was primed with a Not I - oligo(dT) primer [5'

TGTTACCAATCTGAAGTGGAGCGCGCATAGTTTCTTTTCTTTTCTTTTCTTTT

T 3']; double-stranded cDNA was ligated to Eco RI

adaptors (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of the modified pT73 vector.

Library is normalized, and was constructed by Bento

Soares and M.Fatima Bonaldo."

BASE COUNT 64 a 163 c 113 g 69 t 1 others

ORIGIN

alignment\_scores:

Quality: 87.00 Length: 14  
Ratio: 6.214 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

Quality: 87.00 Length: 14  
Ratio: 6.214 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

Quality: 87.00 Length: 14  
Ratio: 6.214 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-155-076-1 x AI360141 ..

Align seg 1/1 to: AI360141 from: 1 to: 410

1 AlaGlupHeHisArgTrpSerTyrMetValHisTrpLys 14

|||||  
119 GCGAGTTCACCGCTGGAGCTCTACATGTCACACTGGAAG 160

seq\_name: gb\_est24:AI690171

seq\_documentation\_block:

LOCUS AI690171 411 bp mRNA EST 16-DEC-1999  
DEFINITION tx33a02.x1 NCI-CGAP\_Lu24 Homo sapiens cDNA clone IMAGE:2271338 3'  
similar to gb:M55040 ACETYLCHOLINESTERASE PRECURSOR  
(HUMAN); contains PTR5.b2 TAR1 repetitive element ;, mRNA sequence.

ACCESSION AI690171

VERSION AI690171.1

KEYWORDS AI690171.1 GI:4901465

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheraia; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 411)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

On Jan 19, 1998 this sequence version replaced gi:2286587.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

DNA Sequencing by: Greg Lennon, Ph.D.

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 458 Std Error: 0.00

Seq primer: -40UP from Gibco.

Location/Qualifiers

1..411

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:2271338"

/clone\_lib="NCI-CGAP\_Lu24"

/tissue\_type="carcinoid"

/lab\_host="DH10B"

/note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a

modified polylinker; Plasmid DNA from the normalized

library NCI-CGAP\_Lu5 was prepared, and ss circles were

made in vitro. Following HAP purification, this DNA was

used as tracer in a subtractive hybridization reaction.

The driver was PCR-amplified cDNAs from a pool of 5,000

clones made from the same library (cloneIDs

1414920-1417991 and 1520904-1522439). Subtraction by Bento

Soares and M. Fatima Bonaldo."

BASE COUNT 66 a 162 c 113 g 70 t

ORIGIN

alignment\_scores:

Quality: 87.00 Length: 14  
Ratio: 6.214 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

Quality: 87.00 Length: 14  
Ratio: 6.214 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

```

US-09-155-076-1 x A1690171
Align seg 1/1 to: A1690171 from: 1 to: 411

1 AlaGluPheHisArgTyrSerTyrMetValHisTrpLys 14
|||||
119 GCCGAGTTCACCGCTGGAGCTCCTACATGGTGCACTGGAAG 160

seq_name: gb_est7:AA401251

seq_documentation_block:
LOCUS AA401251 413 bp mRNA EST 16-MAY-1997
DEFINITION zv56b01.s1 Soares total fetus Nb2HF8_9w Homo sapiens cDNA clone
IMAGE:758569 3' similar to gb:M55040 ACETYLCHOLINESTERASE PRECURSOR
(HUMAN); mRNA sequence.
ACCESSION AA401251
VERSION AA401251.1 GI:2055140
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 413)
AUTHORS Hillier,L., Allien,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
Washu-Merck EST Project 1997
Unpublished (1997)
JOURNAL On Jan 17, 1998 this sequence version replaced gi:2044207.
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: polyT not found
Seq primer: -43ml3 fwd. ET from Amerisham.
FEATURES
Location/Qualifiers
source
1..413
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:758569"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from pooled 8-9 week
(total) fetus material with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCTTAATTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 68 a 163 c 111 g 71 t
ORIGIN

alignment_scores:
Quality: 87.00 Length: 14
Ratio: 6.214 Gaps: 0
Percent Similarity: 100.000

alignment_block:
US-09-155-076-1 x AA401251
Align seg 1/1 to: AA401251 from: 1 to: 413

1 AlaGluPheHisArgTyrSerTyrMetValHisTrpLys 14
|||||
186 GCCGAGTTCACCGCTGGAGCTCCTACATGGTGCACTGGAAG 227

seq_name: gb_est1:AA030863

seq_documentation_block:
LOCUS AA030863 501 bp mRNA EST 21-AUG-1996
DEFINITION m145c07.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus CDNA
clone IMAGE:466476 5' similar to gb:M55040 ACETYLCHOLINESTERASE
PRECURSOR (HUMAN); gb:X56518 Mouse mRNA for acetylcholinesterase
(MOUSE); mRNA sequence.

```

```

seq_name: gb_est45:AW653940
118 GCCGAGTTCACCGCTGGAGCTCCTACATGGTGCACTGGAAG 159

```

```

seq_documentation_block:
LOCUS AW653940 496 bp mRNA EST 05-APR-2000
DEFINITION 102878 MARC LBOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION AW653940
VERSION AW653940.1 GI:7419766
KEYWORDS EST.
SOURCE Bos taurus.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 496)
AUTHORS Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A. and
Keele,J.W.
Design and use of four pooled tissue normalized cDNA libraries for
EST discovery in cattle
Unpublished (2000)
JOURNAL Contact: Smith TPL
COMMENT USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCACGTCACGACG
Plate: 112 row: B column: 5
Seq primer: ATTAGGTGACACTATAG.
FEATURES
Location/Qualifiers
source
1..496
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC LBOV"
/tissue_type="pooled"
/lab_host="DH10B"
/notes="Vector: pCMV SPORT6; Site 1: XbaI; Site 2: XhoI;
Library made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."
BASE COUNT 91 a 177 c 137 g 91 t
ORIGIN

alignment_scores:
Quality: 87.00 Length: 14
Ratio: 6.214 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-1 x AW653940
Align seg 1/1 to: AW653940 from: 1 to: 496

1 AlaGluPheHisArgTyrSerTyrMetValHisTrpLys 14
|||||
186 GCCGAGTTCACCGCTGGAGCTCCTACATGGTGCACTGGAAG 227

seq_name: gb_est1:AA030863

seq_documentation_block:
LOCUS AA030863 501 bp mRNA EST 21-AUG-1996
DEFINITION m145c07.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus CDNA
clone IMAGE:466476 5' similar to gb:M55040 ACETYLCHOLINESTERASE
PRECURSOR (HUMAN); gb:X56518 Mouse mRNA for acetylcholinesterase
(MOUSE); mRNA sequence.

```

```

ACCESSION   AA030863
VERSION     AA030863.1  GI:1500851
KEYWORDS    EST.
SOURCE      Mus musculus
ORGANISM    house mouse.

REFERENCE   1 (bases 1 to 501)
AUTHORS    Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
TITLE       The WashU-HMI Mouse EST Project
JOURNAL     Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:280292
            Seq primer: -28M13 rev2 from Amersham
            High quality sequence stop: 168.
            Location/Qualifiers
                1..501
                /organism="Mus musculus"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="IMAGE:466476"
                /clone_lib="Soares mouse embryo N8ME13.5 14.5"
                /sex="unknown"
                /tissue_type="embryo"
                /dev_stage="13.5-14.5dpc total fetus"
                /lab_host="DH10B"
                /note="vector: p7T73D-Pac (Pharmacia) with a modified
                polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                was primed with a Not I - oligo(dT) primer [5'
                TGTTACCAATCTGAAGTGGGAGCGCGCGAAATTTTTTTTTTTTTTTTTT
                T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
                14.5dpc embryos [total RNA provided by Minoru KO, Wayne
                State Univ., from 2 l; double-stranded cDNA was ligated to
                Eco RI adaptors (Pharmacia), digested with Not I and
                cloned into the Not I and Eco RI sites of the modified
                pT7T3 vector. Library went through one round of
                normalization, and was constructed by Bento Soares and
                M.Fatima Bonaldo."
BASE COUNT   97 a 163 c 138 g 103 t
ORIGIN
alignment_scores:
    Quality: 87.00      Length: 14
    Ratio: 6.214      Gaps: 0
    Percent Similarity: 100.000      Percent Identity: 100.000

alignment_block:
US-09-155-076-1 x AA030863 ..
Align seg 1/1 to: AA030863 from: 1 to: 501
1 AlaGluPheHisArgTrpSerSerTyrMetValHisTrpLys 14
|||||
217 GCCGAGTTCACCGCTGGAGCTCTACATGCTGCTGCTGGAAG 258
seq_name: gb_est2:AA118440

seq_documentation_block:
LOCUS      AA118440          514 bp      mRNA      EST      19-NOV-1996
DEFINITION mo34a07.r1 Life Tech mouse embryo 13 5dpc 10666014 Mus musculus

```

CDNA clone IMAGE:555444 5' similar to gb:M55040  
 ACETYLCHOLINESTERASE PRECURSOR (HUMAN); gb:X56518 Mouse mRNA for  
 acetylcholinesterase (MOUSE);, mRNA sequence.

ACCESSION AA118440  
 VERSION AA118440.1 GI:1676072  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus.

REFERENCE 1 (bases 1 to 514)  
 AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,  
 Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,  
 Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,  
 Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and  
 Waterston,R.

TITLE The WashU-HMI Mouse EST Project  
 JOURNAL Unpublished (1996)  
 COMMENT Contact: Marra M/Mouse EST Project  
 WashU-HMI Mouse EST Project  
 Washington University School of MedicineP  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:336236  
 Seq primer: -28M13 rev1 from Amersham  
 High quality sequence stop: 234.  
 Location/Qualifiers

FEATURES  
 source

1..514  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:555444"  
 /clone\_lib="Life Tech mouse embryo 13 5dpc 10666014"  
 /tissue\_type="embryo"  
 /dev\_stage="13.5dpc embryos"  
 /lab\_host="DH10B"  
 /note="organ: whole embryo; Vector: pCMV-SPORT2; Site\_1:  
 SalI; Site\_2: NotI; Cloned unidirectionally. Primer:  
 Oligo dT. 13.5dpc embryos. pCMV-SPORT2 vector."

BASE COUNT 89 a 180 c 130 g 115 t  
 ORIGIN

alignment\_scores:  
 Quality: 87.00 Length: 14  
 Ratio: 6.214 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

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Align seg 1/1 to: AA118440 from: 1 to: 514

1 AlaGluPheHisArgTrpSerSerTyrMetValHisTrpLys 14  
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 202 GCCGAGTTCACCGCTGGAGCTCTACATGCTGCTGCTGGAAG 243

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 13, 2000, 02:25:26 ; Search time 14.59 Seconds  
(without alignments)  
16.811 Million cell updates/sec

Title: US-09-155-076-2

Perfect score: 16

Sequence: 1 DAEFRHDSGYEVHQQ 16

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 152396 seqs, 15329161 residues

Word size : 0

Total number of hits satisfying chosen parameters: 152396

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Listing first 45 summaries

Database :

Issued\_Patents\_AA:\*  
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3: /cgn2\_6/ptodata/2/iaa/6\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	16	100.0	16	1	US-08-302-808-10
2	16	100.0	16	2	US-08-986-948-10
3	16	100.0	21	2	US-08-659-984A-18
4	16	100.0	27	1	US-08-141-324-11
5	16	100.0	27	1	US-08-141-324-12
6	16	100.0	27	1	US-08-541-902-11
7	16	100.0	27	1	US-08-541-902-12
8	16	100.0	28	1	US-08-346-849-4
9	16	100.0	28	1	US-08-302-808-7
10	16	100.0	28	2	US-08-609-090-2
11	16	100.0	28	2	US-08-986-948-7
12	16	100.0	28	2	US-08-293-284A-4
13	16	100.0	28	2	US-08-461-216-2
14	16	100.0	30	2	US-08-609-090-3
15	16	100.0	33	2	US-08-609-090-4
16	16	100.0	33	2	US-08-659-984A-16
17	16	100.0	35	2	US-08-304-585-6
18	16	100.0	35	2	US-08-612-785B-15
19	16	100.0	35	2	US-08-612-785B-38
20	16	100.0	36	2	US-08-609-090-5
21	16	100.0	38	1	US-08-302-808-1
22	16	100.0	38	2	US-07-737-371E-68
23	16	100.0	38	2	US-08-986-948-1
24	16	100.0	39	1	US-08-302-808-2
25	16	100.0	39	2	US-08-609-090-7
26	16	100.0	39	2	US-08-682-245A-1
27	16	100.0	39	2	US-08-986-948-2
28	16	100.0	40	1	US-07-744-767A-1

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30 16 100.0 40 1 US-08-476-464A-2 Sequence 2, Appli  
31 16 100.0 40 1 US-08-304-585-1 Sequence 1, Appli  
32 16 100.0 40 1 US-08-304-585-8 Sequence 8, Appli  
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34 16 100.0 40 2 US-08-433-734-1 Sequence 1, Appli  
35 16 100.0 40 2 US-08-609-090-8 Sequence 69, Appli  
36 16 100.0 40 2 US-07-737-371E-69 Sequence 2, Appli  
37 16 100.0 40 2 US-08-682-245A-2 Sequence 3, Appli  
38 16 100.0 40 2 US-08-986-948-3 Sequence 1, Appli  
39 16 100.0 40 2 US-08-461-216-1 Sequence 1, Appli  
40 16 100.0 40 4 PCT-US92-05700-1 Sequence 1, Appli  
41 16 100.0 41 1 US-07-819-361-1 Sequence 1, Appli  
42 16 100.0 41 1 US-08-302-808-4 Sequence 4, Appli  
43 16 100.0 41 2 US-08-682-245A-3 Sequence 3, Appli  
44 16 100.0 41 2 US-08-986-948-4 Sequence 4, Appli  
45 16 100.0 42 1 US-07-744-767A-2 Sequence 2, Appli

#### ALIGNMENTS

RESULT 1  
US-08-302-808-10  
; Sequence 10, Application US/08302808  
; Patent No. 5750349  
; GENERAL INFORMATION:  
; APPLICANT: SUZUKI, No. 5750349uhiro  
; APPLICANT: OKADA, Asano  
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR  
; TITLE OF INVENTION: DERIVATIVES AND USE THEREOF  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
; STREET: 130 WATER STREET  
; CITY: BOSTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02019  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/302,808  
; FILING DATE: 15-SEP-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/JP94/00089  
; FILING DATE: 24-JAN-1994  
; APPLICATION NUMBER: 010132/1993  
; FILING DATE: 25-JAN-1993  
; APPLICATION NUMBER: 019035/1993  
; FILING DATE: 05-FEB-1993  
; APPLICATION NUMBER: 286985/1993  
; FILING DATE: 16-NOV-1993  
; APPLICATION NUMBER: 334773/1993  
; FILING DATE: 28-DEC-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DAVID, RESNICK S  
; REGISTRATION NUMBER: 34,235  
; REFERENCE/DOCKET NUMBER: 44631  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-523-3400  
; TELEFAX: 617-523-6440  
; TELEX: 200291 STRE  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single

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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; US-08-302-808-10

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Best Local Similarity 100.0%; Pred. No. 6.8e-12;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
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Db 1 DAEFRHDSGYEVHHQK 16

RESULT 2
US-08-986-948-10
; Sequence 10, Application US/08986948
; Patent No. 595317
; GENERAL INFORMATION:
; APPLICANT: SUZUKI, No. 595317uhiro
; APPLICANT: OKADA, Asano
; APPLICANT: KITADA, Chieko
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
; DERIVATIVES AND USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02019
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/986,948
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/302,808
; FILING DATE: 15-SEP-1994
; APPLICATION NUMBER: PCT/JP94/00089
; FILING DATE: 24-JAN-1994
; APPLICATION NUMBER: 010132/1993
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: 019035/1993
; FILING DATE: 05-FEB-1993
; APPLICATION NUMBER: 286985/1993
; FILING DATE: 16-NOV-1993
; APPLICATION NUMBER: 334773/1993
; FILING DATE: 28-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 44631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: 200291 STRE
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; US-08-986-948-10

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Best Local Similarity 100.0%; Pred. No. 6.8e-12;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 DAEFRHDSGYEVHHQK 16

RESULT 3
US-08-659-984A-18
; Sequence 18, Application US/08659984A
; Patent No. 5942400
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Jacobson-Croak, Kirsten L.
; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
; INHIBITION
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,984A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,152
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-659-984A-18

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Best Local Similarity 100.0%; Pred. No. 8.5e-12;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 6 DAEFRHDSGYEVHHQK 21

RESULT 4

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US-08-141-324-11
; Sequence 11, Application US/08141324
; Patent No. 5475097
; GENERAL INFORMATION:
; APPLICANT: Travis, James
; APPLICANT: Potempa, Jan S.
; APPLICANT: Barr, Philip J.
; APPLICANT: Pavloff, Nadine
; APPLICANT: Pike, Robert N.
; TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis
; TITLE OF INVENTION: Protease
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee and Winner, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/141,324
; FILING DATE: 21-OCT-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 44-93
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-499-8080
; TELEFAX: 303-499-8089
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-141-324-11

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Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
Db 9 DAEFRHDSGYEVHHQK 24
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RESULT 5
US-08-141-324-12
; Sequence 12, Application US/08141324
; Patent No. 5475097
; GENERAL INFORMATION:
; APPLICANT: Travis, James
; APPLICANT: Potempa, Jan S.
; APPLICANT: Barr, Philip J.
; APPLICANT: Pavloff, Nadine
; APPLICANT: Pike, Robert N.
; TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis
; TITLE OF INVENTION: Protease
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee and Winner, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/541,902
; FILING DATE: 21-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/141,324
; FILING DATE: 21-OCT-1993
; ATTORNEY/AGENT INFORMATION:

```

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; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/141,324
; FILING DATE: 21-OCT-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 44-93
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-499-8080
; TELEFAX: 303-499-8089
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-141-324-12

Query Match 100.0%; Score 16; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
Db 9 DAEFRHDSGYEVHHQK 24
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RESULT 6
US-08-541-902-11
; Sequence 11, Application US/08541902
; Patent No. 5707620
; GENERAL INFORMATION:
; APPLICANT: Travis, James
; APPLICANT: Potempa, Jan S.
; APPLICANT: Barr, Philip J.
; APPLICANT: Pavloff, Nadine
; APPLICANT: Pike, Robert N.
; TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis
; TITLE OF INVENTION: Protease
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee and Winner, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/541,902
; FILING DATE: 21-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/141,324
; FILING DATE: 21-OCT-1993
; ATTORNEY/AGENT INFORMATION:

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Wed Sep 13 08:11:34 2000

NAME: Ferber, Donna M.  
REGISTRATION NUMBER: 33,878  
REFERENCE/DOCKET NUMBER: 44-93  
TELEPHONE: 303-499-8080  
TELEFAX: 303-499-8089  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-541-902-11

Query Match 100.0%; Score 16; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 1.1e-11;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHQQ 16  
Db 9 DAEFRHDSGYEVHQQ 24

RESULT 7  
US-08-541-902-12  
Sequence 12, Application US/08541902  
Patent No. 5707620  
GENERAL INFORMATION:  
APPLICANT: Travis, James  
APPLICANT: Potempa, Jan S.  
APPLICANT: Barr, Philip J.  
APPLICANT: Pavloff, Nadine  
APPLICANT: Pike, Robert N.  
TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis  
TITLE OF INVENTION: Protease  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Greenlee and Winner, P.C.  
STREET: 5370 Manhattan Circle, Suite 201  
CITY: Boulder  
STATE: CO  
COUNTRY: US  
ZIP: 80303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE:  
APPLICATION NUMBER: US/08/541,902  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/141,324  
FILING DATE: 21-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Ferber, Donna M.  
REGISTRATION NUMBER: 33,878  
REFERENCE/DOCKET NUMBER: 44-93  
TELEPHONE: 303-499-8080  
TELEFAX: 303-499-8089  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-541-902-12

Query Match 100.0%; Score 16; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 1.1e-11;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHQQ 16  
Db 9 DAEFRHDSGYEVHQQ 24

RESULT 8  
US-08-346-849-4  
Sequence 4, Application US/08346849  
Patent No. 5670483  
GENERAL INFORMATION:  
APPLICANT: Zhang, Shuguang  
APPLICANT: Lockshin, Curtis  
APPLICANT: Rich, Alexander  
APPLICANT: Holmes, Todd  
TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY  
TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02173-4799  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE:  
APPLICATION NUMBER: US/08/346,849  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/973,326  
FILING DATE: 28 DECEMBER 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Brook, David E.  
REGISTRATION NUMBER: 22,592  
REFERENCE/DOCKET NUMBER: MIT-6008  
TELEPHONE: (617) 861-6240  
TELEFAX: (617) 861-9540  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-346-849-4

Query Match 100.0%; Score 16; DB 1; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.1e-11;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHQQ 16  
Db 1 DAEFRHDSGYEVHQQ 16

RESULT 9  
US-08-302-808-7

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; Sequence 7, Application US/08302808
; Patent No. 5750349
; GENERAL INFORMATION:
; APPLICANT: SUZUKI, NO. 5750349uhiro
; APPLICANT: ODAKA, Asano
; APPLICANT: KITADA, Chieko
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
; DERIVATIVES AND USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02019
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/302,808
; FILING DATE: 15-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/00089
; FILING DATE: 24-JAN-1994
; APPLICATION NUMBER: 010132/1993
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: 019035/1993
; FILING DATE: 05-FEB-1993
; APPLICATION NUMBER: 286985/1993
; FILING DATE: 16-NOV-1993
; APPLICATION NUMBER: 334773/1993
; FILING DATE: 28-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 44631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-8440
; TELEX: 200291 STRE
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; US-08-302-808-7

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Query Match      100.0%; Score 16; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 DAEFRHDSGYEVHHQK 16
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Db 1 DAEFRHDSGYEVHHQK 16

```

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RESULT 10
US-08-609-090-2
; Sequence 2, Application US/08609090
; Patent No. 5840838
; GENERAL INFORMATION:
; APPLICANT: HENSLEY, Kenneth

```

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; APPLICANT: BUTTERFIELD, D. A.
; APPLICANT: CARNEY, John M.
; APPLICANT: AKSENOV, Michael
; TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF
; AN OLIGOPEPTIDE OR POLYPEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LOWE PRICE LEBLANC & BECKER
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,090
; FILING DATE: 29-FEB-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kraus, Eric J.
; REGISTRATION NUMBER: 36,190
; REFERENCE/DOCKET NUMBER: 434-059
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-684-1111
; TELEFAX: 703-684-1124
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-609-090-2

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Query Match      100.0%; Score 16; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 DAEFRHDSGYEVHHQK 16
   |||||
Db 1 DAEFRHDSGYEVHHQK 16

```

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RESULT 11
US-08-986-948-7
; Sequence 7, Application US/08986948
; Patent No. 5955317
; GENERAL INFORMATION:
; APPLICANT: SUZUKI, NO. 5955317uhiro
; APPLICANT: ODAKA, Asano
; APPLICANT: KITADA, Chieko
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
; DERIVATIVES AND USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02019
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/986,948

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us-09-155-076-2.ra1

;; FILING DATE: 08/08/293,284A  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA: 07/973,326  
;; APPLICATION NUMBER: 07/973,326  
;; FILING DATE: 28-DEC-1992  
;; FILING DATE: 28-DEC-1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Brook, David E.  
;; REGISTRATION NUMBER: 22,592  
;; REFERENCE/DOCKET NUMBER: MIT-6008A  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (617) 861-6240  
;; TELEFAX: (617) 861-9540  
;; INFORMATION FOR SEQ ID NO: 4:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 28 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; US-08-293-284A-4

Query Match 100.0%; Score 16; DB 2; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.le-11;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 DAEFRHDSGYEVHHQK 16  
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## RESULT 13

US-08-461-216-2  
; Sequence 2, Application US/08461216  
; Patent No. 5958883  
; GENERAL INFORMATION:  
; APPLICANT: Snow, A.D.  
; TITLE OF INVENTION: ANIMAL MODELS OF HUMAN AMYLOIDOSES  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Christensen, O'Connor, Johnson and Kindness  
; STREET: 1420 Fifth Avenue, Suite 2800  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101-2347  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage  
; COMPUTER: IBM PC/386 Compatible  
; OPERATING SYSTEM: MS-DOS 4.01  
; SOFTWARE: Word for Windows-t  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/461,216  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/969,734  
; FILING DATE: October 23, 1992  
; APPLICATION NUMBER: 07/950,417  
; FILING DATE: September 23, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Broderick, Thomas F.  
; REGISTRATION NUMBER: 31,332  
; REFERENCE/DOCKET NUMBER: UOFW-1-6707  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 1-206-682-8100; 1-206-224-0709 (direct)  
; TELEFAX: 1-206-224-0779  
; TELEX: 4938023  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 28 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single

;; FILING DATE: 08/302,808  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA: 07/973,326  
;; APPLICATION NUMBER: 07/973,326  
;; FILING DATE: 28-DEC-1992  
;; FILING DATE: 28-DEC-1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: David, Resnick S  
;; REGISTRATION NUMBER: 34,235  
;; REFERENCE/DOCKET NUMBER: 44631  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 617-523-3400  
;; TELEFAX: 617-523-6440  
;; INFORMATION FOR SEQ ID NO: 7:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 28 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; HYPOTHETICAL: NO  
;; ANTI-SENSE: NO  
;; FRAGMENT TYPE: N-terminal  
;; ORIGINAL SOURCE:  
;; US-08-986-948-7

Query Match 100.0%; Score 16; DB 2; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.le-11;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16  
|||||  
DB 1 DAEFRHDSGYEVHHQK 16  
|||||

## RESULT 12

US-08-293-284A-4  
; Sequence 4, Application US/08293284A  
; Patent No. 5955343  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Todd  
; APPLICANT: Zhang, Shuguang  
; APPLICANT: Rich, Alexander  
; APPLICANT: Dipersio, C. Michael  
; APPLICANT: Lockshin, Curtis  
; TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY  
; TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES  
; TITLE OF INVENTION: THEREFOR  
; NUMBER OF SEQUENCES: 64  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02173-4799  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:

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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; DESCRIPTION: {SYMBOL 98 \f "Symbol"}\A4(1-28);
; DESCRIPTION: page 83, line 31
; US-08-461-216-2

```

```

Query Match 100.0%; Score 16; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 DAEFRHDSGYEVHHQK 16
| | | | | | | | | | | | | | | |
Db 1 DAEFRHDSGYEVHHQK 16

```

```

RESULT 14
US-08-609-090-3
; Sequence 3, Application US/08609090
; Patent No. 5840838
; GENERAL INFORMATION:
; APPLICANT: HENSLEY, Kenneth
; APPLICANT: BUTTERFIELD, D. A.
; APPLICANT: CARNEY, John M.
; APPLICANT: AKSENOV, Michael
; TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF
; AN OLIGOPEPTIDE OR POLYPEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSER: LOWE PRICE LEBLANC & BECKER
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314

```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,090
; FILING DATE: 29-FEB-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kraus, Eric J.
; REGISTRATION NUMBER: 36,190
; REFERENCE/DOCKET NUMBER: 434-059
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-684-1111
; TELEFAX: 703-684-1124
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-609-090-3

```

```

Query Match 100.0%; Score 16; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.2e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 DAEFRHDSGYEVHHQK 16
| | | | | | | | | | | | | | | |
Db 1 DAEFRHDSGYEVHHQK 16

```

```

RESULT 15
US-08-609-090-4
; Sequence 4, Application US/08609090

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; Patent No. 5840838
; GENERAL INFORMATION:
; APPLICANT: HENSLEY, Kenneth
; APPLICANT: BUTTERFIELD, D. A.
; APPLICANT: CARNEY, John M.
; APPLICANT: AKSENOV, Michael
; TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF
; AN OLIGOPEPTIDE OR POLYPEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSER: LOWE PRICE LEBLANC & BECKER
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,090
; FILING DATE: 29-FEB-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kraus, Eric J.
; REGISTRATION NUMBER: 36,190
; REFERENCE/DOCKET NUMBER: 434-059
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-684-1111
; TELEFAX: 703-684-1124
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-609-090-4

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Query Match 100.0%; Score 16; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 DAEFRHDSGYEVHHQK 16
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Db 1 DAEFRHDSGYEVHHQK 16

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Search completed: September 13, 2000, 02:25:26
Job time: 169 sec

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us-09-155-076-2.rai

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Wed Sep 13 08:11:34 2000

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Date: Sep 13, 2000 3:47 AM

About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

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-O=/cgn2.1/USPto\_spool/US09155076/runat\_29082000\_092538\_16909/app\_query.fasta\_1.144  
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-DELEXT=7.000 -START=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45  
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Search information block:

Query: US-09-155-076-2

Query length: 16

Database: GenEmbl.\*

Database sequences: 972840

Database length: 892348106

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gb_pat:AR016774	+	16.00	351.86	1.7e-11	58	AR016774 Sequence 15 from Patent W
gb_pat:AR9528	+	16.00	349.24	2.3e-11	85	A49528 Sequence 10 from Patent W
gb_pat:AR9920	+	16.00	345.07	4.0e-11	156	A69920 Sequence 15 from Patent W
gb_om:SSAPPMR	+	16.00	344.28	4.4e-11	175	X56127 S.scrofa mRNA for amyloid
gb_om:UMAPPMR	+	16.00	344.28	4.4e-11	175	X56128 U.maritimus mRNA for amyloid
gb_om:CFAPPMR	+	16.00	344.25	4.5e-11	176	X56125 C.familiaris mRNA for amyloid
gb_om:ORAPPMR	+	16.00	344.25	4.5e-11	176	X56129 O.ryctolagus sp. mRNA for amyloid
gb_om:CSAPPMR	+	16.00	344.25	4.5e-11	176	X56124 B.taurus mRNA for amyloid
gb_om:BTAPPMR	+	16.00	344.21	4.5e-11	177	X56130 Ovis sp. mRNA for amyloid
gb_om:OVAPPMR	+	16.00	344.17	4.5e-11	178	X56130 Ovis sp. mRNA for amyloid
gb_pr1:HUMAPRA41	+	16.00	343.76	4.7e-11	189	M29269 Human amyloid protein gene
gb_pr1:HUMAMYB1	+	16.00	342.06	5.9e-11	242	M37895 Human amyloid-beta protein
gb_pr2:S60721	+	16.00	341.95	6.0e-11	246	S60721 beta-amyloid peptide precursor
gb_pr2:S61380	+	16.00	341.95	6.0e-11	246	S61380 beta-amyloid peptide precursor
gb_pr2:S61383	+	16.00	341.95	6.0e-11	246	S61383 beta-amyloid peptide precursor
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gb_pat:108767	+	16.00	340.59	7.1e-11	300	I08767 Sequence 14 from Patent W
gb_pat:A69499	+	16.00	339.45	8.2e-11	354	A69499 Sequence 2 from Patent W
gb_pat:A69501	+	16.00	339.45	8.2e-11	354	A69501 Sequence 4 from Patent W
gb_pat:A69503	+	16.00	339.45	8.2e-11	354	A69503 Sequence 6 from Patent W
gb_pat:A69507	+	16.00	339.45	8.2e-11	354	A69507 Sequence 8 from Patent W
gb_pat:A72176	+	16.00	339.45	8.2e-11	354	A72176 Sequence 10 from Patent W
gb_pat:A72178	+	16.00	339.45	8.2e-11	354	A72178 Sequence 4 from Patent W
gb_pat:A72180	+	16.00	339.45	8.2e-11	354	A72180 Sequence 6 from Patent W
gb_pat:A72182	+	16.00	339.45	8.2e-11	354	A72182 Sequence 8 from Patent W
gb_pat:A72184	+	16.00	339.45	8.2e-11	354	A72184 Sequence 10 from Patent W
gb_pat:AR066418	+	16.00	339.45	8.2e-11	354	AR066418 Sequence 2 from Patent W
gb_pat:A69509	+	16.00	339.34	8.4e-11	360	A69509 Sequence 12 from Patent W
gb_pat:A72186	+	16.00	339.34	8.4e-11	360	A72186 Sequence 12 from Patent W
gb_pat:106120	+	16.00	337.28	1.1e-10	486	I06120 Sequence 10 from Patent W
gb_pat:108764	+	16.00	337.28	1.1e-10	486	I08764 Sequence 8 from Patent W
gb_pat:A47565	+	16.00	336.82	1.2e-10	520	A47565 Sequence 9 from Patent W
gb_pat:AR007224	+	16.00	336.39	1.2e-10	553	AR007224 Sequence 9 from Patent W
gb_pr3:HUMAMYB17	+	16.00	336.39	1.2e-10	553	M34878 Human amyloid-beta protein
gb_om:OCAPPEX16	+	16.00	329.76	2.9e-10	1455	X63471 O.cuniculus APP gene for Alzheimer's
gb_om:RABAMPREA	+	16.00	329.54	2.9e-10	1503	M83558 Rabbit ORF1 and amyloid
gb_pat:AR003651	+	16.00	329.46	3.0e-10	1521	AR003651 Sequence 3 from Patent W

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gb\_pat:109368 + 16.00 329.26 3.0e-10 1564 ! I09368 Sequence 1 from Patent W

gb\_pat:124950 + 16.00 329.26 3.0e-10 1564 ! I24950 Sequence 4 from Patent W

gb\_pr1:HUMAMY4A + 16.00 329.26 3.0e-10 1564 ! M18734 Human beta-amyloid A

gb\_pr1:HUMAMOB + 16.00 328.56 3.3e-10 1733 ! M16765 Human cerebrovascula

gb\_pat:129797 + 16.00 327.29 3.9e-10 2085 ! I29797 Sequence 9 from Patent W

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seq\_documentation\_block:

LOCUS AR016774 58 bp DNA PAT

DEFINITION Sequence 15 from patent US 5777194.

ACCESSION AR016774

VERSION AR016774.1 GI:3973051

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 58)

AUTHORS Scott,R.W., Reaume,A.G., Trusko,S.P. and Siman,R.

TITLE Gene-targeted mice with humanized A.beta. sequence and Swedish FAD

MUTATION

JOURNAL Patent: US 5777194-A 15 07-JUL-1998;

FEATURES Location/Qualifiers

source 1..58

BASE COUNT 23 a 11 c 11 g 13 t

ORIGIN

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Quality: 16.00 Length: 16

Ratio: 1.000 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

## alignment\_block:

US-09-155-076-2 x AR016774

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8 GATGAGAATTCAGACATGATTCAGGATATGAAGTCCACCATCAAAA 55

seq\_name: gb\_pat:A49528

seq\_documentation\_block:

LOCUS A49528 85 bp DNA PAT

DEFINITION Sequence 10 from Patent WO9608561.

ACCESSION A49528

VERSION A49528.1 GI:2302985

KEYWORDS

SOURCE unidentified.

ORGANISM unidentified.

REFERENCE 1 (bases 1 to 85)

AUTHORS Chaudhuri,B. and Stephan,C.

TITLE METHOD FOR DETECTION OF MALFOLDED PROTEIN

JOURNAL Patent: WO 9608561-A 10 21-MAR-1996;

COMMENT CIBA GEIGY AG (CH)

Other publication AU 3521595 960329.

FEATURES Location/Qualifiers

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BASE COUNT 22 a 18 c 21 g

ORIGIN

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Ratio: 1.000 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

polymerase chain reaction analysis  
Brain Res. Mol. Brain Res. 10 (4), 299-305 (1991)  
92017079

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BASE COUNT 44 a 33 c 50 g 48 t  
ORIGIN

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Quality: 16.00 Length: 16  
Ratio: 1.000 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
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18 GATGCGAGATTCCGACACGATTCGGGCTATGAGGTTTCATCACAANA 65

seq\_name: gb\_om:UMAPPMR

seq\_documentation\_block:  
LOCUS UMAPPMR 175 bp mRNA MAM 14-JUL-1992  
DEFINITION U.maritimus mRNA for amyloid precursor protein (APP) (partial).  
ACCESSION X56128  
VERSION X56128.1 GI:2165  
KEYWORDS amyloid polypeptide.  
SOURCE polar bear.  
ORGANISM Thalartos maritimus  
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
Carnivora; Fissipedia; Ursidae; Thalartos.  
REFERENCE 1 (bases 1 to 175)  
AUTHORS Johnstone,E.M.  
TITLE Direct Submission  
JOURNAL Submitted (24-SEP-1990) E.M. Johnstone, ELI LILLY AND COMPANY,  
LILLY CORPORATE CENTER 0424, INDIANAPOLIS IN 46285, USA  
REFERENCE 2 (bases 1 to 175)  
AUTHORS Johnstone,E.M., Chaney,M.O., Norris,F.H., Pascual,R. and  
Little,S.P.  
TITLE Conservation of the sequence of the Alzheimer's disease amyloid  
peptide in dog, polar bear and five other mammals by cross-species  
polymerase chain reaction analysis  
JOURNAL Brain Res. Mol. Brain Res. 10 (4), 299-305 (1991)  
MEDLINE 92017079  
FEATURES Location/Qualifiers  
1. .175  
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BASE COUNT 45 a 34 c 50 g 46 t

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Align seg 1/1 to: A49528 from: 1 to: 85

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seq\_name: gb\_pat:A69920

seq\_documentation\_block:  
LOCUS A69920 156 bp DNA PAT 07-MAY-1999  
DEFINITION Sequence 15 from Patent W09807850.  
ACCESSION A69920  
VERSION A69920.1 GI:4774427  
KEYWORDS human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 156)  
AUTHORS Preddie,E.R. and Bergmann,J.E.  
TITLE AGENTS FOR PRE-SYMPTOMATIC DETECTION AND THERAPEUTIC TARGETING OF  
ALZHEIMER'S DISEASE AND DOWN SYNDROME IN HUMANS  
JOURNAL Patent: WO 9807850-A 26-FEB-1998;  
PREDDIE ENRIQUE R (CA)  
FEATURES Location/Qualifiers  
1. .156  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="ALZAS1"

BASE COUNT 54 a 29 c 25 g 48 t  
ORIGIN

alignment\_scores:  
Quality: 16.00 Length: 16  
Ratio: 1.000 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
US-09-155-076-2 x A69920 ..  
Align seg 1/1 to: A69920 from: 1 to: 156

1 AspaLaGluPheArGHisAspSerGlyTyrGluValHisGlnLys 16  
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4 GATGCGAATTCGACATGACTCAGGATATGAAGTTCATCACAANA 51

seq\_name: gb\_om:SSAPPMR

seq\_documentation\_block:  
LOCUS SSAPPMR 175 bp mRNA MAM 14-JUL-1992  
DEFINITION S.scrofa mRNA for amyloid precursor protein.  
ACCESSION X56127  
VERSION X56127.1 GI:1895  
KEYWORDS amyloid polypeptide.  
SOURCE pig.  
ORGANISM Sus scrofa  
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
Artiodactyla; Suidae; Suina; Suidae; Sus.  
REFERENCE 1 (bases 1 to 175)  
AUTHORS Johnstone,E.M.  
TITLE Direct Submission  
JOURNAL Submitted (24-SEP-1990) E.M. Johnstone, ELI LILLY AND COMPANY,  
LILLY CORPORATE CENTER 0424, INDIANAPOLIS IN 46285, USA  
REFERENCE 2 (bases 1 to 175)  
AUTHORS Johnstone,E.M., Chaney,M.O., Norris,F.H., Pascual,R. and  
Little,S.P.  
TITLE Conservation of the sequence of the Alzheimer's disease amyloid  
peptide in dog, polar bear and five other mammals by cross-species



## ORIGIN

alignment\_scores:  
 Quality: 16.00 Length: 16  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
 US-09-155-076-2 x UMAPPMR ..  
 Align seg 1/1 to: UMAPPMR from: 1 to: 175

1 AspaLaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16  
 |||||  
 18 GACGCCGAGTCCGACATGACTCAGGATGAGTTCATCATCAAGAA 65

## seq\_name: gb\_om:CFAPPMR

seq\_documentation\_block:  
 LOCUS CFAPPMR 176 bp mRNA MAM 14-JUL-1992  
 DEFINITION C.familiaris mRNA for amyloid precursor protein (APP) (partial).  
 ACCESSION X56125  
 VERSION X56125.1 GI:872  
 KEYWORDS amyloid polypeptide.  
 SOURCE dog.

## ORGANISM

Canis familiaris  
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
 Carnivora; Fissipedia; Canidae; Canis.

REFERENCE  
 AUTHORS Johnstone, E.M.  
 TITLE Direct Submission

JOURNAL  
 Submitted (24-SEP-1990) E.M. Johnstone, ELI LILLY AND COMPANY,  
 LILLY CORPORATE CENTER 0424, INDIANAPOLIS IN 46285, USA

REFERENCE  
 2 (bases 1 to 176)

AUTHORS Johnstone, E.M., Chaney, M.O., Norris, F.H., Pascual, R. and  
 Little, S.P.

TITLE Conservation of the sequence of the Alzheimer's disease amyloid  
 peptide in dog, polar bear and five other mammals by cross-species  
 polymerase chain reaction analysis  
 JOURNAL Brain Res. Mol. Brain Res. 10 (4), 299-305 (1991)  
 MEDLINE 92017079

## FEATURES

Location/Qualifiers

1..176  
 /organism="Canis familiaris"  
 /db\_xref="taxon:9615"  
 /tissue\_type="kidney"  
 <1..>176

## CDS

/codon\_start=1  
 /product="amyloid precursor protein"  
 /protein\_id="CAA39590.1"  
 /db\_xref="GI:873"  
 /db\_xref="SWISS-PROT:Q28280"  
 /translation="ISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGG  
 VIATVIVILVLMK"

BASE COUNT  
 ORIGIN 47 a 32 c 49 g 48 t

alignment\_scores:  
 Quality: 16.00 Length: 16  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
 US-09-155-076-2 x CFAPPMR ..  
 Align seg 1/1 to: CFAPPMR from: 1 to: 176

1 AspaLaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16  
 |||||  
 19 GATGCCGAGTCCGACATGACTCAGGATGAGTTCATCATCAAGAA 66

## seq\_name: gb\_om:ORAPPMR

seq\_documentation\_block:  
 LOCUS ORAPPMR 176 bp mRNA MAM 14-JUL-1992  
 DEFINITION Oryctolagus sp. mRNA for amyloid precursor protein (APP) (partial).  
 ACCESSION X56129  
 VERSION X56129.1 GI:1817  
 KEYWORDS amyloid polypeptide.  
 SOURCE Oryctolagus cuniculus.  
 ORGANISM Oryctolagus cuniculus

Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
 Lagomorpha; Leporidae; Oryctolagus.

REFERENCE  
 AUTHORS Johnstone, E.M.  
 TITLE Direct Submission

JOURNAL  
 Submitted (24-SEP-1990) E.M. Johnstone, ELI LILLY AND COMPANY,  
 LILLY CORPORATE CENTER 0424, INDIANAPOLIS IN 46285, USA

REFERENCE  
 2 (bases 1 to 176)

AUTHORS Johnstone, E.M., Chaney, M.O., Norris, F.H., Pascual, R. and  
 Little, S.P.

TITLE Conservation of the sequence of the Alzheimer's disease amyloid  
 peptide in dog, polar bear and five other mammals by cross-species  
 polymerase chain reaction analysis  
 JOURNAL Brain Res. Mol. Brain Res. 10 (4), 299-305 (1991)  
 MEDLINE 92017079

## FEATURES

Location/Qualifiers

1..176  
 /organism="Oryctolagus cuniculus"  
 /db\_xref="taxon:9986"  
 /tissue\_type="brain"  
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## CDS

/codon\_start=3  
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 /protein\_id="CAA39594.1"  
 /db\_xref="GI:1818"  
 /db\_xref="SWISS-PROT:Q28748"  
 /translation="SEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGV  
 VIATVIVILVLMK"

BASE COUNT  
 ORIGIN 44 a 28 c 52 g 52 t

## alignment\_scores:

Quality: 16.00 Length: 16  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

## alignment\_block:

US-09-155-076-2 x ORAPPMR ..

Align seg 1/1 to: ORAPPMR from: 1 to: 176

1 AspaLaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16  
 |||||  
 18 GATGCCGAGTCCGACATGATTCGTGATATGAGTTCATCATCAAGAA 65

## seq\_name: gb\_om:CSAPPMR

seq\_documentation\_block:  
 LOCUS CSAPPMR 176 bp mRNA ROD 14-JUL-1992  
 DEFINITION Cavia sp. mRNA for amyloid precursor protein (APP) (partial).  
 ACCESSION X56126  
 VERSION X56126.1 GI:49569  
 KEYWORDS amyloid polypeptide.  
 SOURCE Cavia sp.

## ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
 Rodentia; Hystricognathi; Caviidae; Cavia.

REFERENCE  
 1 (bases 1 to 176)

AUTHORS Johnstone, E.M.

TITLE Direct Submission

JOURNAL  
 Submitted (24-SEP-1990) E.M. Johnstone, ELI LILLY AND COMPANY,  
 LILLY CORPORATE CENTER 0424, INDIANAPOLIS IN 46285, USA

```

REFERENCE
AUTHORS      2 (bases 1 to 176)
              Johnstone,E.M., Chaney,M.O., Norris,F.H., Pascual,R. and
              Little,S.P.
TITLE        Conservation of the sequence of the Alzheimer's disease amyloid
              peptide in dog, polar bear and five other mammals by cross-species
              polymerase chain reaction analysis
JOURNAL      Brain Res. Mol. Brain Res. 10 (4), 299-305 (1991)
MEDLINE      92017079
FEATURES     Location/Qualifiers
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              /organism="Bos taurus"
              /db_xref="taxon:10143"
              /tissue_type="brain"
              <1..>176
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              /product="amyloid precursor protein"
              /protein_id="CAA39591.1"
              /db_xref="GI:49570"
              /translation="ISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGG
              VVIATVIVITLMLK"
              VVIATVIVITLMLK"
BASE COUNT   52 a 30 c 46 g 48 t
ORIGIN

alignment_scores:
  Quality: 16.00      Length: 16
  Ratio: 1.000       Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-2 x CSAPPMR ..
Align seg 1/1 to: CSAPPMR from: 1 to: 176

1 AspaLaGlupheArGHisAspSerGlyTyTGluValHisGlnLys 16
|||||
19 GATCGAGAAATCCGACATGATTCAGGATATGAGATTCATCATCAAAA 66
VVIATVIVITLMLK"

seq_name: gb_om:BTAPPMR

seq_documentation_block: 177 bp mRNA MAM 14-JUL-1992
LOCUS BTAPPMR
DEFINITION B.taurus mRNA for amyloid precursor protein (APP) (partial).
ACCESSION X56124
VERSION X56124.1 GI:82
KEYWORDS amyloid polypeptide.
SOURCE Bos taurus.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Artiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 177)
AUTHORS Johnstone,E.M., Chaney,M.O., Norris,F.H., Pascual,R. and
          Little,S.P.
TITLE Conservation of the sequence of the Alzheimer's disease amyloid
          peptide in dog, polar bear and five other mammals by cross-species
          polymerase chain reaction analysis
JOURNAL Brain Res. Mol. Brain Res. 10 (4), 299-305 (1991)
MEDLINE 92017079
FEATURES Location/Qualifiers
          1..177
          /organism="Bos taurus"
          /db_xref="taxon:9913"
          /tissue_type="brain"
          <1..>177
          /codon_start=1
          /product="amyloid precursor protein"
          /protein_id="CAA39591.1"
          /db_xref="GI:83"
CDS

REFERENCE
AUTHORS      2 (bases 1 to 178)
              Johnstone,E.M., Chaney,M.O., Norris,F.H., Pascual,R. and
              Little,S.P.
TITLE        Conservation of the sequence of the Alzheimer's disease amyloid
              peptide in dog, polar bear and five other mammals by cross-species
              polymerase chain reaction analysis
JOURNAL      Brain Res. Mol. Brain Res. 10 (4), 299-305 (1991)
MEDLINE      92017079
FEATURES     Location/Qualifiers
              1..178
              /organism="Ovis sp."
              /db_xref="taxon:9939"
              /tissue_type="heart"
              <1..>178
              /codon_start=3
              /product="amyloid precursor protein"
              /protein_id="CAA39595.1"
              /db_xref="GI:1830"
              /db_xref="SWISS-PROT:Q28757"
              /translation="SEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGV
              VVIATVIVITLMLK"
              VVIATVIVITLMLK"
BASE COUNT   48 a 31 c 49 g 50 t
ORIGIN

alignment_scores:
  Quality: 16.00      Length: 16
  Ratio: 1.000       Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-2 x OVAPPMR ..
Align seg 1/1 to: OVAPPMR from: 1 to: 178

1 AspaLaGlupheArGHisAspSerGlyTyTGluValHisGlnLys 16
|||||
19 GATCGAGAAATCCGACATGATTCAGGATATGAGATTCATCATCAAAA 66
VVIATVIVITLMLK"

seq_name: gb_om:OVAPPMR

seq_documentation_block: 178 bp mRNA MAM 14-JUL-1992
LOCUS OVAPPMR
DEFINITION Ovis sp. mRNA for amyloid precursor protein (APP) (partial).
ACCESSION X56130
VERSION X56130.1 GI:1829
KEYWORDS amyloid polypeptide.
SOURCE Ovis sp.
ORGANISM Ovis sp.
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Artiodactyla; Ruminantia; Pecora; Bovidae; Caprinae;
REFERENCE 1 (bases 1 to 178)
AUTHORS Johnstone,E.M.
          Direct Submission
          Submitted (24-SEP-1990) E.M. Johnstone, ELI LILLY AND COMPANY,
          LILLY CORPORATE CENTER 0424, INDIANAPOLIS IN 46285, USA
REFERENCE 2 (bases 1 to 178)
AUTHORS Johnstone,E.M., Chaney,M.O., Norris,F.H., Pascual,R. and
          Little,S.P.
TITLE Conservation of the sequence of the Alzheimer's disease amyloid
          peptide in dog, polar bear and five other mammals by cross-species
          polymerase chain reaction analysis
JOURNAL Brain Res. Mol. Brain Res. 10 (4), 299-305 (1991)
MEDLINE 92017079
FEATURES Location/Qualifiers
          1..178
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          /protein_id="CAA39595.1"
          /db_xref="GI:1830"
          /db_xref="SWISS-PROT:Q28757"
          /translation="SEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGV
          VVIATVIVITLMLK"
          VVIATVIVITLMLK"
BASE COUNT   48 a 31 c 49 g 50 t
ORIGIN

alignment_scores:
  Quality: 16.00      Length: 16
  Ratio: 1.000       Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-2 x OVAPPMR ..
Align seg 1/1 to: OVAPPMR from: 1 to: 178

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1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisHisGlnLys 16  
 |||  
 18 GATCGAGAATCCGACATGATTCGGATATGAAGTTCATCATCAAAA 65

seq\_name: gb\_pr1:HUMAPR4A1

seq\_documentation\_block:  
 LOCUS HUMAPR4A1 189 bp DNA PRI 31-OCT-1994  
 DEFINITION Human amyloid protein gene, exon X.  
 ACCESSION M29269  
 VERSION M29269.1 GI:178862  
 KEYWORDS amyloid protein.  
 SEGMENT 1 of 2  
 SOURCE Human DNA (library of T. Maniatis), clone lambda-41.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 189)  
 AUTHORS Johnstone,E.M., Chaney,M.O., Moore,R.E., Ward,K.E., Norris,F.H. and Little,S.P.  
 TITLE Alzheimer's disease amyloid peptide is encoded by two exons and shows similarity to soybean trypsin inhibitor  
 JOURNAL Biochem. Biophys. Res. Commun. 163 (3), 1248-1255 (1989)  
 MEDLINE 89392030  
 FEATURES  
 source Location/Qualifiers  
 1..189  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /map="21q21.2"  
 <1..42  
 /gene="APP"  
 /note="intron X-1; G00-119-692"  
 43..143  
 /gene="APP"  
 /note="exon X; G00-119-692"  
 59 a 32 c  
 /note="73 bp upstream of BglII site; chromosome 21q21.2."

intron  
 exon  
 BASE COUNT 59 a 32 c 60 t  
 ORIGIN 73 bp upstream of BglII site; chromosome 21q21.2.

alignment\_scores:  
 Quality: 16.00 Length: 16  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
 US-09-155-076-2 x HUMAPR4A1 ..  
 Align seg 1/1 to: HUMAPR4A1 from: 1 to: 189

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisHisGlnLys 16  
 |||  
 93 GATCGAGAATCCGACATGATTCGGATATGAAGTTCATCATCAAAA 140

seq\_name: gb\_pr1:HUMAMYBBI

seq\_documentation\_block:  
 LOCUS HUMAMYBBI 242 bp DNA PRI 31-OCT-1994  
 DEFINITION Human amyloid-beta protein DNA, exon 14.  
 ACCESSION M37895  
 VERSION M37895.1 GI:178617  
 KEYWORDS amyloid-beta protein.  
 SEGMENT 1 of 2  
 SOURCE Human (Dutch patient with hereditary cerebral hemorrhage with amyloidosis) DNA.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 242)  
 AUTHORS Levy,E., Carman,M.D., Fernandez-Madrid,I.J., Power,M.D., Lieberburg,I., van Duinen,S.G., Bots,G.T., Luyendijk,W. and Frangione,B.  
 TITLE Mutation of the Alzheimer's disease amyloid gene in hereditary

JOURNAL cerebral hemorrhage, Dutch type  
 MEDLINE Science 248 (4959), 1124-1126 (1990)  
 FEATURES 90260663  
 source Location/Qualifiers  
 1..242  
 /organism="Homo sapiens"  
 /isolate="hereditary cerebral hemorrhage with amyloidosis of Dutch type patient"  
 /db\_xref="taxon:9606"  
 /map="21q21.2"  
 <1..103  
 /gene="APP"  
 104..204  
 /note="G00-119-692"  
 /number=1  
 205..242  
 /gene="APP"  
 intron  
 exon  
 BASE COUNT 75 a 35 c 52 g 80 t  
 ORIGIN

alignment\_scores:  
 Quality: 16.00 Length: 16  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
 US-09-155-076-2 x HUMAMYBBI ..  
 Align seg 1/1 to: HUMAMYBBI from: 1 to: 242

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisHisGlnLys 16  
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 154 GATCGAGAATCCGACATGATTCGGATATGAAGTTCATCATCAAAA 201

seq\_name: gb\_pr2:S60721

seq\_documentation\_block:  
 LOCUS S60721 246 bp mRNA PRI 23-JUL-1993  
 DEFINITION beta-amyloid peptide precursor [clone 1] [human, mRNA Partial Mutant, 246 nt].

ACCESSION S60721  
 VERSION S60721.1 GI:299644  
 KEYWORDS  
 SOURCE human.

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 246)  
 AUTHORS Denman,R.B., Rosenczwaig,R. and Miller,D.L.  
 TITLE A system for studying the effect(s) of familial Alzheimer disease mutations on the processing of the beta-amyloid peptide precursor

JOURNAL Biochem. Biophys. Res. Commun. 192 (1), 96-103 (1993)  
 MEDLINE 93236601  
 REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 129915] from the original journal article.  
 Map location: 21  
 This sequence comes from Fig. 1.

FEATURES  
 source Location/Qualifiers  
 1..246  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 1..246  
 /partial  
 /gene="beta-amyloid peptide precursor, beta APP"

gene  
 CDS  
 1..246  
 /partial  
 /gene="beta-amyloid peptide precursor, beta APP"

REFERENCE 1  
 /note="This sequence comes from Fig. 1; Protein sequence is in conflict with the conceptual translation; mismatches(44[K->N],73[W->Y],76[I->N]); beta APP"  
 /codon\_start=1  
 /product="beta-amyloid peptide precursor"

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alignment_block:
US-09-155-076-2 x S61380
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Align seg 1/1 to: S61380 from: 1 to: 246

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisHisGlnLys 16
|||||
52 GATGCAGATTCCGACATGACTCAGGATATGAAGTTCATCATCAAAAA 99

seq_name: gb_pr2:S61383

seq_documentation_block:
LOCUS S61383 246 bp mRNA 23-JUL-1993
DEFINITION beta-amyloid peptide precursor [clone 3] [human, mRNA Partial
Mutant, 246 nt].
ACCESSION S61383
VERSION S61383.1 GI:299648
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 246)
AUTHORS Denman,R.B., Rosenzwaig,R. and Miller,D.L.
TITLE A system for studying the effect(s) of familial Alzheimer disease
mutations on the processing of the beta-amyloid peptide precursor
JOURNAL Biochem. Biophys. Res. Commun. 192 (1), 96-103 (1993)
MEDLINE 93236601
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 132966] from the original journal article.
This sequence comes from Fig. 1.
Map location: 21.

FEATURES
Location/Qualifiers
Source 1..246
/organism="Homo sapiens"
/db_xref="taxon:9606"
gene 1..246
/partial
/gene="beta-amyloid peptide precursor, beta APP"
CDS 1..246
/partial
/gene="beta-amyloid peptide precursor, beta APP"
/note="this sequence comes from Fig. 1; Protein sequence
is in conflict with the conceptual translation;
mismatches(698[K->N],727[W->Y],730[I->N]); beta APP"
/codon_start=1
/product="beta-amyloid peptide precursor"
/protein_id="AAB26265.1"
/db_xref="GI:299649"
/translation="GSGLTNKTETISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSK
KGAIIGLMGVGVVIAIVITLVLMLKKQWTSIHGVE"

BASE COUNT 72 a 40 c 71 g 63 t
ORIGIN

alignment_scores:
Quality: 16.00 Length: 16
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-2 x S60721
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Align seg 1/1 to: S60721 from: 1 to: 246

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisHisGlnLys 16
|||||
52 GATGCAGATTCCGACATGACTCAGGATATGAAGTTCATCATCAAAAA 99

seq_name: gb_pr2:S61380

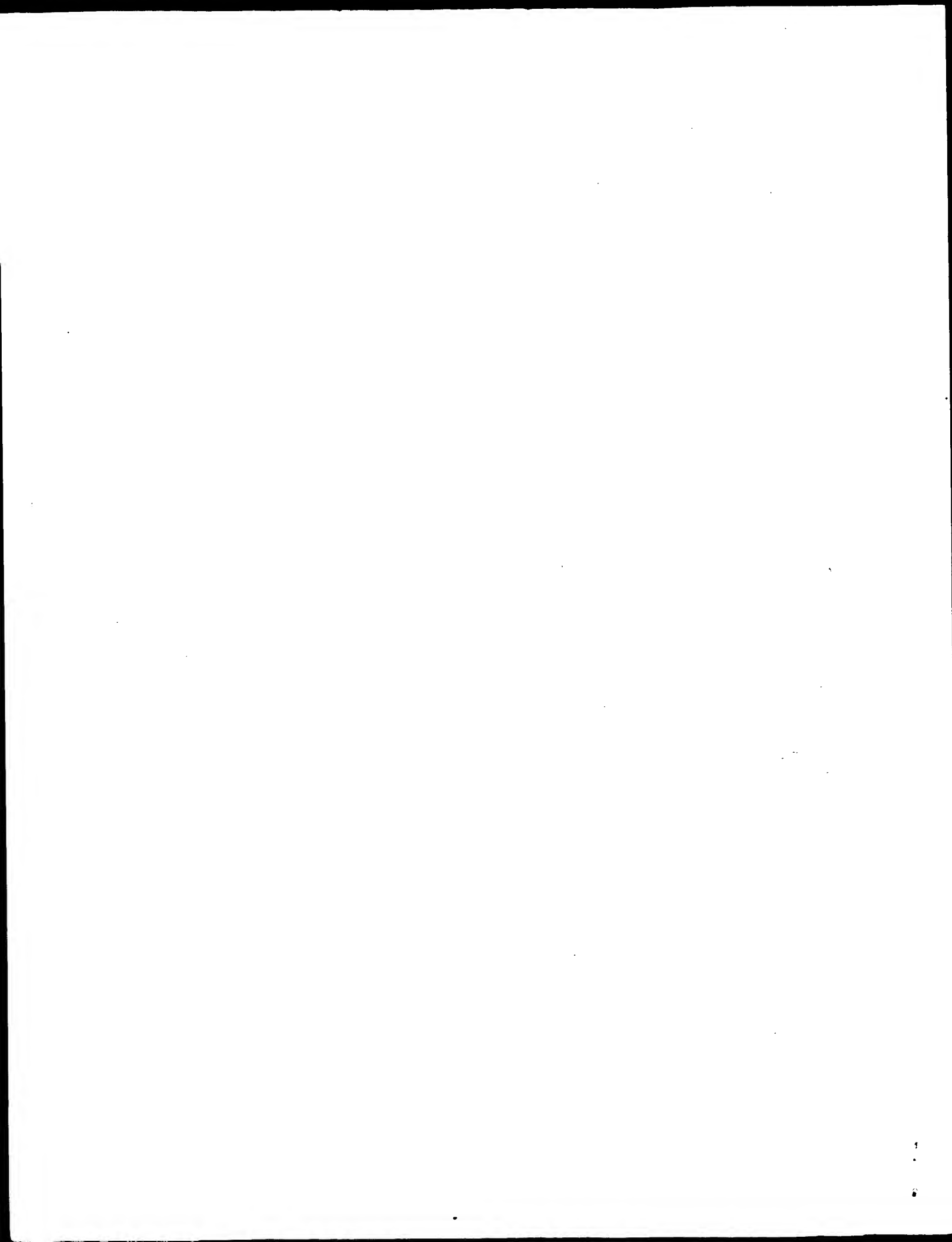
seq_documentation_block:
LOCUS S61380 246 bp mRNA 23-JUL-1993
DEFINITION beta-amyloid peptide precursor [clone 2] [human, mRNA Partial
Mutant, 246 nt].
ACCESSION S61380
VERSION S61380.1 GI:299646
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 246)
AUTHORS Denman,R.B., Rosenzwaig,R. and Miller,D.L.
TITLE A system for studying the effect(s) of familial Alzheimer disease
mutations on the processing of the beta-amyloid peptide precursor
JOURNAL Biochem. Biophys. Res. Commun. 192 (1), 96-103 (1993)
MEDLINE 93236601
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 132963] from the original journal article.
This sequence comes from Fig. 1.
Map location: 21.

FEATURES
Location/Qualifiers
Source 1..246
/organism="Homo sapiens"
/db_xref="taxon:9606"
gene 1..246
/partial
/gene="beta-amyloid peptide precursor, beta APP"
CDS 1..246
/partial
/gene="beta-amyloid peptide precursor, beta APP"
/note="this sequence comes from Fig. 1; Protein sequence
is in conflict with the conceptual translation;
mismatches(44[K->N],73[W->Y],76[I->N]); beta APP"
/codon_start=1
/product="beta-amyloid peptide precursor"
/protein_id="AAB26264.1"
/db_xref="GI:299647"
/translation="GSGLTNKTETISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSK
KGAIIGLMGVGVVIAIVITLVLMLKKQWTSIHGVE"

BASE COUNT 73 a 40 c 69 g 64 t
ORIGIN

alignment_scores:
Quality: 16.00 Length: 16
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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OM of: US-09-155-076-2 to: N\_Geneseq\_36.\* out\_format : pfs  
 Date: Sep 13, 2000 3:50 AM  
 About: Results were produced by the GenCore software, version 4.5,  
 Copyright (c) 1993-2000 CompuGen Ltd.

## Command line parameters:

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 -O=/cgn2.1/USPTO.spool/US09155076/runat\_29082000\_092539\_16943/app\_query.fasta\_1.144  
 -DB=N\_Geneseq\_36 -QFMT=fastap -SUFFIX=ring -GAPOP=4.500  
 -GAPEXT=0.050 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000  
 -GAPOP=4.500 -GAPEXT=0.050 -GAPOP=60.000 -GAPEXT=60.000  
 -DELOP=6.000 -FGAPEXT=7.000 -GAPOP=60.000 -GAPEXT=60.000  
 -TRANS-human40.cdi -LST=45 -DOCALLIGN=200 -THR\_SCORE=quality  
 -THR\_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0  
 -MAXLEN=1000000 -USER=US09155076 -CGNI\_1.75 -NCPU=6 -ICPU=3  
 -LONGLOG -NO\_XLPXY -WAIT -THREADS=1

## Search information block:

Query: US-09-155-076-2  
 Query length: 16  
 Database: N\_Geneseq\_36.\*  
 Database sequences: 311585  
 Database length: 125096042  
 Search time (sec): 75.910000

WARN: XGAPOP and XGAPEXT must be equal. Assuming XGAPOP=XGAPEXT=60.000  
 WARN: XGAPEXT and XGAPEXT must be equal. Assuming XGAPEXT=XGAPEXT=60.000

## score\_list:

Sequence	Std	Orig	ZScore	EScore	Len	Documentation
N_Geneseq_36:T38687	+	16.00	336.34	3.9e-11	58	Mouse amyloid precursor protein
N_Geneseq_36:T14516	+	16.00	333.80	5.4e-11	85	Beta-amyloid peptide coding sequence
N_Geneseq_36:N92266	+	16.00	328.94	1.0e-10	177	Region of pre-APP coding sequence
N_Geneseq_36:Q77992	+	16.00	326.50	1.1e-10	189	CDNA encoding the APP leader sequence
N_Geneseq_36:V23754	+	16.00	326.34	1.4e-10	262	Alz1 coding sequence. Nucleic
N_Geneseq_36:Q88696	+	16.00	325.51	1.6e-10	297	Beta-amyloid precursor protein
N_Geneseq_36:Q88697	+	16.00	325.51	1.6e-10	297	Beta-amyloid precursor protein
N_Geneseq_36:Q88698	+	16.00	325.51	1.6e-10	297	Beta-amyloid precursor protein
N_Geneseq_36:Q10017	+	16.00	325.44	1.6e-10	300	Sequence encoding beta-amyloid
N_Geneseq_36:Q42665	+	16.00	325.44	1.6e-10	300	Full-length beta-amyloid protein
N_Geneseq_36:Q88699	+	16.00	325.24	1.6e-10	309	Beta-amyloid precursor protein
N_Geneseq_36:Q88700	+	16.00	325.24	1.6e-10	309	Beta-amyloid precursor protein
N_Geneseq_36:T18082	+	16.00	324.69	1.7e-10	336	Familial Alzheimer's disease APP
N_Geneseq_36:V20377	+	16.00	324.34	1.8e-10	354	DNA for APP C-terminal fragment
N_Geneseq_36:V20380	+	16.00	324.34	1.8e-10	354	DNA for APP C-terminal fragment
N_Geneseq_36:V20381	+	16.00	324.34	1.8e-10	354	DNA for APP C-terminal fragment
N_Geneseq_36:V20379	+	16.00	324.34	1.8e-10	354	DNA for APP C-terminal fragment
N_Geneseq_36:V20378	+	16.00	324.34	1.8e-10	354	DNA for APP C-terminal fragment
N_Geneseq_36:V07188	+	16.00	324.34	1.8e-10	354	Flag-amyloid precursor protein
N_Geneseq_36:X08982	+	16.00	324.34	1.8e-10	354	Amyloid precursor protein (APP)
N_Geneseq_36:V20382	+	16.00	324.23	1.9e-10	360	DNA for APP C-terminal fragment
N_Geneseq_36:N80605	+	16.00	322.24	2.4e-10	486	Lambda SM2 encoding first 18 am
N_Geneseq_36:Q10015	+	16.00	322.24	2.4e-10	486	Genomic clone including beta-am
N_Geneseq_36:Q42662	+	16.00	322.24	2.4e-10	486	Clone Lambda SM2 encoding beta-am
N_Geneseq_36:Q82910	+	16.00	321.79	2.5e-10	520	Human beta amyloid fusion prote
N_Geneseq_36:V23753	+	16.00	321.59	2.6e-10	536	Alz1 coding sequence. Nucleic
N_Geneseq_36:N90437	+	16.00	324.75	6.2e-10	1504	CDNA sequence of clone amy 37
N_Geneseq_36:V36456	+	16.00	314.68	6.3e-10	1521	Maltose binding protein-APP (S
N_Geneseq_36:N90397	+	16.00	314.50	6.4e-10	1562	CDNA sequence of amy 37 clone.
N_Geneseq_36:N90396	+	16.00	313.86	7.0e-10	1721	APP-REP 751 amyloid precursor
N_Geneseq_36:Q54257	+	16.00	313.59	8.2e-10	2085	Mouse amyloid precursor protei
N_Geneseq_36:Q69003	+	16.00	312.58	8.3e-10	2088	APP695. Polynucleotide probe c
N_Geneseq_36:Q27801	+	16.00	312.06	8.8e-10	2256	Lambda APCP16814, amino acids
N_Geneseq_36:Q10014	+	16.00	312.06	8.8e-10	2256	Sequence of clone lambdaAPCP16
N_Geneseq_36:Q20532	+	16.00	312.06	8.8e-10	2256	Lambda clone APCP16814 encodes
N_Geneseq_36:Q42661	+	16.00	312.06	8.8e-10	2256	APP751. Polynucleotide probe c
N_Geneseq_36:Q27802	+	16.00	312.04	8.8e-10	2265	Amyloid precursor protein (APP)
N_Geneseq_36:X08983	+	16.00	311.91	9.0e-10	2310	Human APP770 cDNA. Identifying

N\_Geneseq\_36:Q48860 + 16.00 311.90 9.0e-10 2313 ! Mutated APP770 exon 17 DNA.  
 N\_Geneseq\_36:Q74708 + 16.00 311.90 9.0e-10 2313 ! cDNA of APP 770 gene contg.  
 N\_Geneseq\_36:N91050 + 16.00 310.29 1.1e-09 2949 ! Sequence encoding novel amy  
 N\_Geneseq\_36:Q05086 + 16.00 310.29 1.1e-09 2949 ! Sequence encodes NAP-2 gene  
 N\_Geneseq\_36:N91049 + 16.00 310.16 1.1e-09 3006 ! Sequence encoding novel amy  
 N\_Geneseq\_36:Q05085 + 16.00 310.16 1.1e-09 3006 ! Sequence encodes NAP gene a

seq\_name: N\_Geneseq\_36:T38687

seq\_documentation\_block:

ID T38687 standard; DNA; 58 BP.

AC T38687;

DE 21-JUL-1997 (first entry)

DE Mouse amyloid precursor protein exon 16 primer ST61.

KW Exon 16; murine; mouse; amyloid; precursor; protein; APP;

KW humanisation; homozygous; heterozygous; human; Abeta; Swedish;

KW familial; Alzheimer's; disease; FAD; mutation; tool; model;

KW elucidation; pathology; symptomatology; screen; inhibition;

KW transgenic; polymerase chain reaction; primer; PCR;

KW amplification; ss.

OS Synthetic.

PN W09634097-A1.

PD 31-OCT-1996.

PF 26-APR-1996; U05824.

PF 26-APR-1995; US-429207.

PR 23-APR-1996; US-636876.

PA (CEPH-) CEPHALON INC.

PI Hoffman EK, Reaume AG, Scott RW, Siman R, Trusko SP;

DR WPI; 96-497629/49.

PT Transgenic mice with humanised amyloid precursor protein gene -

PT having at least 1 Swedish FAD mutation, useful as tools or models to

PT elucidate role of human A-beta in Alzheimer's disease

PS Example 1; Page 75; 123pp; English.

CC The present sequence is a primer for the PCR amplification of exon

CC 16 of the mouse amyloid precursor protein (APP) gene, into which 6

CC humanising base pair changes was introduced. The exon was then used

CC in the preparation of mice homozygous or heterozygous for a

CC targeted APP encoding gene, comprising a human Abeta peptide

CC encoding sequence in place of the endogenous murine sequence, and

CC at least 1 Swedish Familial Alzheimer's Disease (FAD) mutation. The

CC mice can be used as tools, or models to elucidate the role of human

CC Abeta in AD pathology and symptomatology. They can also be used to

CC screen chemical compounds for the ability to inhibit in vivo

CC processing of APP, to yield the human Abeta peptide by

CC administering the chemical compounds to a mouse and measuring the

CC relative amounts of amyloidogenic and nonamyloidogenic processing

CC of APP in a sample from the mouse at an appropriate interval after

CC administration of the chemical compounds.

SQ Sequence 58 BP; 23 A; 11 C; 13 T;

## alignment\_scores:

Quality: 16.00 Length: 16  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

## alignment\_block:

US-09-155-076-2 x T38687 ..

Align seg 1/1 to: T38687 from: 1 to: 58

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16  
 |||||  
 8 GATGCAGAAATTCAGACATGATTCAGGATATGAAGTCCACCATCAAAA 55

seq\_name: N\_Geneseq\_36:T14516

seq\_documentation\_block:

ID T14516 standard; DNA; 85 BP.

AC T14516;

DT 30-OCT-1996 (first entry)

DE Beta-amyloid4 peptide coding sequence.

KW Unfolded-protein-response element; UPR; BiP; expression cassette; p53;

reporter element; protein malforming; prion; beta-amyloid peptide; plant; host cell; animal; insect cell; fungal cell; saccharomyces cerevisiae; protein aggregation inhibitor; Alzheimer's disease; cancer; therapy; ds Synthetic.

Key misc\_feature 1. .60 Location/Qualifiers  
1. .60  
/\*tag= a  
/note= "5' overhang"  
complement (85)  
/\*tag= b  
/note= "site of 60 bp 5' overhang"

WO9608561-AL.  
21-MAR-1996.  
04-SEP-1995; EQ3475.  
16-SEP-1994; EP-810536.  
(CIBA ) CIBA GEIGY AG.  
Chaudhuri B, Stephan C;  
WPI; 96-179938/18.  
Host used to determined influence of cpd. on appearance of malformed protein - also to identify cpds. that inhibit the aggregation of protein, pref. beta-amyloid, useful in treatment of Alzheimer's disease

Example 10: Page 18: 59pp: English.  
This sequence represents the beta-amyloid4 peptide. This sequence is amplified using the primers shown in T14517 and T14518, and is used in one of the expression cassettes of the invention. The first expression cassette contains one or more copies of the unfolded-protein-response (UPR) element (see T14511) operably linked to a reporter element. The second expression cassette comprises a promoter operably linked to a signal sequence, a DNA encoding a protein whose malforming is to be studied, and a terminator sequence. The protein encoding sequence in the second expression cassette is preferably a prion, p53, beta-amyloid peptide, or functional derivatives of these. The two cassettes are used to transform a host cell that is capable of excreting proteins. The host cell can be a plant, animal or insect cell, but is preferably a fungal cell (especially saccharomyces cerevisiae). The transformed host can be used to determine the influence of a compound on the appearance of a malformed protein. This is done by culturing the host cell under suitable conditions, applying the compound to be tested and measuring the amount of reporter gene activation. Compounds identified by this method can be used to inhibit protein aggregation, especially for the treatment of Alzheimer's disease or cancer.

Sequence 85 BP; 22 A; 21 C; 24 T;

alignment\_scores:  
Quality: 16.00 Length: 16  
Ratio: 1.000 Caps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
US-09-155-076-2 x T14516 ..

Align seg 1/1 to: T14516 from: 1 to: 85

1 AspAlaGluPheargHisaspSerGlyTyrGluValHisHisGlnlys 16  
|||||  
11 GACGCTGAATTAGACACGACTCTGTTACGAAGTTCACCAACAAAG 58

seq\_name: N\_Geneseq\_36:N92266

seq\_documentation\_block:  
ID N92266 standard; RNA; 177 BP.  
AC N92266;  
DE 23-APR-1990 (first entry)  
DT Region of pre-APC coding sequence.  
KW Alzheimer's disease; pre-APC coding sequence; APC protein.  
PN EP-341491-A.  
PD 15-NOV-1989.  
PF 26-APR-1989; 107531.  
PR 13-MAY-1988; US-194053.  
PT (MOLE-) Molecular Therapeutics Inc.  
PI Scangos G. Rae P, Unterbeck A, Kamarck ME;



1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16  
 |||||  
 58 GATCAGAAATTCGACATGACTCAGGATATGAGATTCATCATCAAAA 105

seq\_name: N\_Geneseq\_36:V23754

seq\_documentation\_block:

ID V23754 standard; DNA; 262 BP.  
 AC V23754;  
 DT 18-AUG-1998 (first entry)  
 DE Alzasl coding sequence.  
 KW DSas; DSASP; alzsa; Down's syndrome; diagnosis; therapy; human;  
 KW Alzheimer's disease; ss.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT CDS 50..205  
 FT /\*tag= a  
 FT /product= ALZASpl  
 FT /note= "specifically claimed fragment"

PN WO9807850-A2.  
 PD 26-FEB-1998.  
 PF 22-AUG-1997; E04599.  
 PR 22-AUG-1996; CA-183901.  
 PA (BERG/) BERGMANN J E.  
 PA (PRED/) PREDDIE E R.  
 PI Bergmann JE, Preddie ER;  
 DR WPI; 98-169155/15.  
 DR P-PSDB; W53984.  
 PT Nucleic acid molecules dsas, and alzsa - used for detecting and  
 PT treating Down's syndrome and Alzheimer's disease  
 PS Claim 13; Fig 11; 96pp; English.  
 CC This sequence represents the human alzsa1 nucleic acid. The dsas  
 CC and alzsa DNA sequences are the nucleic acids of the invention. Reagents  
 CC specifically for DSASP can be used for the diagnosis of Down's syndrome  
 CC in humans and especially in pregnant women. Molecules that inhibit the  
 CC activity of the promoters (PDS1, PDS2, PDS3, and PDS4) for dsas can be  
 CC used for treating Down's syndrome. The reagent capable of detecting  
 CC alzsa can be used for detecting Alzheimer's disease, especially in the  
 CC pre-symptomatic stage. Substances that inhibit the promoters for alzsa  
 CC can be used in treating Alzheimer's disease.  
 SQ Sequence 262 BP; 96 A; 43 C; 52 G; 71 T;

alignment\_scores:

Quality: 16.00 Length: 16  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-155-076-2 x V23754 ..

Align seg 1/1 to: V23754 from: 1 to: 262

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16  
 |||||  
 53 GATCAGAAATTCGACATGACTCAGGATATGAGATTCATCATCAAAA 100

seq\_name: N\_Geneseq\_36:Q88696

seq\_documentation\_block:

ID Q88696 standard; cDNA to mRNA; 297 BP.  
 AC Q88696;  
 DT 11-NOV-1995 (first entry)  
 DE Beta-amyloid precursor protein C-terminal peptide gene.  
 KW Human; beta-amyloid precursor protein; C-terminal peptide;  
 KW gene transfer; transgenic animal; Alzheimer disease model;  
 KW gene therapy; ss.  
 OS Homo sapiens.  
 PN EP-653154-A.  
 PD 17-MAY-1995.  
 PF 07-NOV-1994; 117512.  
 PR 12-NOV-1993; JP-306026.  
 PA (FARH ) HOECHST JAPAN LTD.

PA (FARH ) HOECHST JAPAN KK.  
 PI Kawarabayashi T, Kobayashi T, Sato M, Shoji M, Tada N;  
 DR WPI; 95-180492/24.  
 DR P-PSDB; R74694.

PT Transgenic animal model for Alzheimer's disease - contains DNA encoding  
 PT part of beta-amyloid precursor protein in a gene construct designed for  
 PT over-expression in various cell types  
 PT Claim 2; Page 11; 32pp; English.

CC The sequence encodes a human brain beta-amyloid precursor protein  
 CC (APP) C-terminal peptide. The DNA may be transferred along with an  
 CC APP signal peptide gene (e.g. Q88695) into somatic and germ cells of  
 CC a non-human mammal, and the resulting transgenic animal may be used  
 CC as a model for Alzheimer disease (AD). The animal model exhibits  
 CC symptoms similar to AD, producing large quantities of APP C-terminal  
 CC peptide, death of neuron cells in pyramidal cells at cerebral  
 CC amyloid regions, increases in glial cells and deposition of  
 CC abnormally phosphorylated tau protein. The animal model may be  
 CC used to develop new therapies for AD, including gene therapy  
 CC strategies.  
 SQ Sequence 297 BP; 86 A; 64 C; 78 G; 69 T;

alignment\_scores:

Quality: 16.00 Length: 16  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-155-076-2 x Q88696 ..

Align seg 1/1 to: Q88696 from: 1 to: 297

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16  
 |||||  
 1 GATCAGAAATTCGACATGACTCAGGATATGAGATTCATCATCAAAA 48

seq\_name: N\_Geneseq\_36:Q88697

seq\_documentation\_block:

ID Q88697 standard; cDNA to mRNA; 297 BP.  
 AC Q88697;  
 DT 11-NOV-1995 (first entry)  
 DE Beta-amyloid precursor protein C-terminal peptide mutant gene.  
 KW Human; beta-amyloid precursor protein mutant; C-terminal peptide;  
 KW gene transfer; transgenic animal; Alzheimer disease model;  
 KW gene therapy; ss.  
 OS Homo sapiens.  
 PN EP-653154-A.  
 PD 17-MAY-1995.  
 PF 07-NOV-1994; 117512.  
 PR 12-NOV-1993; JP-306026.

PA (FARH ) HOECHST JAPAN LTD.

PA (FARH ) HOECHST JAPAN KK.

PI Kawarabayashi T, Kobayashi T, Sato M, Shoji M, Tada N;

DR WPI; 95-180492/24.

DR P-PSDB; R74695.

PT Transgenic animal model for Alzheimer's disease - contains DNA encoding  
 PT part of beta-amyloid precursor protein in a gene construct designed for  
 PT over-expression in various cell types  
 PT Claim 2; Page 12-13; 32pp; English.

CC The sequence encodes a human brain beta-amyloid precursor protein  
 CC (APP) mutant C-terminal peptide, and differs from Q88696 by a Glu  
 CC to Gln conversion at codon-22. The DNA may be transferred along  
 CC with an APP signal peptide gene (e.g. Q88695) into somatic and germ  
 CC cells of a non-human mammal, and the resulting transgenic animal may  
 CC be used as a model for Alzheimer disease (AD). The animal model  
 CC exhibits symptoms similar to AD, producing large quantities of APP  
 CC C-terminal peptide, death of neuron cells in pyramidal cells at  
 CC cerebral amyloid regions, increases in glial cells and deposition  
 CC of abnormally phosphorylated tau protein. The animal model may  
 CC be used to develop new therapies for AD, including gene therapy  
 CC strategies.  
 SQ Sequence 297 BP; 86 A; 65 C; 77 G; 69 T;

AC Q10017;  
 DE 14-MAR-1991 (first entry)  
 DT Sequence encoding beta-amyloid-related protein.  
 KW Alzheimer's disease; AD; acute pancreatitis; ds.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT cds 1..300  
 FT /\*tag= a

PN WO9014840-A.  
 PD 13-DEC-1990.  
 PF 04-JUN-1989; U03141.  
 PR 06-JUN-1989; US-361912.  
 PR 29-MAR-1990; US-502273.  
 PA (CALB-) CALIF BIOTECH INC.  
 PI Schilling JW, Ponte PA, Cordell B;  
 DR WPI; 91-006983/01.  
 DR R-PSDB; R10024.  
 DT DNA sequences, and protease inhibitors encoded by them and  
 PT antibodies - for diagnosis and treatment of alzheimers disease  
 PS Disclosure; Fig 5; 96pp; English.  
 CC Sequence may be useful in prognosis and diagnosis of human  
 CC Alzheimer's disease (AD). Abs may be raised to the gene product, and  
 CC probes derived from the encoding sequence allowing diagnosis and  
 CC determination of genetic predisposition.  
 CC The gene product is a protease inhibitor and may also have utility  
 CC in treatment of acute pancreatitis.  
 SQ Sequence 300 BP; 87 A; 63 C; 80 G; 70 T;

alignment\_scores:  
 Quality: 16.00 Length: 16  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
 US-09-155-076-2 x Q10017 ..

Align seg 1/1 to: Q10017 from: 1 to: 300

seq\_name: N\_Geneseq\_36:Q42665

seq\_documentation\_block:  
 ID Q42665 standard; cDNA; 300 BP.  
 AC Q42665;  
 DT 27-OCT-1993 (first entry)  
 DE Full-length beta-amyloid protein coding region.  
 KW Alzheimer's Disease; Amyloid Plaque Core Protein; APCP;  
 KW neuritic plaque; ds.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT cds 1..300  
 FT /\*tag= a  
 FT /product= beta-amyloid protein  
 FT /note= "full-length coding sequence obtained by  
 FT combining overlapping clones SM2W3 and  
 FT SM2W4 (Q42664 and Q42663, respectively)"  
 FT misc\_difference 160..162  
 FT /\*tag= b  
 FT /codon= seq: AAC; aa: Lys  
 FT /note= "this codon is AAG in Q42664"

US5220013-A.  
 15-JUN-1993.  
 17-NOV-1986; US-932193.  
 17-NOV-1986; US-932193.  
 31-DEC-1986; US-948376.  
 30-JAN-1987; US-008810.  
 18-AUG-1987; US-087002.  
 30-NOV-1989; US-444118.  
 (SCIO-) SCIOS NOVA INC.

AC Q10017;  
 DE 14-MAR-1991 (first entry)  
 DT Sequence encoding beta-amyloid-related protein.  
 KW Alzheimer's disease; AD; acute pancreatitis; ds.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT cds 1..300  
 FT /\*tag= a

PN WO9014840-A.  
 PD 13-DEC-1990.  
 PF 04-JUN-1989; U03141.  
 PR 06-JUN-1989; US-361912.  
 PR 29-MAR-1990; US-502273.  
 PA (CALB-) CALIF BIOTECH INC.  
 PI Schilling JW, Ponte PA, Cordell B;  
 DR WPI; 91-006983/01.  
 DR R-PSDB; R10024.  
 DT DNA sequences, and protease inhibitors encoded by them and  
 PT antibodies - for diagnosis and treatment of alzheimers disease  
 PS Disclosure; Fig 5; 96pp; English.  
 CC Sequence may be useful in prognosis and diagnosis of human  
 CC Alzheimer's disease (AD). Abs may be raised to the gene product, and  
 CC probes derived from the encoding sequence allowing diagnosis and  
 CC determination of genetic predisposition.  
 CC The gene product is a protease inhibitor and may also have utility  
 CC in treatment of acute pancreatitis.  
 SQ Sequence 300 BP; 87 A; 63 C; 80 G; 70 T;

alignment\_scores:  
 Quality: 16.00 Length: 16  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
 US-09-155-076-2 x Q10017 ..

Align seg 1/1 to: Q10017 from: 1 to: 300

seq\_name: N\_Geneseq\_36:Q42665

seq\_documentation\_block:  
 ID Q42665 standard; cDNA; 300 BP.  
 AC Q42665;  
 DT 27-OCT-1993 (first entry)  
 DE Full-length beta-amyloid protein coding region.  
 KW Alzheimer's Disease; Amyloid Plaque Core Protein; APCP;  
 KW neuritic plaque; ds.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT cds 1..300  
 FT /\*tag= a  
 FT /product= beta-amyloid protein  
 FT /note= "full-length coding sequence obtained by  
 FT combining overlapping clones SM2W3 and  
 FT SM2W4 (Q42664 and Q42663, respectively)"  
 FT misc\_difference 160..162  
 FT /\*tag= b  
 FT /codon= seq: AAC; aa: Lys  
 FT /note= "this codon is AAG in Q42664"

US5220013-A.  
 15-JUN-1993.  
 17-NOV-1986; US-932193.  
 17-NOV-1986; US-932193.  
 31-DEC-1986; US-948376.  
 30-JAN-1987; US-008810.  
 18-AUG-1987; US-087002.  
 30-NOV-1989; US-444118.  
 (SCIO-) SCIOS NOVA INC.

PI Cordell B, Ponte PA;  
 DR WPI: 93-205383/25.  
 DR P-PSDB; R37866.  
 PT DNA sequence useful for detection of Alzheimer's disease - for  
 encoding beta amyloid core protein  
 PS Disclosure; Fig 5; 4Opp; English.  
 CC A clone was obtained from the genomic library described in Lawn et al.,  
 CC Cell, 15:1157-1174 (1978) which included a 57 base pair segment which  
 CC encodes amino acids 1-18 of the beta-amyloid protein, immediately  
 CC preceded by a Methionine. A HindIII/KsaI fragment derived from the  
 CC genomic clone and containing the 57bp segment was used to isolate cDNA  
 CC fragments from a library prepared from temporal and parietal cortical  
 CC tissue from a normal human brain. Lambda clone SM2W3 (Q42664) contains  
 CC a 5' region segment which has a 6bp overlap with the 3' end of clone  
 CC SM2W4 (Q42663). The full-length beta-amyloid protein coding sequence  
 CC (Q42665), including an initiator Met residue which is probably  
 CC processed in vivo, was obtained by combining the sequences of the  
 CC two overlapping clones.  
 SQ Sequence 300 BP; 87 A; 65 C; 78 G; 70 T;

alignment\_scores:  
 Quality: 16.00 Length: 16  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

## alignment\_block:

US-09-155-076-2 x Q42665 ..

Align seg 1/1 to: Q42665 from: 1 to: 300

1 AspaLaGlupheArgHisAspSerGlyTyrGluValHisGlnLys 16  
 |||||  
 4 GATGCAGAAATCCGACATGACTCAGGATATGAAGTTCATCATCAAAAA 51

seq\_name: N\_Geneseq\_36:Q88699

## seq\_documentation\_block:

ID Q88699 standard; cDNA to mRNA; 309 BP.

AC Q88699;

DT 11-NOV-1995 (first entry)

DE Beta-amyloid precursor protein C-terminal peptide gene.

KW Human; beta-amyloid precursor protein; C-terminal peptide;

KW gene transfer; transgenic animal; Alzheimer disease model;

KW gene therapy; ss.

OS Homo sapiens.

PN EP-653154-A.

PD 17-MAY-1995.

PF 07-NOV-1994; 117512.

PR 12-NOV-1993; JP-306026.

PA (FARH ) HOECHST JAPAN LTD.

PI (FARH ) HOECHST JAPAN KK.

PI Kawarabayashi T, Kobayashi T, Sato M, Shoji M, Tada N;

DR WPI: 95-180492/24.

DR P-PSDB; R74697.

PT Transgenic animal model for Alzheimer's disease - contains DNA encoding

PT part of beta-amyloid precursor protein in a gene construct designed for

PT over-expression in various cell types

PS Claim 2; Page 15; 32pp; English.

CC The sequence encodes a human brain beta-amyloid precursor protein

CC (APP) C-terminal peptide. The DNA may be transferred along with an

CC APP signal peptide gene (e.g. Q88695) into somatic and germ cells

CC of a non-human mammal, and the resulting transgenic animal may be

CC used as a model for Alzheimer disease (AD). The animal model

CC exhibits symptoms similar to AD, producing large quantities of APP

CC C-terminal peptide, death of neuron cells in pyramidal cells at

CC cerebral amyloid regions, increases in glial cells and deposition

CC of abnormally phosphorylated tau protein. The animal model may

CC be used to develop new therapies for AD, including gene therapy

CC strategies. 309 BP; 91 A; 64 C; 83 G; 71 T;

SQ

alignment\_scores:  
 Quality: 16.00 Length: 16  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

## alignment\_block:

US-09-155-076-2 x Q88699 ..

Align seg 1/1 to: Q88699 from: 1 to: 309

1 AspaLaGlupheArgHisAspSerGlyTyrGluValHisGlnLys 16  
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 13 GATGCAGAAATCCGACATGACTCAGGATATGAAGTTCATCATCAAAAA 60

seq\_name: N\_Geneseq\_36:Q88700

## seq\_documentation\_block:

ID Q88700 standard; cDNA to mRNA; 309 BP.

AC Q88700;

DT 11-NOV-1995 (first entry)

DE Beta-amyloid precursor protein C-terminal peptide mutant gene.

KW Human; beta-amyloid precursor protein mutant; C-terminal peptide;

KW gene transfer; transgenic animal; Alzheimer disease model;

KW gene therapy; ss.

OS Homo sapiens.

PN EP-653154-A.

PD 17-MAY-1995.

PF 07-NOV-1994; 117512.

PR 12-NOV-1993; JP-306026.

PA (FARH ) HOECHST JAPAN LTD.

PA (FARH ) HOECHST JAPAN KK.

PI Kawarabayashi T, Kobayashi T, Sato M, Shoji M, Tada N;

DR WPI: 95-180492/24.

DR P-PSDB; R74698.

PT Transgenic animal model for Alzheimer's disease - contains DNA encoding

PT part of beta-amyloid precursor protein in a gene construct designed for

PT over-expression in various cell types

PS Claim 2; Page 16-17; 32pp; English.

CC The sequence encodes a human brain beta-amyloid precursor protein

CC (APP) mutant C-terminal peptide, and differs from Q88699 by

CC conversion of Lys to Asn at codon-3 and Met to Leu at codon-4. The

CC DNA may be transferred along with an APP signal peptide gene (e.g.

CC Q88695) into somatic and germ cells of a non-human mammal, and the

CC resulting transgenic animal may be used as a model for Alzheimer

CC disease (AD). The animal model exhibits symptoms similar to AD,

CC producing large quantities of APP C-terminal peptide, death of

CC neuron cells in pyramidal cells at cerebral amyloid regions,

CC increases in glial cells and deposition of abnormally

CC phosphorylated tau protein. The animal model may be used to develop

CC new therapies for AD, including gene therapy strategies.

CC Sequence 309 BP; 90 A; 65 C; 82 G; 72 T;

## alignment\_scores:

Quality: 16.00 Length: 16

Ratio: 1.000 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

## alignment\_block:

US-09-155-076-2 x Q88700 ..

Align seg 1/1 to: Q88700 from: 1 to: 309

1 AspaLaGlupheArgHisAspSerGlyTyrGluValHisGlnLys 16  
 |||||  
 13 GATGCAGAAATCCGACATGACTCAGGATATGAAGTTCATCATCAAAAA 60

seq\_name: N\_Geneseq\_36:TI8082

## seq\_documentation\_block:

ID TI8082 standard; DNA; 336 BP.

AC TI8082;

DT 10-OCT-1996 (first entry)

DE	Familial Alzheimer's disease APP isoform 751 gene fragment.
APP	Amyloid precursor protein; isoform 751; inherent; familial;
KW	Alzheimer's disease; mutation; diagnosis; transgenic model; study;
KW	cognitive; beta A4 domain; exon 17; senility; ss.
OS	Homo sapiens.
Key	Location/Qualifiers
FT	1..336
FT	/*tag= a
FT	/note= "stop codon not given"
PN	WO9803643-A2.
PD	29-JAN-1998.
PF	17-JUL-1997; E03960.
PR	08-MAY-1997; GB-009239.
PR	22-JUL-1996; GB-015351.
PR	09-SEP-1996; GB-018804.
PA	(SMIK ) SMITHKLINE BEECHAM AUSTRALIA PTY LTD.
PA	(SMIK ) SMITHKLINE BEECHAM PHARMA GMBH.
PI	Beyreuther K, Lichtenthaler S, Masters CL, Prior P;
PI	WPI; 98-120768/11.
DR	P-PDSB; W50027.
PT	Construct containing sequence for mutant form of amyloid precursor
PT	protein - or its C-terminal fragment, and related transgenic animals
PT	or transformed cells, used for identifying potential drugs for
PT	Alzheimer's disease
PS	Claim 10; Page 10; 15pp; English.
CC	The present sequence encodes the human amyloid precursor protein
CC	(APP) C-terminal fragment (A4CT) mutant SPA4CT Thr43Ser.
CC	The mutation results in a higher ratio of beta A4 1-42 to beta A4
CC	1-40, useful in disease models to identify potential drugs for the
CC	treatment of Alzheimer's disease.
SQ	Sequence 354 BP; 89 A; 83 C; 99 G; 83 T;
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Ratio:	1.000 Gaps: 0
Percent Similarity:	100.000 Percent Identity: 100.000
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58 GATGCAGAATTCGACATCAGCATGATGAAGTTCAATCAATAAAA 105	
seq_name: N_Geneseq_36:V20380	
seq_documentation_block:	
ID V20380 standard; DNA; 354 BP.	
AC V20380:	
DT 26-JUN-1998 (first entry)	
DE DNA for APP C-terminal fragment mutant SPA4CT Thr43Ala/Val46Phe.	
KW Human; amyloid precursor protein; APP; carboxy-terminal fragment;	
KW A4CT; mutant SPA4CT Thr43Ala/Val46Phe; disease model; treatment;	
KW Alzheimer's disease; ss.	
OS Homo sapiens.	
OS Synthetic.	
Key	Location/Qualifiers
FT	1..354
FT	/*tag= a
FT	/note= "stop codon not given"
PN	WO9803643-A2.
PD	29-JAN-1998.
PF	17-JUL-1997; E03960.
PR	08-MAY-1997; GB-009239.
PR	22-JUL-1996; GB-015351.
PR	09-SEP-1996; GB-018804.
PA	(SMIK ) SMITHKLINE BEECHAM AUSTRALIA PTY LTD.
PA	(SMIK ) SMITHKLINE BEECHAM PHARMA GMBH.
PI	Beyreuther K, Lichtenthaler S, Masters CL, Prior P;
PI	WPI; 98-120768/11.
DR	P-PDSB; W50030.
PT	Construct containing sequence for mutant form of amyloid precursor
PT	protein - or its C-terminal fragment, and related transgenic animals
PT	or transformed cells, used for identifying potential drugs for
PT	Alzheimer's disease
PS	Claim 10; Page 10; 15pp; English.
CC	The present sequence encodes the human amyloid precursor protein
CC	(APP) C-terminal fragment (A4CT) mutant SPA4CT Thr43Ser.
CC	The mutation results in a higher ratio of beta A4 1-42 to beta A4
CC	1-40, useful in disease models to identify potential drugs for the
CC	treatment of Alzheimer's disease.
SQ	Sequence 354 BP; 89 A; 83 C; 99 G; 83 T;
alignment_scores:	
Quality:	16.00 Length: 16
Ratio:	1.000 Gaps: 0
Percent Similarity:	100.000 Percent Identity: 100.000
alignment_block:	
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1 ASPAGLAPheArgHisAspSerGlyTyrGIUValHisHisGlnIys 16	
40 GATGCAGAATTCGACATCAGCATGATGAAGTTCAATCAATAAAA 87	
seq_name: N_Geneseq_36:V20377	
seq_documentation_block:	
ID V20377 standard; DNA; 354 BP.	
AC V20377:	
DT 26-JUN-1998 (first entry)	
DE DNA for APP C-terminal fragment mutant SPA4CT Thr43Ser.	
KW Human; amyloid precursor protein; APP; carboxy-terminal	
KW A4CT; mutant SPA4CT Thr43Ser; disease model; treatment;	
KW Alzheimer's disease; ss.	
OS Homo sapiens.	
OS Synthetic.	
Key	Location/Qualifiers
FT	1..336
FT	/*tag= a
FT	/note= "stop codon not given"
PN	WO9803643-A2.
PD	29-JAN-1998.
PF	17-JUL-1997; E03960.
PR	08-MAY-1997; GB-009239.
PR	22-JUL-1996; GB-015351.
PR	09-SEP-1996; GB-018804.
PA	(SMIK ) SMITHKLINE BEECHAM AUSTRALIA PTY LTD.
PA	(SMIK ) SMITHKLINE BEECHAM PHARMA GMBH.
PI	Beyreuther K, Lichtenthaler S, Masters CL, Prior P;
PI	WPI; 98-120768/11.
DR	P-PDSB; W50030.
PT	Construct containing sequence for mutant form of amyloid precursor
PT	protein - or its C-terminal fragment, and related transgenic animals
PT	or transformed cells, used for identifying potential drugs for
PT	Alzheimer's disease
PS	Claim 10; Page 10; 15pp; English.
CC	The present sequence encodes the human amyloid precursor protein
CC	(APP) C-terminal fragment (A4CT) mutant SPA4CT Thr43Ser.
CC	The mutation results in a higher ratio of beta A4 1-42 to beta A4
CC	1-40, useful in disease models to identify potential drugs for the
CC	treatment of Alzheimer's disease.
SQ	Sequence 336 BP; 102 A; 69 C; 88 G; 77 T;
alignment_scores:	
Quality:	16.00 Length: 16
Ratio:	1.000 Gaps: 0
Percent Similarity:	100.000 Percent Identity: 100.000
alignment_block:	
US-09-155-076-2 x T18082 ..	
Align seg 1/1 to: T18082 from: 1 to: 336	
1 ASPAGLAPheArgHisAspSerGlyTyrGIUValHisHisGlnIys 16	
40 GATGCAGAATTCGACATCAGCATGATGAAGTTCAATCAATAAAA 87	
seq_name: N_Geneseq_36:V20377	
seq_documentation_block:	
ID V20377 standard; DNA; 354 BP.	
AC V20377:	
DT 26-JUN-1998 (first entry)	
DE DNA for APP C-terminal fragment mutant SPA4CT Thr43Ser.	
KW Human; amyloid precursor protein; APP; carboxy-terminal	
KW A4CT; mutant SPA4CT Thr43Ser; disease model; treatment;	
KW Alzheimer's disease; ss.	
OS Homo sapiens.	
OS Synthetic.	

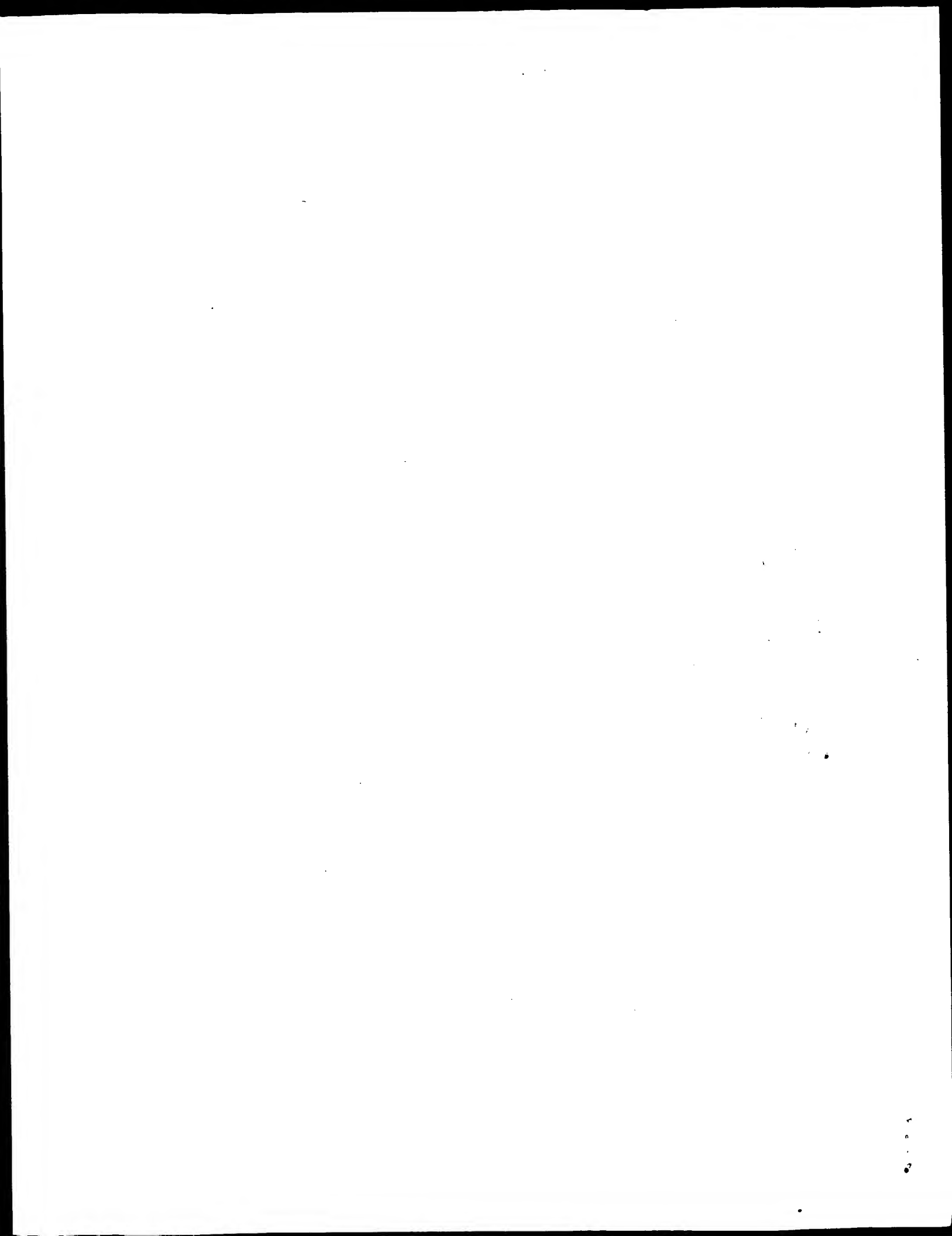
PT or transformed cells, used for identifying potential drugs for  
PS Alzheimer's disease  
CC Claim 10: Page 11: 15pp: English.  
CC The present sequence encodes the human amyloid precursor protein  
CC (APP) C-terminal fragment (A4CT) mutant SPA4CT Thr43Ala/Val46Phe.  
CC The mutation results in a higher ratio of beta A4 1-42 to beta A4  
CC 1-40, useful in disease models to identify potential drugs for the  
CC treatment of Alzheimer's disease.  
SQ Sequence 354 BP; 91 A; 82 C; 98 G; 83 T;

alignment\_scores:  
Quality: 16.00 Length: 16  
Ratio: 1.000 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
US-09-155-076-2 x V20380 ..

Align seg 1/1 to: V20380 from: 1 to: 354

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16  
|||||  
58 GATCCAGAAATCCGACATGACTCAGGATATGAGTTTCATCAAAA 105





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; TITLE OF INVENTION: Transgenic Animal Models for Alzheimer's Disease
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower - 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/04026
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, Ph.D, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 31188
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 189 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; ORIGINAL SOURCE: Human
; ORGANISM: Human
; PCT-US94-04026-8

alignment_scores:
  Quality: 16.00      Length: 16
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US-09-155-076-2 x PCT-US94-04026-8 ..
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58 GATGCAGATTCCGACATGACTGAGTATGAGTTTCATCATCAAAA 105

seq_name: /cgn2_6/ptodata/2/1na/6_COMB.seq:US-08-339-708A-3

seq_documentation_block:
; Sequence 3, Application US/08339708A
; Patent No. 6037521
; GENERAL INFORMATION:
; APPLICANT: Sato, Masahiro
; APPLICANT: Takashi, Kobayashi
; APPLICANT: Tada, No. 6037521hiro
; APPLICANT: Shoji, Mikio
; APPLICANT: Kawarabayashi, Takeshi
; TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR ALZHEIMER'S
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:

; TITLE OF INVENTION: Transgenic Animal Models for Alzheimer's Disease
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower - 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,708A
; FILING DATE: 14-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 306026/93
; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SANDERCOCK, COLIN G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 026083/0159
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 297 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: homo sapiens
; STRAIN: human brain
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..297
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; OTHER INFORMATION: precursor; 2. C-terminal peptide"
; US-08-339-708A-3

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  Percent Similarity: 100.000  Percent Identity: 100.000

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seq_documentation_block:
; Sequence 5, Application US/08339708A
; Patent No. 6037521
; GENERAL INFORMATION:
; APPLICANT: Sato, Masahiro
; APPLICANT: Takashi, Kobayashi
; APPLICANT: Tada, No. 6037521hiro
; APPLICANT: Shoji, Mikio
; APPLICANT: Kawarabayashi, Takeshi
; TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR ALZHEIMER'S
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,708A
; FILING DATE: 14-NOV-1994
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: JP 306026/93
; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SANDERCOCK, COLIN G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 026083/0159
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 297 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: homo sapiens
; STRAIN: human brain
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..297
; OTHER INFORMATION: /note= "1. human beta-amyloid
; OTHER INFORMATION: precursor; 2. C-terminal peptide"
; US-08-339-708A-5

alignment_scores:
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seq_documentation_block:
; Sequence 7, Application US/08339708A
; Patent No. 6037521
; GENERAL INFORMATION:
; APPLICANT: Sato, Masahiro
; APPLICANT: Takashi, Kobayashi
; APPLICANT: Tada, No. 6037521hiro
; APPLICANT: Shoji, Mikio
; APPLICANT: Kawarabayashi, Takeshi
; TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR ALZHEIMER'S
; TITLE OF INVENTION: DISEASE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA

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; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,708A
; FILING DATE: 14-NOV-1994
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: JP 306026/93
; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SANDERCOCK, COLIN G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 026083/0159
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 297 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: homo sapiens
; STRAIN: human brain
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..297
; OTHER INFORMATION: /note= "1. human beta-amyloid
; OTHER INFORMATION: precursor; 2. C-terminal peptide"
; US-08-339-708A-7

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seq_documentation_block:
; Patent No. 5220013
; APPLICANT: PONTE, PHYLLIS A.;CORDELL, BARBARA
; TITLE OF INVENTION: DNA SEQUENCE USEFUL FOR THE DETECTION
; OF ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/444,118
; FILING DATE: 30-NOV-1989
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 87,002
; FILING DATE: 18-AUG-1987
; APPLICATION NUMBER: 8,810
; FILING DATE: 30-JAN-1987
; APPLICATION NUMBER: 948,376
; FILING DATE: 31-DEC-1986
; APPLICATION NUMBER: 932,193

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us-09-155-076-2.rni

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; FILING DATE: 17-NOV-1986
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5220013-9

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seq_documentation_block:
; Patent No. 5223482
; APPLICANT: SCHILLING, JAMES W.; PONTE, PHYLLIS A.; CORDELL, BARBARA
; TITLE OF INVENTION: RECOMBINANT ALZHEIMER'S PROTEASE
; INHIBITORY AMYLOID PROTEIN AND METHOD OF USE
; NUMBER OF SEQUENCES: 34
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/361,912
; FILING DATE: 06-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 359,911
; FILING DATE: 12-MAY-1989
; APPLICATION NUMBER: 87,002
; FILING DATE: 18-AUG-1987
; APPLICATION NUMBER: 8,810
; FILING DATE: 30-JAN-1987
; APPLICATION NUMBER: 948,376
; FILING DATE: 31-DEC-1986
; APPLICATION NUMBER: 932,193
; FILING DATE: 17-NOV-1986
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5223482-9

alignment_scores:
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    Percent Similarity: 100.000    Percent Identity: 100.000

alignment_block:
US-09-155-076-2 x 5223482-9 ..

Align seg 1/1 to: 5223482-9 from: 1 to: 300

1 AspaAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
|||||
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seq_name: /cgn2_6/ptodata/2/ina/6_COMB.seq:US-08-339-708A-9

seq_documentation_block:
; Sequence 9, Application US/08339708A
; Patent No. 6037521
; GENERAL INFORMATION:
; APPLICANT: Sato, Masahiro
; APPLICANT: Takashi, Kobayashi
; APPLICANT: Tada, No. 6037521hiro
; APPLICANT: Shoji, Mikio
; APPLICANT: Kawarabayashi, Takeshi
;
; TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR ALZHEIMER'S
; TITLE OF INVENTION: DISEASE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,708A
; FILING DATE: 14-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 306026/93
; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SANDERCOCK, COLIN G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 026083/0159
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: homo sapiens
; STRAIN: human brain
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..309
; OTHER INFORMATION: /note= "1. human beta-amyloid
; OTHER INFORMATION: precursor; 2. C-terminal peptide"
US-08-339-708A-9

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US-09-155-076-2 x US-08-339-708A-9 ..

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1 AspaAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
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seq_name: /cgn2_6/ptodata/2/ina/6_COMB.seq:US-08-339-708A-11

seq_documentation_block:
; Sequence 11, Application US/08339708A
; Patent No. 6037521
; GENERAL INFORMATION:
; APPLICANT: Sato, Masahiro
; APPLICANT: Takashi, Kobayashi
; APPLICANT: Tada, No. 6037521hiro
; APPLICANT: Shoji, Mikio
; APPLICANT: Kawarabayashi, Takeshi

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; APPLICANT: Kavarabayashi, Takeshi
; TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR ALZHEIMER'S
; TITLE OF INVENTION: DISEASE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,708A
; FILING DATE: 14-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 306026/93
; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SANDERCOCK, COLIN G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 026083/0159
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: homo sapiens
; STRAIN: human brain
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..309
; OTHER INFORMATION: /note= "1. human beta-amyloid
; OTHER INFORMATION: precursor; 2. C-terminal peptide"
; US-08-339-708A-11

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  Quality: 16.00      Length: 16
  Ratio: 1.000       Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

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1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
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13 GATGCGAATTCCGACATGACTCAGGATGATGAGTTCATCATCAAAA 60

seq_name: /cgn2_6/ptodata/2/lna/5C_COMB.seq:US-08-729-345-2

seq_documentation_block:
; Patent No. 584999
; APPLICANT: Neve, Rachael L. Joanne
; TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR ALZHEIMER'S
; TITLE OF INVENTION: DISEASE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/729,345
; FILING DATE: 16-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 04843/027001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 354 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1..351
; OTHER INFORMATION:
; US-08-729-345-2

alignment_scores:
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  Ratio: 1.000       Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
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seq_name: /cgn2_6/ptodata/2/lna/backfiles1.seq:5187153-3

seq_documentation_block:
; Patent No. 5187153
; APPLICANT: CORDELL, BARBARA; SCHILLING, JAMES W.; KATUNUMA, NOBUHIKO
; TITLE OF INVENTION: METHODS OF TREATMENT USING ALZHEIMER'S
; AMYLOID POLYPEPTIDE DERIVATIVES
; NUMBER OF SEQUENCES: 33
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/502,273
; FILING DATE: 29-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 361,912
; FILING DATE: 06-JUN-1989
; APPLICATION NUMBER: 359,911
; FILING DATE: 12-MAY-1989
; APPLICATION NUMBER: 87,002

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; FILING DATE: 18-AUG-1987
; APPLICATION NUMBER: 8,810
; FILING DATE: 30-JAN-1987
; APPLICATION NUMBER: 948,376
; FILING DATE: 31-DEC-1986
; APPLICATION NUMBER: 932,193
; FILING DATE: 17-NOV-1986
; SEQ ID NO:3
; LENGTH: 485
5187153-3

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    Ratio: 1.000        Gaps: 0
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Align seg 1/1 to: 5187153-3 from: 1 to: 485

1 AspaGluPheArgHisAspSerGlyTyrGluValHisHisGlnIlys 16
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240 GATGCAGAAATTCGACATGACTCAGGATATGAGTTTCATCAAAAA 287

seq_name: /cgn2_6/ptodata/2/ina/backfiles1.seq:5220013-3

seq_documentation_block:
; Patent No. 5220013
; APPLICANT: PONTE, PHYLLIS A.;CORDELL, BARBARA
; TITLE OF INVENTION: DNA SEQUENCE USEFUL FOR THE DETECTION
; OF ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/444,118
; FILING DATE: 30-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 87,002
; FILING DATE: 18-AUG-1987
; APPLICATION NUMBER: 8,810
; FILING DATE: 30-JAN-1987
; APPLICATION NUMBER: 948,376
; FILING DATE: 31-DEC-1986
; APPLICATION NUMBER: 932,193
; FILING DATE: 17-NOV-1986
; SEQ ID NO:3
; LENGTH: 486
5220013-3

alignment_scores:
    Quality: 16.00      Length: 16
    Ratio: 1.000        Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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Align seg 1/1 to: 5220013-3 from: 1 to: 486

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241 GATGCAGAAATTCGACATGACTCAGGATATGAGTTTCATCAAAAA 288

seq_name: /cgn2_6/ptodata/2/ina/backfiles1.seq:5223482-3

seq_documentation_block:
; Patent No. 5223482
; APPLICANT: SCHILLING, JAMES W.;PONTE, PHYLLIS A.;CORDELL,
; BARBARA
; TITLE OF INVENTION: RECOMBINANT ALZHEIMER'S PROTEASE
; INHIBITORY AMYLOID PROTEIN AND METHOD OF USE

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; NUMBER OF SEQUENCES: 34
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/361,912
; FILING DATE: 06-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 359,911
; FILING DATE: 12-MAY-1989
; APPLICATION NUMBER: 87,002
; FILING DATE: 18-AUG-1987
; APPLICATION NUMBER: 8,810
; FILING DATE: 30-JAN-1987
; APPLICATION NUMBER: 948,376
; FILING DATE: 31-DEC-1986
; APPLICATION NUMBER: 932,193
; FILING DATE: 17-NOV-1986
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; LENGTH: 486
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Percent Similarity: 100.000 Percent Identity: 100.000

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1 AspaGluPheArgHisAspSerGlyTyrGluValHisHisGlnIlys 16
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seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-268-348A-9

seq_documentation_block:
; Sequence 9, Application US/08268348A
; Patent No. 5750374
; GENERAL INFORMATION:
; APPLICANT: Dobelli, Heinz
; APPLICANT: Draeger, Nicholas
; APPLICANT: Trotman, Gerda H
; APPLICANT: Jakob, Peter
; APPLICANT: Stuber, Dietrich
; TITLE OF INVENTION: Process for Producing Hydrophobic
; POLYPEPTIDES AND PROTEINS, AND FUSION PROTEINS FOR USE IN
; TISSUE ENGINEERING
; TITLE OF INVENTION: Producing Same
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/268,348A
; FILING DATE: 29-JUN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93110755.1
; FILING DATE: 06-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Parise, John P.
; REGISTRATION NUMBER: 34,403
; REFERENCE/DOCKET NUMBER: 4105/157
; TELECOMMUNICATION INFORMATION:

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; TELEPHONE: (201) 235-6326
; TELEFAX: (201) 235-3500
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 520 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 115..516
; OTHER INFORMATION: /product= "Amyloid Protein AA"
US-08-268-348A-9

* alignment_scores:
  Quality: 16.00      Length: 16
  Ratio: 1.000       Gaps: 0
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US-09-155-076-2 x US-08-268-348A-9 ..

Align seg 1/1 to: US-08-268-348A-9 from: 1 to: 520

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seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-480-498-3

seq_documentation_block:
; Sequence 3, Application US/08480498
; Patent No. 5744346
; GENERAL INFORMATION:
; APPLICANT: Chrysler, Susanna M.S.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Keim, Pamela S.
; APPLICANT: Anderson, John P.
; TITLE OF INVENTION: Beta-Secretase
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,498
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 015270-002200
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1521 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-480-498-3
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us-09-155-076-2.rni

Wed Sep 13 08:11:35 2000

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 13, 2000, 02:25:55 ; Search time 17.58 seconds  
(without alignments)  
56,323 Million cell updates/sec

Title: US-09-155-076-2

Perfect score: 16

Sequence: 1 DAEFRHDSGYEVHHQK 16

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 178050 seqs, 61884766 residues

Word size : 0

Total number of hits satisfying chosen parameters: 178050

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

Database :

PIR\_64.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	100.0	42	PN0512	beta-amyloid prote
2	16	100.0	57	E60045	Alzheimer's diseas
3	16	100.0	57	F60045	Alzheimer's diseas
4	16	100.0	57	G60045	Alzheimer's diseas
5	16	100.0	57	D60045	Alzheimer's diseas
6	16	100.0	57	A60045	Alzheimer's diseas
7	16	100.0	57	B60045	Alzheimer's diseas
8	16	100.0	82	PQ0438	Alzheimer's diseas
9	16	100.0	695	A49795	Alzheimer's diseas
10	16	100.0	770	QRH044	Alzheimer's diseas
11	7	43.8	747	2 JH0773	Alzheimer's diseas
12	6	37.5	122	2 S54715	Alzheimer's diseas
13	6	37.5	284	2 S04723	probable aspartate
14	6	37.5	313	2 J00960	genome polyprotein
15	6	37.5	327	2 S11435	polyprotein - pota
16	6	37.5	330	2 A26205	genome polyprotein
17	6	37.5	379	2 S13556	coat protein precu
18	6	37.5	380	2 G69277	genome polyprotein
19	6	37.5	397	2 T11786	aspartate transam
20	6	37.5	427	2 JA0073	genome polyprotein
21	6	37.5	453	2 C69543	hypothetical prote
22	6	37.5	519	2 PC1072	nuclear inclusion
23	6	37.5	761	2 T15776	hypothetical prote
24	6	37.5	846	2 A60678	genome polyprotein
25	6	37.5	1555	2 J00959	polyprotein - pota
26	6	37.5	3061	1 JN0545	genome polyprotein
27	6	37.5	3063	2 JS0166	genome polyprotein
28	5	31.2	58	2 D69449	hypothetical prote
29	5	31.2	112	2 B72019	periplasmic divale

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31	5	31.2	123	2	H72479	probable translati
32	5	31.2	125	2	S68170	ig heavy chain v r
33	5	31.2	132	2	JQ0737	RnpA protein - Mic
34	5	31.2	135	1	R3TW12	ribosomal protein
35	5	31.2	135	2	A34653	cell adhesion prot
36	5	31.2	141	2	H72693	hypothetical prote
37	5	31.2	144	2	S23658	superoxide dismuta
38	5	31.2	145	2	S62510	hypothetical prote
39	5	31.2	161	2	S30698	cyax protein - Esc
40	5	31.2	167	2	T34963	hypothetical prote
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43	5	31.2	195	2	B70577	hypothetical prote
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#### ALIGNMENTS

##### RESULT 1

PN0512  
beta-amyloid protein - guinea pig (fragment)

C:Species: Cavia porcellus (guinea pig)

C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 17-Mar-1999

C:Accession: PN0512

R:Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno Biochem. Biophys. Res. Commun. 193, 624-630, 1993

A:Title: Receptor-mediated specific biological activity of a beta-amyloid protein fra

A:Reference number: PN0512; MUID:93290653

A:Accession: PN0512

A:Molecule type: protein

A:Residues: 1-42 <SH1>

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas

C:Keywords: alternative splicing; amyloid

Query Match 100.0%; Score 16; DB 2; Length 42;

Best Local Similarity 100.0%; Pred. No. 4.2e-12;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16

Db 1 DAEFRHDSGYEVHHQK 16

##### RESULT 2

E60045  
Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)

C:Species: Ovis sp. (sheep)

C:Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995

C:Accession: E60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d

A:Reference number: A60045; MUID:92017079

A:Accession: E60045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

A:Cross-references: EMBL:X56130

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 16; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 5.5e-12;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16

Db 6 DAEFRHDSGYEVHHQK 21

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RESULT 3
F60045
Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C:Accession: F60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079
A:Accession: F60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56127; NID:g1895; PIDN:CAA39592.1; PID:g1896
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 16; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 5.5e-12;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
Db 6 DAEFRHDSGYEVHHQK 21

RESULT 4
F60045
Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)
C:Species: Cavia porcellus (guinea pig)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: G60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079
A:Accession: G60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56126
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 16; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 5.5e-12;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
Db 6 DAEFRHDSGYEVHHQK 21

RESULT 5
D60045
Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: D60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079
A:Accession: D60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56124
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 16; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 5.5e-12;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
Db 6 DAEFRHDSGYEVHHQK 21

```

```

Query Match 100.0%; Score 16; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 5.5e-12;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
Db 6 DAEFRHDSGYEVHHQK 21

RESULT 6
A60045
Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: A60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079
A:Accession: A60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56125
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 16; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 5.5e-12;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
Db 6 DAEFRHDSGYEVHHQK 21

RESULT 7
B60045
Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)
C:Species: Ursus maritimus (polar bear)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C:Accession: B60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079
A:Accession: B60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56128; NID:g2165; PIDN:CAA39593.1; PID:g2166
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 16; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 5.5e-12;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
Db 6 DAEFRHDSGYEVHHQK 21

RESULT 8
PQ0438
Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C:Accession: PQ0438; C60045
R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.
Biochem. Biophys. Res. Commun. 188, 905-911, 1992
A:Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precurs
A:Reference number: PQ0438; MUID:93075180

```



A:Accession: PQ0438  
 A:Molecule type: DNA  
 A:Residues: 1-82 <DAV>  
 A:Cross-references: GB:M83558; GB:M83657  
 R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
 Brain Res. Mol. Brain Res. 10, 299-305, 1991  
 A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,  
 A:Reference number: A60045; MUID:92017079  
 A:Accession: C60045  
 A:Molecule type: mRNA  
 A:Residues: 12-68 <JOH>  
 A:Cross-references: EMBL:X56129  
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase  
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 100.0%; Score 16; DB 2; Length 82;  
 Best Local Similarity 100.0%; Pred. No. 7.6e-12;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAFFRHDSDGYEVHQQ 16  
 |||||  
 DB 17 DAFFRHDSDGYEVHQQ 32

RESULT 9  
 A49795  
 Alzheimer's disease amyloid beta protein precursor - crab-eating macaque  
 C:Species: Macaca fascicularis (crab-eating macaque)  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C:Accession: A49795  
 R:Podlinsky, M.B.; Tolan, D.R.; Selkoe, D.J.  
 Am. J. Pathol. 138, 1423-1435, 1991  
 A:Title: Homology of the amyloid beta protein precursor in monkey and human supports a  
 A:Reference number: A49795; MUID:91273117  
 A:Accession: A49795  
 A>Status: Preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-695 <POD>  
 A:Cross-references: GB:M58727; NID:q342062; PIDN:AAA36829.1; PID:q342063  
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase  
 C:Keywords: alternative splicing

Query Match 100.0%; Score 16; DB 1; Length 695;  
 Best Local Similarity 100.0%; Pred. No. 5e-11;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAFFRHDSDGYEVHQQ 16  
 |||||  
 DB 597 DAFFRHDSDGYEVHQQ 612

RESULT 10  
 QRHUA  
 Alzheimer's disease amyloid beta protein precursor - human  
 N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor Xia inhibitor  
 N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular  
 protein precursor splice form APP(770)  
 C:Species: Homo sapiens (man)  
 C:Date: 30-Jun-1987 #sequence\_revision 28-Jul-1995 #text\_change 24-Nov-1999  
 C:Accession: S02260; S05194; A32277; A33260; A33486; I39451; I39453; I59562; A44  
 468; A28583; A29302; A60805; JLO038; S06121; A60355; A59011; A38384; S29076; S38252; S3  
 R:Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Bey  
 Nucleic Acids Res. 17, 517-522, 1989  
 A:Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded b  
 A:Reference number: S02260; MUID:89128427  
 A:Accession: S02260  
 A:Molecule type: DNA  
 A:Residues: 1-288, 'V', 365-770 <LEMI>  
 A:Cross-references: EMBL:X13466  
 A:Note: alternative splice form APP(695)  
 R:Lemaire, H.G.

submitted to the EMBL Data Library, November 1988  
 A:Reference number: S05194  
 A:Accession: S05194  
 A:Molecule type: DNA  
 A:Residues: 1-14, 'VW', 17-288, 'V', 365-770 <LEM2>  
 A:Cross-references: EMBL:X13466; NID:q35598; PIDN:CAA31830.1; PID:g871360  
 A:Note: alternative splice form APP(695)  
 R:La Fauce, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.  
 Biochem. Biophys. Res. Commun. 159, 297-304, 1989  
 A:Title: Characterization of the 5'-end region and the first two exons of the beta-pr  
 A:Reference number: A32277; MUID:89165870  
 A:Accession: A32277  
 A:Molecule type: DNA  
 A:Residues: 1-75 <LAF>  
 A:Cross-references: GB:M24546; GB:M24547; NID:q341202; PIDN:AAC13654.1; PID:g516074  
 R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.  
 Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989  
 A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows simila  
 A:Reference number: A33260; MUID:89392030  
 A:Accession: A33260  
 A:Molecule type: DNA  
 A:Residues: 656-737 <JOH>  
 A:Cross-references: GB:M29270; NID:q178863; PIDN:AAA51768.1; PID:g178865  
 R:Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B  
 Biochem. Biophys. Res. Commun. 170, 301-307, 1990  
 A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid  
 A:Reference number: A35486; MUID:90321244  
 A:Accession: A35486  
 A:Molecule type: DNA  
 A:Residues: 672-710 <PRE1>  
 A:Note: 693-Gln was found in DNA isolated from HCHWA-D patients  
 R:Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuha, H.; Sasaki, Y.  
 Gene 87, 257-263, 1990  
 A:Title: Genomic organization of the human amyloid beta-protein precursor gene.  
 A:Reference number: I39451; MUID:90236318  
 A:Accession: I39451  
 A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/  
 A:Molecule type: DNA  
 A:Residues: 1-770 <YOS1>  
 A:Cross-references: GB:M33112; NID:q178613; PIDN:AAB59502.1; PID:g178616  
 A:Accession: I39451  
 A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/  
 A:Molecule type: DNA  
 A:Residues: 1-530, 'QWLMPVPAFWFAKVG' <YOS2>  
 A:Cross-references: GB:M34875; NID:q178608; PIDN:AAB59501.1; PID:g178615  
 R:Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuha, H.; Sasaki, Y.  
 Gene 102, 291-292, 1991  
 A:Reference number: A59020; MUID:91340168  
 A:Accession: A59020  
 A:Contents: annotation; erratum  
 A:Note: revised physical map for reference I39451  
 R:Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Du  
 Science 248, 1124-1126, 1990  
 A:Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemo  
 A:Reference number: I39453; MUID:90260663  
 A:Accession: I39453  
 A>Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 656-737 <LEV>  
 A:Cross-references: GB:M37896; NID:q178618; PIDN:AAA51727.1; PID:g178620  
 R:Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.  
 Science 254, 97-99, 1991  
 A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzhe  
 A:Reference number: I59562; MUID:92022553  
 A:Accession: I59562  
 A>Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 689-716, 'F', 718-737 <MUR>  
 A:Cross-references: GB:S57665; NID:q236720; PIDN:AAB19991.1; PID:g236721  
 R:Kamino, K.; Orr, H.T.; Payami, H.; Wajsbom, E.M.; Alonso, M.E.; Pulst, S.M.; Anders  
 arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Mart  
 Am. J. Hum. Genet. 51, 998-1014, 1992  
 A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for t

Wed Sep 13 08:11:36 2000

A:Cross-references: GB:X06989; EMBL:X00297; NID:g28720; PIDN:CAA30050.1; PID:g28721  
 A:Note: alternative splice form APP(751)  
 R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.  
 Nature 331, 530-532, 1988  
 A:Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibi  
 A:Reference number: A38949; MUID:88122641  
 A:Accession: A38949  
 A:Molecule type: mRNA  
 A:Residues: 287-367 <KIT>  
 A:Cross-references: GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:g929611  
 A:Experimental source: glioblastoma cell line  
 A:Note: alternative splice form APP(770)  
 R:Vitek, M.P.; Rascol, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ash  
 Brain Res. Mol. Brain Res. 4, 121-131, 1988  
 A:Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three  
 A:Reference number: A30320  
 A:Accession: A30320  
 A:Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 284-288, 'V', 365-770 <VIT1>  
 A:Accession: B30320  
 A:Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 122-288, 'V', 365-770 <VIT2>  
 A:Accession: C30320  
 A:Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 606-770 <VIT3>  
 R:Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta,  
 Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988  
 A:Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease  
 A:Reference number: A31087; MUID:88124954  
 A:Accession: A31087  
 A:Molecule type: mRNA  
 A:Residues: 507-770 <ZAI>  
 A:Cross-references: GB:M18734; NID:g178572; PIDN:AAA51726.1; PID:g178573  
 A:Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue  
 8 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue  
 A:Note: the cited Genbank accession number, J03394, is not in release 101.0  
 R:Masters, C.L.; Multhaup, G.; Simms, G.; Pottgiesser, J.; Martins, R.N.; Beyreuther,  
 Query Match 100.0%; Score 16; DB 1; Length 770;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-11;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DAEFRHDSGYEVHOK 16  
 |||||  
 DB 672 DAEFRHDSGYEVHOK 687  
 RESULT 11  
 JH0773  
 Alzheimer's disease amyloid beta protein precursor - African clawed frog  
 C:Species: Xenopus laevis (African clawed frog)  
 C:Date: 10-Jun-1993 #sequence\_revision 10-Jun-1993 #text\_change 13-Aug-1999  
 C:Accession: JH0773  
 R:Okado, H.; Okamoto, H.  
 Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992  
 A:Title: A Xenopus homologue of the human beta-amyloid precursor protein: development  
 A:Reference number: JH0773; MUID:93129227  
 A:Accession: JH0773  
 A:Molecule type: mRNA  
 A:Residues: 1-747 <OKA>  
 A:Cross-references: GB:S52417; NID:g263150; PIDN:AAB24853.1; PID:g263151  
 A:Experimental source: larva  
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas  
 C:Keywords: alternative splicing; amyloid  
 P:287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>  
 Query Match 43.8%; Score 7; DB 2; Length 747;  
 Best Local Similarity 100.0%; Pred. No. 1.2;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

A:Reference number: A44017; MUID:93035397  
 A:Accession: A44017  
 A:Molecule type: DNA  
 A:Residues: 687-718 <KAM2>  
 A:Cross-references: GB:AAB23646.1; PID:g257380  
 A:Experimental source: familial Alzheimer disease family LIT  
 A:Note: sequence extracted from NCB1 backbone (NCBIP:115376)  
 A:Note: this sequence has a silent mutation  
 R:Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;  
 Nature 325, 733-736, 1987  
 A:Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surfac  
 A:Reference number: A03134; MUID:87144572  
 A:Accession: A03134  
 A:Molecule type: mRNA  
 A:Residues: 1-288, 'V', 365-770 <KAN>  
 A:Cross-references: GB:X00264; NID:g28525; PIDN:CAA68374.1; PID:g28526  
 A:Note: alternative splice form APP(695)  
 R:Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.  
 Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987  
 A:Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular a  
 A:Reference number: A29030; MUID:87231971  
 A:Accession: A29030  
 A:Molecule type: mRNA  
 A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>  
 A:Cross-references: GB:M16765; NID:g178539; PIDN:AAA51722.1; PID:g178540  
 A:Note: the authors translated the codon GAG for residue 647 as Asp  
 R:Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.  
 Science 235, 877-880, 1987  
 A:Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid  
 A:Reference number: A47584; MUID:87120328  
 A:Accession: A47584  
 A:Molecule type: mRNA  
 A:Residues: 674-756, 'S', 758-770 <GOL>  
 A:Cross-references: GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:g178707  
 A:Experimental source: brain  
 R:Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke  
 Science 235, 880-884, 1987  
 A:Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th  
 A:Reference number: A47585; MUID:87120329  
 A:Accession: A47585  
 A:Molecule type: mRNA  
 A:Residues: 674-703 <TANI>  
 A:Cross-references: GB:M15532; NID:g177957; PIDN:AAA51564.1; PID:g177958  
 R:Dykes, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muelle  
 EMBO J. 7, 949-957, 1988  
 A:Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 prec  
 A:Reference number: S02638; MUID:88296437  
 A:Accession: S02638  
 A:Molecule type: mRNA  
 A:Residues: 672-678 <DYK>  
 R:Tanzi, R.E.; McClatchey, A.I.; Lampert, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve  
 Nature 331, 528-530, 1988  
 A:Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat  
 A:Reference number: S00707; MUID:88122640  
 A:Accession: S00707  
 A:Molecule type: mRNA  
 A:Residues: 286-344, 'I', 365-366 <TAN2>  
 A:Cross-references: EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:g929612  
 A:Experimental source: promyelocytic leukemia cell line HL60  
 A:Note: alternative splice form APP(751)  
 R:Ponte, P.; Gonzalez-Dewhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Da  
 Nature 331, 525-527, 1988  
 A:Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibi  
 A:Reference number: S00925; MUID:88122639  
 A:Accession: S00925  
 A:Molecule type: mRNA  
 A:Residues: 1-344, 'I', 365-770 <PO2>

QY 10 YEVHHQ 16  
 |||||  
 Db 658 YEVHHQ 664

## RESULT 12

S54715  
 probable aspartate transaminase (EC 2.6.1.1) - Streptomyces coelicolor (fragment)  
 C:Species: Streptomyces coelicolor  
 C:Date: 23-Aug-1995 #sequence\_revision 12-Dec-1997 #text\_change 13-Sep-1998  
 C:Accession: S54715  
 R:Puttkhant, C.; Nihira, T.; Yamada, Y.  
 Mol. Gen. Genet. 247, 118-122, 1995  
 A:Title: Cloning, nucleotide sequence, and transcriptional analysis of the nusG gene of  
 A:Reference number: S54715; MUID:95231511  
 A:Accession: S54715  
 A:Molecule type: DNA  
 A:Residues: 1-122 <PUT>  
 A:Cross-references: EMBL:D32254  
 A:Experimental source: strain A3(2), substrain SC  
 C:Superfamily: aspartate transaminase  
 C:Keywords: aminotransferase

Query Match 37.5%; Score 6; DB 2; Length 122;  
 Best Local Similarity 100.0%; Pred. No. 3.3;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DSGYEV 12  
 |||||  
 Db 93 DSGYEV 98

## RESULT 13

S04723  
 genome polyprotein - potato virus Y (strain o) (fragment)  
 N:Contains: coat protein; replicase  
 C:Species: potato virus Y, PVY  
 C:Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 20-Sep-1999  
 C:Accession: S04723  
 R:Bravo-Almonacid, F.; Mentaberry, A.N.  
 Nucleic Acids Res. 17, 4401, 1989  
 A:Title: Nucleotide cDNA sequence coding for the PVY coat protein.  
 A:Reference number: S04723; MUID:89296509  
 A:Accession: S04723  
 A:Status: translation not shown  
 A:Molecule type: genomic RNA  
 A:Residues: 1-284 <BRA>  
 A:Cross-references: EMBL:X14136; NID:961445; PIDN:CAA32356.1; PID:61446  
 C:Superfamily: tobacco etch virus genome polyprotein; DEAD/H box helicase homology  
 C:Keywords: polyprotein

Query Match 37.5%; Score 6; DB 2; Length 284;  
 Best Local Similarity 100.0%; Pred. No. 6.9;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 YEVHHQ 15  
 |||||  
 Db 12 YEVHHQ 17

## RESULT 14

JT0960  
 polyprotein - potato virus Y  
 N:Contains: coat protein  
 C:Species: potato virus Y, PVY  
 C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 29-May-1998  
 C:Accession: JT0960  
 R:Hidaka, M.  
 submitted to JIPID, November 1991  
 A:Reference number: JT0959

A:Accession: JT0960  
 A:Molecule type: genomic RNA  
 A:Residues: 1-313 <HID>  
 A:Experimental source: necrotic strain T  
 C:Superfamily: tobacco etch virus genome polyprotein; DEAD/H box helicase homology  
 C:Keywords: polyprotein  
 F:46-313/Product: coat protein #status predicted <COA>

Query Match 37.5%; Score 6; DB 2; Length 313;  
 Best Local Similarity 100.0%; Pred. No. 7.6;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 YEVHHQ 15  
 |||||  
 Db 41 YEVHHQ 46

## RESULT 15

S11435  
 genome polyprotein - potato virus Y (fragment)  
 N:Contains: coat protein; NIB protein  
 C:Species: potato virus Y, PVY  
 C:Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 20-Sep-1999  
 C:Accession: S11435; S11549; JC1526  
 R:Zhou, X.R.; Fang, R.X.; Wang, C.Q.; Mang, K.Q.  
 Nucleic Acids Res. 18, 5554, 1990  
 A:Title: cDNA sequence of the 3'-coding region of PVY genome (the Chinese isolate).  
 A:Reference number: S11435; MUID:91016851  
 A:Accession: S11435  
 A:Molecule type: mRNA  
 A:Residues: 1-327 <ZHO1>  
 A:Cross-references: EMBL:X54058  
 R:Zhou, X.R.  
 submitted to the EMBL Data Library, July 1990  
 A:Reference number: S11549  
 A:Accession: S11549  
 A:Molecule type: mRNA  
 A:Residues: 1-90, 'E', 92-327 <ZHO2>  
 A:Cross-references: EMBL:X54058; NID:961219; PIDN:CAA37993.1; PID:98333159  
 R:Onshima, K.; Hataya, T.; Sano, T.; Inoue, A.K.; Shikata, E.  
 Ann. Phytopathol. Soc. Jpn. 57, 615-622, 1991  
 A:Title: Comparison of biological properties, serological characteristics and amino a

A:Reference number: JC1526  
 A:Accession: JC1526  
 A:Molecule type: genomic RNA  
 A:Residues: 61-88, 'E', 71-73, 'ES', 76-111, 'S', 113-201, 'E', 203-327 <OHS>  
 C:Genetics:

A:Start codon: GCA  
 C:Superfamily: tobacco etch virus genome polyprotein; DEAD/H box helicase homology  
 C:Keywords: coat protein; polyprotein  
 F:61-327/Product: coat protein #status predicted <COP>

Query Match 37.5%; Score 6; DB 2; Length 327;  
 Best Local Similarity 100.0%; Pred. No. 7.9;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 YEVHHQ 15  
 |||||  
 Db 55 YEVHHQ 60

Search completed: September 13, 2000, 02:25:56  
 Job time: 139 sec

Wed Sep 13 08:11:36 2000

us-09-155-076-2.rpr

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 13, 2000, 02:27:53 : Search time 10.69 seconds  
(without alignments)  
46.382 Million cell updates/sec

Title: US-09-155-076-2

Perfect score: 16

Sequence: 1 DAEFRHDSGYEVHHOK 16

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 85661 seqs, 30989116 residues

Word size : 0

Total number of hits satisfying chosen parameters: 85661

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Listing first 45 summaries

Database : SwissProt\_38.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	100.0	57	1	A4_PIG
2	16	100.0	57	1	A4_URDMA
3	16	100.0	58	1	A4_CANFA
4	16	100.0	58	1	A4_RABIT
5	16	100.0	58	1	A4_SHEEP
6	16	100.0	59	1	A4_BOVIN
7	16	100.0	751	1	A4_SAISC
8	16	100.0	770	1	A4_HUMAN
9	6	37.5	213	1	AAT_STRGR
10	6	37.5	284	1	POLG_PVYHO
11	6	37.5	327	1	POLG_PVYCH
12	6	37.5	330	1	COAT_PEMV
13	6	37.5	397	1	AAT_STRVG
14	6	37.5	3061	1	POLG_PVYHU
15	6	37.5	3063	1	POLG_PVYN
16	5	31.2	90	1	EFIB_AERPE
17	5	31.2	132	1	RNPA_MICLU
18	5	31.2	135	1	RS12_THETH
19	5	31.2	144	1	SODM_BRAFL
20	5	31.2	145	1	YAF4_SCHPO
21	5	31.2	150	1	RNK6_MIOTA
22	5	31.2	161	1	YZCX_ECOLI
23	5	31.2	203	1	RUVA_ECOLI
24	5	31.2	214	1	ACUB_BACSU
25	5	31.2	218	1	COAT_SMWLM
26	5	31.2	235	1	YVCF_BACSU
27	5	31.2	237	1	CD63_HUMAN
28	5	31.2	237	1	CD63_MOUSE
29	5	31.2	237	1	CD63_RABIT
30	5	31.2	237	1	CD63_RAT
31	5	31.2	258	1	FABI_SYNY3
32	5	31.2	285	1	PNMT_RAT
33	5	31.2	294	1	ATHE_MOUSE
34	5	31.2	303	1	COPB_HUMAN
35	5	31.2	317	1	MAD3_HUMAN
36	5	31.2	329	1	TECB_CHICK
37	5	31.2	331	1	GALR_LACCA
38	5	31.2	331	1	UL38_HCMVA
39	5	31.2	336	1	Y724_MERTH
40	5	31.2	340	1	ASTQ_PSEAE
41	5	31.2	369	1	T1B_PARTE
42	5	31.2	372	1	GM4D_VIBCH
43	5	31.2	373	1	GM4D_EGOLI
44	5	31.2	382	1	MTLD_BACST
45	5	31.2	398	1	TAP_DROME

#### ALIGNMENTS

RESULT 1  
ID A4\_PIG STANDARD; PRT; 57 AA.  
AC Q29023;  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID  
DE PROTEIN (BETA-APP)] (FRAGMENT).  
GN APP.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-BRAIN;  
RX MEDLINE; 92017079.  
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;  
RT "Conservation of the sequence of the Alzheimer's disease amyloid  
RT peptide in dog, polar bear and five other mammals by cross-species  
RT polymerase chain reaction analysis".  
RL Brain Res. Mol. Brain Res. 10:299-305(1991).  
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO  
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN  
CC G(O) (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.  
CC -----  
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CC -----  
DR EMBL; X56127; CAA39592.1; -  
DR HSSP; P05067; IAML.  
DR PROSITE; PS00319; A4\_EXTRA; PARTIAL.  
DR PROSITE; PS00320; A4\_INTRA; PARTIAL.  
KW Glycoprotein; Amyloid; Neurone; Transmembrane.  
FT NON\_TER 1  
FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).  
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 34 57 POTENTIAL.  
FT NON\_TER 57  
SQ SEQUENCE 57 AA; 6172 MW; 84209D98EBA82DFA CRC64;

Query Match 100.0%; Score 16; DB 1; Length 57;

Best Local Similarity 100.0%; Pred. No. 9.7e-12;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOK 16

|||||

6 DAEFRHDSGYEVHHOK 21

DB

```

[1]
RN SEQUENCE FROM N.A.
RP TISSUE-KIDNEY;
RX MEDLINE; 92017079.
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC PROTEIN (BETA-APP) (FRAGMENT).
CC APP.
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
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CC
CC -----
CC DR EMBL; X56125; CAA39593.1; -.
CC HSP; P05067; IAML.
CC DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
CC DR PROSITE; PS00320; A4_INTRA; PARTIAL.
CC KW Glycoprotein; Amyloid; Neurone; Transmembrane.
CC FT NON_TER 1 49 BETA-AMYLOID PROTEIN (POTENTIAL).
CC FT CHAIN 7 34 EXTRACELLULAR (POTENTIAL).
CC FT DOMAIN <1 34
CC FT TRANSMEM 35 58
CC FT NON_TER 58 58
CC FT SEQUENCE 58 AA; 6285 MW; 8469D488A2E12DFA CRC64;
CC
CC Query Match 100.0%; Score 16; DB 1; Length 58;
CC Best Local Similarity 100.0%; Pred. No. 9.9e-12; Indels 0; Gaps 0;
CC Matches 16; Conservative 0; Mismatches 0;
CC
CC QY 1 DAEFRHDSGYEVHHQK 16
CC Db | | | | | | | | | | | | | | | |
CC 7 DAEFRHDSGYEVHHQK 22
CC
CC RESULT 4
CC A4_RABIT ID A4_RABIT STANDARD; PRT; 58 AA.
CC AC Q28748;
CC DT 01-NOV-1997 (Rel. 35, Created)
CC DT 01-NOV-1997 (Rel. 35, Last sequence update)
CC DT 15-JUL-1999 (Rel. 38, Last annotation update)
CC DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID
CC DE PROTEIN (BETA-APP)] (FRAGMENT).
CC GN APP.
CC OS Oryctolagus cuniculus (Rabbit).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
CC [1]
CC RN SEQUENCE FROM N.A.
CC RP TISSUE-BRAIN;
CC RX MEDLINE; 92017079.
CC RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
CC RT "Conservation of the sequence of the Alzheimer's disease amyloid
CC RT peptide in dog, polar bear and five other mammals by cross-species
CC RT polymerase chain reaction analysis."
CC RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC CC PROTEIN (BETA-APP) (FRAGMENT).
CC CC APP.
CC CC G(O) (BY SIMILARITY).
CC CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
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CC CC -----
CC DR EMBL; X56128; CAA39593.1; -.
CC HSP; P05067; IAML.
CC DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
CC DR PROSITE; PS00320; A4_INTRA; PARTIAL.
CC KW Glycoprotein; Amyloid; Neurone; Transmembrane.
CC FT NON_TER 1 48 BETA-AMYLOID PROTEIN (POTENTIAL).
CC FT CHAIN 6 48 EXTRACELLULAR (POTENTIAL).
CC FT DOMAIN <1 33
CC FT TRANSMEM 34 57
CC FT NON_TER 57 57
CC FT SEQUENCE 57 AA; 6172 MW; 84209D88EBA82DFA CRC64;
CC
CC Query Match 100.0%; Score 16; DB 1; Length 57;
CC Best Local Similarity 100.0%; Pred. No. 9.7e-12; Indels 0; Gaps 0;
CC Matches 16; Conservative 0; Mismatches 0;
CC
CC QY 1 DAEFRHDSGYEVHHQK 16
CC Db | | | | | | | | | | | | | | | |
CC 6 DAEFRHDSGYEVHHQK 21
CC
CC RESULT 3
CC A4_CANFA ID A4_CANFA STANDARD; PRT; 58 AA.
CC AC Q28280;
CC DT 01-NOV-1997 (Rel. 35, Created)
CC DT 01-NOV-1997 (Rel. 35, Last sequence update)
CC DT 15-JUL-1999 (Rel. 38, Last annotation update)
CC DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID
CC DE PROTEIN (BETA-APP)] (FRAGMENT).
CC GN APP.
CC OS Canis familiaris (Dog).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

```

```

[1]
RN SEQUENCE FROM N.A.
RP TISSUE-KIDNEY;
RX MEDLINE; 92017079.
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC PROTEIN (BETA-APP) (FRAGMENT).
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
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CC
CC -----
CC DR EMBL; X56125; CAA39590.1; -.
CC HSP; P05067; IAML.
CC DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
CC DR PROSITE; PS00320; A4_INTRA; PARTIAL.
CC KW Glycoprotein; Amyloid; Neurone; Transmembrane.
CC FT NON_TER 1 49 BETA-AMYLOID PROTEIN (POTENTIAL).
CC FT CHAIN 7 34 EXTRACELLULAR (POTENTIAL).
CC FT DOMAIN <1 34
CC FT TRANSMEM 35 58
CC FT NON_TER 58 58
CC FT SEQUENCE 58 AA; 6285 MW; 8469D488A2E12DFA CRC64;
CC
CC Query Match 100.0%; Score 16; DB 1; Length 58;
CC Best Local Similarity 100.0%; Pred. No. 9.9e-12; Indels 0; Gaps 0;
CC Matches 16; Conservative 0; Mismatches 0;
CC
CC QY 1 DAEFRHDSGYEVHHQK 16
CC Db | | | | | | | | | | | | | | | |
CC 7 DAEFRHDSGYEVHHQK 22
CC
CC RESULT 4
CC A4_RABIT ID A4_RABIT STANDARD; PRT; 58 AA.
CC AC Q28748;
CC DT 01-NOV-1997 (Rel. 35, Created)
CC DT 01-NOV-1997 (Rel. 35, Last sequence update)
CC DT 15-JUL-1999 (Rel. 38, Last annotation update)
CC DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID
CC DE PROTEIN (BETA-APP)] (FRAGMENT).
CC GN APP.
CC OS Oryctolagus cuniculus (Rabbit).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
CC [1]
CC RN SEQUENCE FROM N.A.
CC RP TISSUE-BRAIN;
CC RX MEDLINE; 92017079.
CC RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
CC RT "Conservation of the sequence of the Alzheimer's disease amyloid
CC RT peptide in dog, polar bear and five other mammals by cross-species
CC RT polymerase chain reaction analysis."
CC RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC CC PROTEIN (BETA-APP) (FRAGMENT).
CC CC APP.
CC CC G(O) (BY SIMILARITY).
CC CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
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CC CC
CC CC -----
CC DR EMBL; X56128; CAA39593.1; -.
CC HSP; P05067; IAML.
CC DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
CC DR PROSITE; PS00320; A4_INTRA; PARTIAL.
CC KW Glycoprotein; Amyloid; Neurone; Transmembrane.
CC FT NON_TER 1 48 BETA-AMYLOID PROTEIN (POTENTIAL).
CC FT CHAIN 6 48 EXTRACELLULAR (POTENTIAL).
CC FT DOMAIN <1 33
CC FT TRANSMEM 34 57
CC FT NON_TER 57 57
CC FT SEQUENCE 57 AA; 6172 MW; 84209D88EBA82DFA CRC64;
CC
CC Query Match 100.0%; Score 16; DB 1; Length 57;
CC Best Local Similarity 100.0%; Pred. No. 9.7e-12; Indels 0; Gaps 0;
CC Matches 16; Conservative 0; Mismatches 0;
CC
CC QY 1 DAEFRHDSGYEVHHQK 16
CC Db | | | | | | | | | | | | | | | |
CC 6 DAEFRHDSGYEVHHQK 21
CC
CC RESULT 3
CC A4_CANFA ID A4_CANFA STANDARD; PRT; 58 AA.
CC AC Q28280;
CC DT 01-NOV-1997 (Rel. 35, Created)
CC DT 01-NOV-1997 (Rel. 35, Last sequence update)
CC DT 15-JUL-1999 (Rel. 38, Last annotation update)
CC DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID
CC DE PROTEIN (BETA-APP)] (FRAGMENT).
CC GN APP.
CC OS Canis familiaris (Dog).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

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 CC -----

DR EMBL; X56129; CAA39594.1; -;  
 DR HSSP; P05067; 1AML.  
 DR PROSITE; PS00319; A4\_EXTRA; PARTIAL.  
 DR PROSITE; PS00320; A4\_INTRA; PARTIAL.  
 KW Glycoprotein; Amyloid; Neurone; Transmembrane.  
 FT NON\_TER 1 1  
 FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).  
 FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 34 57 POTENTIAL.  
 FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).  
 FT NON\_TER 58 58  
 SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 100.0%; Score 16; DB 1; Length 58;  
 Best Local Similarity 100.0%; Pred. No. 9.9e-12;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQK 16  
 Db 6 DAEFRHDSGYEVHHQK 21  
 |||||

RESULT 5  
 ID A4\_SHEEP STANDARD; PRT; 58 AA.  
 AC Q28757;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID  
 DE PROTEIN (BETA-APP)] (FRAGMENT).  
 GN APP.

OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
 OC Bovidae; Caprinae; Ovis.  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC TISSUE=HEART;  
 RX MEDLINE; 92017079.  
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;  
 RT "Conservation of the sequence of the Alzheimer's disease amyloid  
 RT peptide in dog, polar bear and five other mammals by cross-species  
 RT polymerase chain reaction analysis."  
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).  
 CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO  
 CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN  
 CC G(O) (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.  
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 CC -----

DR EMBL; X56130; CAA39595.1; -;  
 DR HSSP; P05067; 1AML.  
 DR PROSITE; PS00319; A4\_EXTRA; PARTIAL.  
 DR PROSITE; PS00320; A4\_INTRA; PARTIAL.  
 KW Glycoprotein; Amyloid; Neurone; Transmembrane.

FT NON\_TER 1 1  
 FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).  
 FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 34 57 POTENTIAL.  
 FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).  
 FT NON\_TER 58 58  
 SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 100.0%; Score 16; DB 1; Length 58;  
 Best Local Similarity 100.0%; Pred. No. 9.9e-12;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQK 16  
 Db 6 DAEFRHDSGYEVHHQK 21  
 |||||

RESULT 6  
 ID A4\_BOVIN STANDARD; PRT; 59 AA.  
 AC Q28053;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID  
 DE PROTEIN (BETA-APP)] (FRAGMENT).  
 GN APP.

OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
 OC Bovidae; Bovinae; Bos.  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC TISSUE=BRAIN;  
 RX MEDLINE; 92017079.  
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;  
 RT "Conservation of the sequence of the Alzheimer's disease amyloid  
 RT peptide in dog, polar bear and five other mammals by cross-species  
 RT polymerase chain reaction analysis."  
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).  
 CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO  
 CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN  
 CC G(O) (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.  
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 CC -----

DR EMBL; X56124; CAA39589.1; -;  
 DR EMBL; X56126; CAA39591.1; -;  
 DR HSSP; P05067; 1AML.  
 DR PROSITE; PS00319; A4\_EXTRA; PARTIAL.  
 DR PROSITE; PS00320; A4\_INTRA; PARTIAL.  
 KW Glycoprotein; Amyloid; Neurone; Transmembrane.

FT NON\_TER 1 1  
 FT CHAIN 7 49 BETA-AMYLOID PROTEIN (POTENTIAL).  
 FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 35 58 POTENTIAL.  
 FT DOMAIN 59 >59 CYTOPLASMIC (POTENTIAL).  
 FT NON\_TER 59 59  
 SQ SEQUENCE 59 AA; 6414 MW; F43469D488A2E12D CRC64;

Query Match 100.0%; Score 16; DB 1; Length 59;  
 Best Local Similarity 100.0%; Pred. No. 1e-11;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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us-09-155-076-2.isp

Qy 1 DAEFRHDSGYEVHHQK 16  
 Db 7 DAEFRHDSGYEVHHQK 22

RESULT 7  
 A4\_SAISC STANDARD; PRT; 751 AA.  
 AC Q95241; 1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-FEB-2000 (Rel. 39, Last annotation update)  
 DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN PRECURSOR [CONTAINS: BETA-AMYLOID PROTEIN (BETA-APP)]  
 GN APP.  
 OS Saimiri sciureus (Common squirrel monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LIVER, AND KIDNEY;  
 RX MEDLINE; 96108492.  
 RA Levy E., Anzini A., Frangione B., Walker L.C.;  
 RT "Beta-amyloid precursor protein gene in squirrel monkeys with cerebral amyloid angiopathy";  
 RL Neurobiol. Aging 16:805-808(1995).  
 CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O).  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.  
 CC  
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 CC  
 CC EMBL; S81024; AAD14347.1;  
 CC PFAM; PF00014; Kunitz\_BPTI; 1.  
 CC PRINTS; PR00203; AMYLOIDA.  
 CC PRINTS; PR00204; BETAAMYLOID.  
 CC PRINTS; PR00759; BASICPTASE.  
 CC PROSITE; PS00280; BPTI\_KUNITZ; 1.  
 CC PROSITE; PS00319; A4\_EXTRA; 1.  
 CC PROSITE; PS00320; A4\_INTRA; 1.  
 CC Glycoprotein; Amyloid; Neutone; Transmembrane; Alternative splicing;  
 KW Signal; Serine protease inhibitor.  
 FT SIGNAL 1 17 BY SIMILARITY.  
 FT CHAIN 18 751 A4 PROTEIN.  
 FT CHAIN 653 695 BETA-AMYLOID PROTEIN (POTENTIAL).  
 FT DOMAIN 18 680 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 681 704 POTENTIAL.  
 FT DOMAIN 705 751 CYTOPLASMIC (POTENTIAL).  
 FT SITE 740 743 CLATHRIN-BINDING (BY SIMILARITY).  
 FT CARBOHYD 523 523 PROBABLE.  
 FT CARBOHYD 552 552 PROBABLE.  
 FT DOMAIN 287 345 BPTI/KUNITZ INHIBITOR.  
 FT ACT\_SITE 301 302 REACTIVE BOND.  
 FT DISULFID 291 341 BY SIMILARITY.  
 FT DISULFID 300 324 BY SIMILARITY.  
 FT DISULFID 316 337 BY SIMILARITY.  
 SQ SEQUENCE 751 AA; 84893 MB; 6C3E431089569049 CRC64;

Query Match 100.0%; Score 16; DB 1; Length 751;  
 Best Local Similarity 100.0%; Pred. No. 8.2e-11;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQK 16

Db 653 DAEFRHDSGYEVHHQK 668

RESULT 8  
 A4\_HUMAN STANDARD; PRT; 770 AA.  
 AC P05067; P09000; Q16011;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 01-NOV-1991 (Rel. 20, Last sequence update)  
 DT 15-FEB-2000 (Rel. 39, Last annotation update)  
 DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN PRECURSOR (PROTEASE NEXIN-II)  
 DE (PN-II) (APPI) [CONTAINS: BETA-AMYLOID PROTEIN (BETA-APP)]  
 GN APP OR A4 OR CVAP OR ADL.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BRAIN;  
 RX MEDLINE; 87144572.  
 RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L., Grzeschik K.H., Multhaup G., Beyreuther K., Mueller-Hill B.;  
 RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface receptor";  
 RL Nature 325:733-736(1987).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 88122639.  
 RA Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D., Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F., Cordell B.;  
 RT "A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibitors";  
 RL Nature 331:525-527(1988).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 89128427.  
 RA Lemaire H.G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M., Unterbeck A., Beyreuther K., Mueller-Hill B.;  
 RT "The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded by 16 exons";  
 RL Nucleic Acids Res. 17:517-522(1989).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 97263807.  
 RA Hattori M., Tsukahara F., Furuhashi Y., Tanahashi H., Hirose M., Saito M., Tsukuni S., Sakaki Y.;  
 RT "A novel method for making nested deletions and its application for sequencing of a 300 kb region of human APP locus";  
 RL Nucleic Acids Res. 25:1802-1808(1997).  
 RN [5]  
 RP SEQUENCE OF 286-345 AND 365-366 FROM N.A.  
 RX MEDLINE; 88122640.  
 RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L., Gusella J.F., Neve R.L.;  
 RT "Protease inhibitor domain encoded by an amyloid protein precursor mRNA associated with Alzheimer's disease";  
 RL Nature 331:528-530(1988).  
 RN [6]  
 RP SEQUENCE OF 287-367 FROM N.A.  
 RX MEDLINE; 88122641.  
 RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;  
 RT "Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitory activity";  
 RL Nature 331:530-532(1988).  
 RN [7]  
 RP SEQUENCE OF 284-289 AND 365-770 FROM N.A.  
 RX MEDLINE; 87231971.  
 RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;  
 RT "Molecular cloning and characterization of a cDNA encoding the cerebrovascular and the neuritic plaque amyloid peptides";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).



RN [8] SEQUENCE OF 507-770 FROM N.A.  
 RX MEDLINE: 88124954.  
 RA Zain S.B., Selim M., Chou W.G., Saydel-Sulkowska E.M., Majocha R.E.,  
 RA Marotta C.A.;  
 RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer  
 RT disease brain: coding and noncoding regions of the fetal precursor  
 RT mRNA are expressed in the cortex.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).  
 RN [9]  
 RN SEQUENCE OF 672-681.  
 RX MEDLINE: 88035004.  
 RA Partridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,  
 RA Tourtellotte W.W., Huebner V., Shively J.E.;  
 RT "Amyloid angiopathy of Alzheimer's disease: amino acid composition  
 RT and partial sequence of a 4,200-dalton peptide isolated from cortical  
 RT microvessels.";  
 RL J. Neurochem. 49:1394-1401(1987).  
 RN [10]  
 RN SEQUENCE OF 739-770 FROM N.A.  
 RX MEDLINE: 90236318.  
 RA Yoshikai S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;  
 RT "Genomic organization of the human amyloid beta-protein precursor  
 RT gene.";  
 RL Gene 87:257-263(1990).  
 RN [11]  
 RN SEQUENCE OF 1-10 FROM N.A.  
 RX MEDLINE: 89016647.  
 RA Schon E.A., Mita S., Sadlock J., Herbert J.;  
 RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)  
 RT encodes a 95-kDa polypeptide.";  
 RL Nucleic Acids Res. 16:9351-9351(1988).  
 RN [12]  
 RN SEQUENCE OF 18-50.  
 RX MEDLINE: 87250462.  
 RA van Nostrand W.E., Cunningham D.D.;  
 RT "Purification of protease nexin II from human fibroblasts.";  
 RL J. Biol. Chem. 262:8508-8514(1987).  
 RN [13]  
 RN IDENTITY OF APP WITH NEXIN-II.  
 RX MEDLINE: 89384866.  
 RA Oltersdorf T., Fritz L.C., Schenk D.B., Lieberburg I.,  
 RA Johnson-Wood K.L., Beattie E.C., Ward P.J., Blacher R.W., Dovey H.F.,  
 RA Sinha S.;  
 RT "The secreted form of the Alzheimer's amyloid precursor protein with  
 RT the Kunitz domain is protease nexin-II.";  
 RL Nature 341:144-147(1989).  
 RN [14]  
 RN PROTEASE-SPECIFICITY OF INHIBITOR DOMAIN.  
 RX MEDLINE: 90211252.  
 RA Kido H., Fukutomi A., Schilling J., Wang Y., Cordell B., Katunuma N.;  
 RT "Protease-specificity of Kunitz inhibitor domain of Alzheimer's  
 RT disease amyloid protein precursor.";  
 RL Biochem. Biophys. Res. Commun. 167:716-721(1990).  
 RN [15]  
 RN COMPLEX WITH G(O).  
 RX MEDLINE: 93188965.  
 RA Nishimoto I., Okamoto T., Matsuura Y., Takahashi S., Okamoto T.,  
 RA Murayama Y., Ogata E.;  
 RT "Alzheimer amyloid protein precursor complexes with brain GTP-binding  
 RT protein G(O).";  
 RL Nature 362:75-79(1993).  
 RN [16]  
 RN X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 28-133.  
 RX MEDLINE: 92215582.  
 RA Rossjohn J., Cappai R., Fell S.C., Henry A., McKinstry W.J.,  
 RA Galatis D., Hesse L., Multhaup G., Beyreuther K., Masters C.L.,  
 RA Parker M.W.;  
 RT "Crystal structure of the N-terminal, growth factor-like domain of  
 RT Alzheimer amyloid precursor protein.";  
 RL Nat. Struct. Biol. 6:327-331(1999).  
 RN [17]

RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 287-344.  
 RX MEDLINE: 91104913.  
 RA Hynes T.R., Randal M., Kennedy L.A., Eigenbrot C., Kosiakof A.A.;  
 RT "X-ray crystal structure of the protease inhibitor domain of  
 RT Alzheimer's amyloid beta-protein precursor.";  
 RL Biochemistry 29:10018-10022(1990).  
 RN [18]  
 RN STRUCTURE BY NMR OF 289-344.  
 RX MEDLINE: 92031488.  
 RA Heald S.L., Tilton R.F. Jr., Hammond L.S., Lee A., Bayne R.M.,  
 RA Kamark M.E., Ramabhadran T.V., Dreyer R.N., Davis G., Unterbeck A.,  
 RA Tamburini P.P.;  
 RT "Sequential NMR resonance assignment and structure determination of  
 RT the Kunitz-type inhibitor domain of the Alzheimer's beta-amyloid  
 RT precursor protein.";  
 RL Biochemistry 30:10467-10478(1991).  
 RN [19]  
 RN STRUCTURE BY NMR OF 672-699.  
 RX MEDLINE: 94281210.  
 RA Talafous J., Marciniowski K.J., Klopman G., Zagorski M.G.;  
 RT "Solution structure of residues 1-28 of the amyloid beta-peptide.";  
 RL Biochemistry 33:7788-7796(1994).  
 RN [20]  
 RN STRUCTURE BY NMR OF 696-706.  
 RX MEDLINE: 97128622.  
 RA Kohno T., Kobayashi K., Maeda T., Sato K., Takashima A.;  
 RT "Three-dimensional structures of the amyloid beta peptide (25-35) in  
 RT membrane-mimicking environment.";  
 RL Biochemistry 35:16094-16104(1996).  
 RN [21]  
 RN STRUCTURE BY NMR OF 672-711.  
 RX MEDLINE: 98359783.  
 RA Coles M., Bicknell W., Watson A.A., Fairlie D.P., Craik D.J.;  
 RT "Solution structure of amyloid beta-peptide(1-40) in a water-micelle  
 RT environment. Is the membrane-spanning domain where we think it is?";  
 RL Biochemistry 37:11064-11077(1998).  
 RN [22]  
 RN STRUCTURE BY NMR OF 672-699.  
 RA Poulsen S.A., Watson A.A., Craik D.J.;  
 RT Submitted (JUN-1998) to the PDB data bank.  
 RN [23]  
 RN SIGNAL SEQUENCE CLEAVAGE SITE, AND TOPOLOGY.  
 RX MEDLINE: 88296437.  
 RA Dyvks T., Weidemann A., Multhaup G., Salbaum J.M., Lemaire H.-G.,  
 RA Kang J., Mueller-Hill B., Masters C.L., Beyreuther K.;  
 RT "Identification, transmembrane orientation and biogenesis of the  
 RT amyloid A4 precursor of Alzheimer's disease.";  
 RL EMBO J. 7:949-957(1988).  
 RN [24]  
 RN REVIEW.  
 RX MEDLINE: 92271194.  
 RA Kosik K.S.;  
 RT "Alzheimer's disease: a cell biological perspective.";  
 RL Science 256:780-783(1992).  
 RN [25]  
 RN REVIEW ON VARIANTS.  
 RX MEDLINE: 93250996.  
 RA Hardy J.;  
 RT "Framing beta-amyloid.";  
 RL Nat. Genet. 1:233-234(1992).  
 RN [26]

Query Match 100.0%; Score 16; DB 1; Length 770;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-11;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16  
 Db - 672 DAEFRHDSGYEVHHQK 687  
 |||||

RESULT 9

AAT\_STRGR

ID AAT\_STRGR STANDARD; PRT; 213 AA.

P36692;  
 AC 01-JUN-1994 (Rel. 29, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-FEB-2000 (Rel. 39, Last annotation update)  
 DE PROBABLE ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1) (TRANSMINASE A)  
 DE (ASPART) (FRAGMENT).  
 GN ASPC OR AATA.  
 OS Streptomyces griseus.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=N2-3-11;  
 RC MEDLINE; 94314177.  
 RA Kuberski S., Kasberg T., Distler J.;  
 RT "The nusG gene of Streptomyces griseus: cloning of the gene and  
 RT analysis of the A-factor binding properties of the gene product.";  
 RL FEMS Microbiol. Lett. 119:33-39(1994).  
 RN [2]  
 RP SEQUENCE OF 1-64 FROM N.A.  
 RC STRAIN=IFO 13350;  
 RC MEDLINE; 94114580.  
 RA Miyake K., Onaka H., Horinouchi S., Beppu T.;  
 RT "Organization and nucleotide sequence of the secE-nusG region of  
 RT Streptomyces griseus";  
 RL Biochim. Biophys. Acta 1217:97-100(1994).  
 CC -1- CATALYTIC ACTIVITY: L-ASPARTATE + 2-OXOGLOUTARATE -> OXALOACETATE +  
 CC L-GLUTAMATE.  
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.  
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT  
 CC AMINOTRANSFERASES.  
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 CC -----  
 CC EMBL; X72787; CAA51294.1; -;  
 CC EMBL; D17464; -; NOT\_ANNOTATED\_CDS.  
 DR PIR; S41059; S41059.  
 DR PROSITE; PS00105; AA\_TRANSFER\_CLASS\_1; PARTIAL.  
 KW Transferase; Aminotransferase; Pyridoxal phosphate.  
 FT NON\_TER 213 213  
 SQ SEQUENCE 213 AA; 22693 MW; C380BF59DA55A429 CRC64;  
 Query Match 37.5%; Score 6; DB 1; Length 213;  
 Best Local Similarity 100.0%; Pred. No. 3.6;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 DSGVEV 12  
 Db 92 DSGVEV 97  
 RESULT 10  
 POLG\_PVYVO STANDARD; PRT; 284 AA.  
 ID POLG\_PVYVO  
 AC P11897;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE GENOME POLYPROTEIN [CONTAINS: NUCLEAR INCLUSION PROTEIN B (NI-B) (NIB)  
 DE (RNA-DIRECTED RNA POLYMERASE) (EC 2.7.7.48); COAT PROTEIN (CP)]  
 DE (FRAGMENT).  
 OS Potato virus Y (strain Yo) (PVY).  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;  
 OC Potyvirus.  
 RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE; 89296509.  
 RA Bravo-Almonacid F.F., Mentaberry A.N.;  
 RT "Nucleotide cDNA sequence coding for the PVYO coat protein.";  
 RL Nucleic Acids Res. 17:4401-4401(1989).  
 CC -1- PTM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE  
 CC POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC  
 CC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT  
 CC INDIVIDUAL PROTEINS.  
 CC -1- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.  
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 CC -----  
 CC EMBL; X14136; CAA32356.1; -;  
 DR PIR; S04723; S04723.  
 DR PFAM; PF00767; Pocy\_coat; 1.  
 KW Transferase; RNA-directed RNA polymerase; Coat protein; Polyprotein.  
 FT NON\_TER 1 1  
 FT CHAIN <1 17 NUCLEAR INCLUSION PROTEIN B.  
 FT CHAIN 18 284 COAT PROTEIN.  
 SQ SEQUENCE 284 AA; 31971 MW; E98535C4607898E2 CRC64;  
 Query Match 37.5%; Score 6; DB 1; Length 284;  
 Best Local Similarity 100.0%; Pred. No. 4.5;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 10 YEYVHQ 15  
 Db 12 YEYVHQ 17  
 RESULT 11  
 POLG\_PVYCH STANDARD; PRT; 327 AA.  
 ID POLG\_PVYCH  
 AC P21294;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE GENOME POLYPROTEIN [CONTAINS: NUCLEAR INCLUSION PROTEIN B (NI-B) (NIB)  
 DE (RNA-DIRECTED RNA POLYMERASE) (EC 2.7.7.48); COAT PROTEIN (CP)]  
 DE (FRAGMENT).  
 OS Potato virus Y (strain Chinese isolate) (PVY).  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;  
 OC Potyvirus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 91016851.  
 RA Zhou X.R., Fang R.X., Wang C.O., Mang K.Q.;  
 RT "cDNA sequence of the 3'-coding region of PVY genome (the Chinese  
 RT isolate).";  
 RL Nucleic Acids Res. 18:5554-5554(1990).  
 CC -1- PTM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE  
 CC POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC  
 CC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT  
 CC INDIVIDUAL PROTEINS.  
 CC -1- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.  
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 CC -----  
 CC EMBL; X54058; CAA37993.1; -;  
 DR EMBL; X54058; CAA37993.1; -;

DR PIR; S11549; S11549.  
 DR HSP; P05067; 1AMB.  
 DR PFAM; PF00767; Poty\_coat; 1.  
 KW Transferase; RNA-directed RNA polymerase; Coat protein; Polypotein.  
 FT NON\_TER 1  
 FT CHAIN <1 60 NUCLEAR INCLUSION PROTEIN B.  
 FT CHAIN 61 327 COAT PROTEIN.  
 SQ SEQUENCE 327 AA; 36868 MW; 8F8355E2DB6F2F18 CRC64;

Query Match 37.5%; Score 6; DB 1; Length 327;  
 Best Local Similarity 100.0%; Pred. No. 5.1;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 YEYHHQ 15  
 |||||  
 Db 55 YEYHHQ 60

RESULT 12  
 COAT\_PMW  
 ID COAT\_PMW STANDARD; PRT; 330 AA.  
 AC P07993;

DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-AUG-1988 (Rel. 08, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE COAT PROTEIN.  
 OS Pepper mottle virus (PeMV).  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;  
 OC Potyvirus.

[1]  
 SEQUENCE FROM N.A.  
 DR Dougherty W.G., Allison R.F., Parks T.D., Johnston R.E., Feild M.J.,  
 RA Armstrong F.B.;  
 RT "Nucleotide sequence at the 3' terminus of pepper mottle virus  
 RT genomic RNA: evidence for an alternative mode of potyvirus capsid  
 RT protein gene organization.";  
 RL Virology 146:282-291(1985).

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CC EMBL; M11598; AA046902.1; -  
 DR PIR; A26205; A26205.  
 DR PFAM; PF00767; Poty\_coat; 1.  
 KW Coat protein.  
 SQ SEQUENCE 330 AA; 37028 MW; C63A2F810D95820E CRC64;

Query Match 37.5%; Score 6; DB 1; Length 330;  
 Best Local Similarity 100.0%; Pred. No. 5.1;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 YEYHHQ 15  
 |||||  
 Db 58 YEYHHQ 63

RESULT 13  
 AAT\_STRVG  
 ID AAT\_STRVG STANDARD; PRT; 397 AA.  
 AC Q60013;

DT 15-FEB-2000 (Rel. 39, Created)  
 DT 15-FEB-2000 (Rel. 39, Last sequence update)  
 DT 15-FEB-2000 (Rel. 39, Last annotation update)  
 DE ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1) (TRANSMINASE A) (ASPAR).  
 GN ASPC OR AAT.  
 OS Streptomyces virginiae.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomycetes.  
 [1]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE; 96257210.  
 RA Katayama M., Sakai Y., Okamoto S., Ihara F., Nihira T., Yamada Y.;  
 RT "Gene organization in the ada-rpL region of Streptomyces virginiae.";  
 RL Gene 171:135-136(1996).  
 CC -1- CATALYTIC ACTIVITY: L-ASPARTATE + 2-OXOGLUTARATE = OXALOACETATE +  
 CC L-GLUTAMATE.  
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT  
 CC AMINOTRANSFERASES.  
 -----  
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 -----  
 CC EMBL; D50624; BAA09299.1; -  
 DR PFAM; PF00155; aminotran\_1; 1.  
 DR PROSITE; PS00105; AA-TRANSFER CLASS 1; 1.  
 KW Transferase; Aminotransferase; Pyridoxal phosphate.  
 FT BINDING 236 236 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 SQ SEQUENCE 397 AA; 42381 MW; EEFDECB7D923065 CRC64;

Query Match 37.5%; Score 6; DB 1; Length 397;  
 Best Local Similarity 100.0%; Pred. No. 6;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DSGYEV 12  
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 Db 82 DSGYEV 87

RESULT 14  
 POLG\_PVYHU

ID POLG\_PVYHU STANDARD; PRT; 3061 AA.  
 AC Q02963;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE GENOME POLYPROTEIN (CONTAINS: N-TERMINAL PROTEIN (P1); HELPER  
 DE COMPONENT PROTEINASE (EC 3.4.22.-) (HC-PRO); PROTEIN P3; 6 KDA PROTEIN  
 DE 1 (6K1); CYTOPLASMIC INCLUSION PROTEIN (CI); 6 KDA PROTEIN 2 (6K2);  
 DE GENOME-LINKED PROTEIN (VPG); NUCLEAR INCLUSION PROTEIN A (NI-A) (NIA)  
 DE (EC 3.4.22.-) (49 KDA PROTEINASE) (49 KDA-PRO); NUCLEAR INCLUSION  
 DE PROTEIN B (NI-B) (NIB) (RNA-DIRECTED RNA POLYMERASE) (EC 2.7.7.48);  
 DE COAT PROTEIN (CP)].  
 OS Potato virus Y (strain Hungarian) (PVY).  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;  
 OC Potyvirus.

[1]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE; 93154578.  
 RA Thole V., Dalmay T., Burgyn J., Balazs E.;  
 RT "Cloning and sequencing of potato virus Y (Hungarian isolate) genomic  
 RT RNA.";  
 RL Gene 123:149-156(1993).  
 CC -1- FUNCTION: HELPER COMPONENT-PROTEINASE IS REQUIRED FOR APHD  
 CC TRANSMISSION AND ALSO HAS PROTEOLYTIC ACTIVITY.  
 CC -1- FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICASE ACTIVITY. IT  
 CC MAY BE INVOLVED IN REPLICATION.  
 CC -1- FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.  
 CC -1- PTM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.  
 CC -1- PTM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE  
 CC POLYPEPTIDE WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC  
 CC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT  
 CC INDIVIDUAL PROTEINS.

```

CC CC -!- SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.
CC CC -!- SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4.
CC CC -!- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.
CC CC -----
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CC CC -----
CC CC EMBL; M95491; AAB59762.1; -.
CC CC PIR; JN0345; JN0545.
CC CC PFAM; PF00270; DEAD; 1.
CC CC PFAM; PF00863; Peptidase_C4; 1.
CC CC PFAM; PF00851; Peptidase_C6; 1.
CC CC PFAM; PF01577; Poty_P1; 1.
CC CC PFAM; PF00767; Poty_coat; 1.
CC CC PFAM; PF00680; RNA_dep_RNA_pol; 1.
CC CC PFAM; PF00271; helicase_C; 1.
CC CC PRINTS; PR00966; NIAPOTYPTASE.
CC CC Hydrolase; Transferase; Thiol protease; RNA-directed RNA polymerase;
CC CC Coat protein; Polyprotein; Covalent protein-RNA linkage; Helicase;
CC CC ATP-binding.
CC CC CHAIN 1 275 N-TERMINAL PROTEIN.
CC CC CHAIN 276 824 HELPER COMPONENT PROTEINASE.
CC CC CHAIN 825 ? PROTEIN P3.
CC CC CHAIN ? 1157 6 kDa PROTEIN 1.
CC CC CHAIN 1158 1791 CYTOPLASMIC INCLUSION PROTEIN.
CC CC CHAIN 1792 1843 6 kDa PROTEIN 2.
CC CC CHAIN 1844 ? GENOME-LINKED PROTEIN.
CC CC CHAIN ? 2275 NUCLEAR INCLUSION PROTEIN A.
CC CC CHAIN 2276 2794 NUCLEAR INCLUSION PROTEIN B.
CC CC CHAIN 2795 3061 COAT PROTEIN.
CC CC CHAIN 1907 1907 COVALENT LINKAGE OF VIRAL RNA (BY
CC CC BINDING SIMILARITY).
CC CC NP_BIND 1242 1249 ATP (POTENTIAL).
CC CC SEQUENCE 3061 AA; 347326 MW; 737FFBA215B56F99 CRC64;

Query Match 37.5%; Score 6; DB 1; Length 3061;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 YEVHHQ 15
Db 2789 YEVHHQ 2794
|||||

RESULT 15
POLG_PVYN STANDARD; PRT; 3063 AA.
AC P18247; Q85266; Q85267; Q85268; Q85269; Q85270; Q85271; Q85272;
AC Q85273;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER
DE COMPONENT PROTEINASE (EC 3.4.22.-) (HC-PRO); PROTEIN P3; 6 kDa PROTEIN
DE 1 (6K1); CYTOPLASMIC INCLUSION PROTEIN (CI); 6 kDa PROTEIN 2 (6K2);
DE GENOME-LINKED PROTEIN (VPG); NUCLEAR INCLUSION PROTEIN A (NI-A) (NIA)
DE (EC 3.4.22.-) (49 kDa PROTEINASE) (49 kDa-PRO); NUCLEAR INCLUSION
DE PROTEIN B (NI-B) (NIB) (RNA-DIRECTED RNA POLYMERASE) (EC 2.7.7.48);
DE COAT PROTEIN (CP)].
OS Potato virus Y (strain N) (PVY).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89279275.
RA Robaglia C., Durand-Tardif M., Tronchet M., Boudazin G.,
RA Astier-Manificier S., Casse-Delbart F.;

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RT "Nucleotide sequence of potato virus Y (N Strain) genomic RNA.";
RL J. Gen. Virol. 70:935-947(1989).
RN [2]
RP REVISIONS.
RA Durand-Tardif M.;
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: HELPER COMPONENT-PROTEINASE IS REQUIRED FOR APHID
CC TRANSMISSION AND ALSO HAS PROTEOLYTIC ACTIVITY.
CC -!- FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICASE ACTIVITY. IT
CC MAY BE INVOLVED IN REPLICATION.
CC -!- FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.
CC -!- PTM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.
CC -!- PTM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE
CC POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC
CC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT
CC INDIVIDUAL PROTEINS.
CC -!- SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.
CC -!- SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4.
CC -!- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.
CC -----
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CC CC or send an email to license@isb-sib.ch).
CC CC -----
CC CC EMBL; X12456; CA30988.1; -.
CC CC EMBL; D00441; BAA00342.1; -.
CC CC PIR; JS0166; JS0166.
CC CC PFAM; PF00270; DEAD; 1.
CC CC PFAM; PF00863; Peptidase_C4; 1.
CC CC PFAM; PF00851; Peptidase_C6; 1.
CC CC PFAM; PF01577; Poty_P1; 1.
CC CC PFAM; PF00767; Poty_coat; 1.
CC CC PFAM; PF00680; RNA_dep_RNA_pol; 1.
CC CC PFAM; PF00271; helicase_C; 1.
CC CC PRINTS; PR00966; NIAPOTYPTASE.
CC CC Hydrolase; Transferase; Thiol protease; RNA-directed RNA polymerase;
CC CC Coat protein; Polyprotein; Covalent protein-RNA linkage; Helicase;
CC CC ATP-binding.
CC CC CHAIN 1 275 N-TERMINAL PROTEIN.
CC CC CHAIN 276 824 HELPER COMPONENT PROTEINASE.
CC CC CHAIN 825 ? PROTEIN P3.
CC CC CHAIN ? 1157 6 kDa PROTEIN 1.
CC CC CHAIN 1158 1791 CYTOPLASMIC INCLUSION PROTEIN.
CC CC CHAIN 1792 1843 6 kDa PROTEIN 2.
CC CC CHAIN 1844 ? GENOME-LINKED PROTEIN.
CC CC CHAIN ? 2275 NUCLEAR INCLUSION PROTEIN A.
CC CC CHAIN 2276 2796 NUCLEAR INCLUSION PROTEIN B.
CC CC CHAIN 2797 3063 COAT PROTEIN.
CC CC CHAIN 1907 1907 COVALENT LINKAGE OF VIRAL RNA (BY
CC CC BINDING SIMILARITY).
CC CC NP_BIND 1242 1249 ATP (POTENTIAL).
CC CC SEQUENCE 3063 AA; 347535 MW; 3EC79125DE33F1BB CRC64;

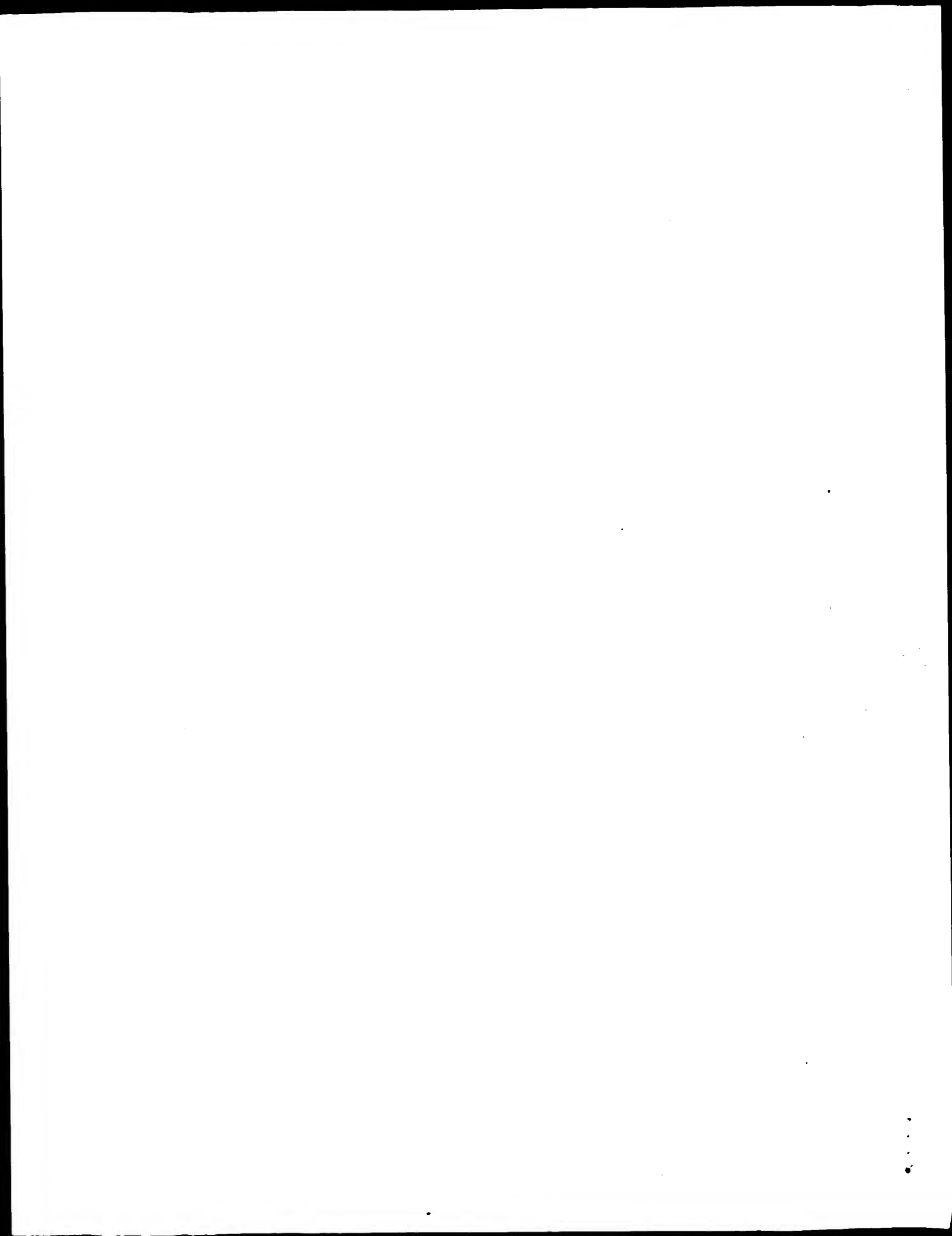
Query Match 37.5%; Score 6; DB 1; Length 3063;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 YEVHHQ 15
Db 2791 YEVHHQ 2796
|||||

Search completed: September 13, 2000, 02:27:54
Job time: 171 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 13, 2000, 02:27:31 ; Search time 22.45 Seconds  
(without alignments)  
49.392 Million cell updates/sec

Title: US-09-155-076-2

Perfect score: 16  
Sequence: 1 DAEFRHDSGYEVHOK 16

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 225878 seqs, 69334122 residues

Word size : 0

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL\_12.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phase.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	100.0	82	4	Q16020
2	16	100.0	82	4	Q16019
3	16	100.0	82	4	Q16014
4	16	100.0	82	4	P78438
5	16	100.0	534	13	O93296
6	16	100.0	695	11	O60496
7	14	87.5	37	4	Q13778
8	10	62.5	699	13	O57394
9	7	43.8	747	13	Q91963
10	7	43.8	780	13	O73683
11	6	37.5	123	2	O53951
12	6	37.5	292	12	O85276
13	6	37.5	292	12	O85108
14	6	37.5	313	12	O85259
15	6	37.5	365	12	O9W605
16	6	37.5	379	12	O85257
17	6	37.5	380	1	O30016
18	6	37.5	447	10	O04340
19	6	37.5	453	1	O30322

20	6	37.5	533	11	O08569
21	6	37.5	704	13	Q90865
22	6	37.5	761	5	Q18468
23	6	37.5	976	12	O85104
24	6	37.5	1555	12	O85274
25	6	37.5	3051	12	O85265
26	5	31.2	58	1	O28675
27	5	31.2	76	2	P70764
28	5	31.2	105	2	O87879
29	5	31.2	112	2	O94629
30	5	31.2	123	1	Q9Y304
31	5	31.2	130	12	O9WY3
32	5	31.2	130	12	Q9WY3
33	5	31.2	132	3	P78948
34	5	31.2	141	1	Q9YDE5
35	5	31.2	142	5	O16896
36	5	31.2	174	2	O52573
37	5	31.2	178	5	Q17803
38	5	31.2	186	5	Q17303
39	5	31.2	195	2	O06241
40	5	31.2	195	12	Q87073
41	5	31.2	196	2	Q49789
42	5	31.2	208	5	O62213
43	5	31.2	209	2	O86679
44	5	31.2	230	4	Q13267
45	5	31.2	232	2	Q9ZHS1

## ALIGNMENTS

RESULT 1  
Q16020  
ID Q16020 PRELIMINARY: PRT: 82 AA.  
AC Q16020;  
DT 01-NOV-1996 (TREMREL. 01, Created)  
DT 01-NOV-1996 (TREMREL. 01, Last sequence update)  
DT 01-NOV-1999 (TREMREL. 12, Last annotation update)  
DE BETA-AMYLLOID PEPTIDE (FRAGMENT).  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 93236501.  
RA DENMAN R.B., ROSENZWAIG R., MILLER D.L.;  
RT "A system for studying the effect(s) of familial Alzheimer disease mutations on the processing of the beta-amyloid peptide precursor.";  
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).  
DR EMBL; S61383; CAB32008.1; -.  
DR HSSP; P05067; 1AML.  
FT NON\_TER 1  
FT NON\_TER 82  
SQ SEQUENCE 82 AA; 8882 MW; 55734509 CRC32;

Query Match 100.0%; Score 16; DB 4; Length 82;  
Best Local Similarity 100.0%; Pred. No. 9.7e-12;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHOK 16  
Db 18 DAEFRHDSGYEVHOK 33

RESULT 2  
Q16019  
ID Q16019 PRELIMINARY: PRT: 82 AA.  
AC Q16019;  
DT 01-NOV-1996 (TREMREL. 01, Created)  
DT 01-NOV-1996 (TREMREL. 01, Last sequence update)  
DT 01-NOV-1999 (TREMREL. 12, Last annotation update)  
DE BETA-AMYLLOID PEPTIDE (FRAGMENT).

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RX MEDLINE; 93236601.
RA DENMAN R.B., ROSENZWAIG R., MILLER D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RL mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S61380; CAB32007.1; -.
DR HSSP; P05067; 1AML.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 8938 MW; 4C8B0B56E CRC32;

Query Match 100.0%; Score 16; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 9.7e-12;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
Db 18 DAEFRHDSGYEVHHQK 33

RESULT 3
Q16014 PRELIMINARY; PRT; 82 AA.
AC Q16014;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)
DE BETA-AMYLLOID PEPTIDE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RX MEDLINE; 93236601.
RA DENMAN R.B., ROSENZWAIG R., MILLER D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RL mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S60721; CAB31888.1; -.
DR HSSP; P05067; 1AML.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 8972 MW; 30147E4F CRC32;

Query Match 100.0%; Score 16; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 9.7e-12;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
Db 18 DAEFRHDSGYEVHHQK 33

RESULT 4
P78438 PRELIMINARY; PRT; 82 AA.
AC P78438;
DT 01-MAY-1997 (TRENBLrel. 03, Created)
DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)
DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)
DE AMYLOID PROTEIN (BETA-AMYLLOID PROTEIN) (FRAGMENT).
GN APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]

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SEQUENCE FROM N.A.
RX MEDLINE; 8932030.
RA JOHNSTONE E.M., CHANEY M.O., MOORE R.E., WARD K.E., NORRIS F.H.,
RA LITTLE S.P.;
RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows
RL similarity to soybean trypsin inhibitor.";
RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
RN [2]
RP SEQUENCE OF 19-48 FROM N.A.
RX MEDLINE; 87120329.
RA TANZI R.E., GUSELLA J.F., WATKINS P.C., BRUNS G.A., GEORGE-HYSLOP P.,
RA VAN KEUREN M.L., PATTERSON D., PAGAN S., KURNIT D.M., NEVE R.L.;
RT "Amyloid beta protein gene: cDNA, mRNA distribution, and genetic
RL linkage near the Alzheimer locus.";
RL Science 235:880-884(1987).
RN [3]
RP SEQUENCE OF 32-63 FROM N.A.
RX MEDLINE; 93035397.
RA KAMINO K., ORR H.T., PAYAMI H., WIJSMAN E.M., ALONSO M.E., PULST S.M.,
RA ANDERSON L., O'DAHL S., NEMENS E., WHITE J.A.;
RT "Linkage and mutational analysis of familial Alzheimer disease
RL kindreds for the APP gene region.";
RL Am. J. Hum. Genet. 51:998-1014(1992).
DR EMBL; M29270; AAA51768.1; -.
DR EMBL; M29269; AAA51768.1; JOINED.
DR EMBL; M15532; AAA51564.1; -.
DR EMBL; S45136; AAB23646.1; -.
DR HSSP; P05067; 1AML.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 8994 MW; 5399FFA4 CRC32;

Query Match 100.0%; Score 16; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 9.7e-12;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
Db 17 DAEFRHDSGYEVHHQK 32

RESULT 5
O93296 PRELIMINARY; PRT; 534 AA.
AC O93296;
DT 01-NOV-1998 (TRENBLrel. 08, Created)
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)
DE AMYLOID PRECURSOR PROTEIN (FRAGMENT).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RA BARNES N.Y., LING L., YOSHIKAWA K., SCHWARTZ L.M., OPPENHEIM R.W.,
RA MILLIGAN C.E.;
RT "Increased production of amyloid precursor protein provides a
RL substrate for Caspase 3 in dying motoneurons.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF042098; AAC35052.1; -.
DR HSSP; P05067; 1AML.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 534 AA; 60597 MW; 6F117D2F CRC32;

Query Match 100.0%; Score 16; DB 13; Length 534;
Best Local Similarity 100.0%; Pred. No. 4.7e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16

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Db 436 DAEFRHDSGYEVHHQK 451

RESULT 6  
Q60496 PRELIMINARY; PRT; 695 AA.  
AC Q60496;  
DT 01-NOV-1996 (TREMELrel. 01, Created)  
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)  
DT 01-NOV-1999 (TREMELrel. 12, Last annotation update)  
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN.  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-BRAIN;  
RA BECK M., MOELLER D., BIGL V.;  
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO  
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN  
CC (G(O)).  
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -!- SIMILARITY: TO OTHER SPECIES APP ANALOGUES.  
DR EMBL; X97631; CAA66230.1; -.  
DR HSP; P05067; IAML.  
DR PRINTS; PR00203; AMYLOIDA4.  
DR PRINTS; PR00204; BETAAMYLOID.  
SQ SEQUENCE 695 AA; 78701 MW; CE05C651 CRC32;

Query Match 100.0%; Score 16; DB 11; Length 695;  
Best Local Similarity 100.0%; Pred. No. 5.8e-11; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 0;  
QY 1 DAEFRHDSGYEVHHQK 16  
Db 597 DAEFRHDSGYEVHHQK 612  
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RESULT 7  
Q13778 PRELIMINARY; PRT; 97 AA.  
AC Q13778;  
DT 01-NOV-1996 (TREMELrel. 01, Created)  
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)  
DT 01-NOV-1999 (TREMELrel. 12, Last annotation update)  
DE AMYLOID PROTEIN (AD-AP) (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 87130328.  
RA GOLDGABER D., LERMAN M.I., MCBRIDE O.W., SAFFIOTTI U., GAJDUSEK D.C.;  
RT "Characterization and chromosomal localization of a cDNA encoding  
RT brain amyloid of Alzheimer's disease.";  
RL Science 235:877-880(1987).  
DR EMBL; M15533; AAA35540.1; -.  
DR HSP; P05067; IAML.  
FT NON\_TER 1  
SQ SEQUENCE 97 AA; 10884 MW; C4D32AA2 CRC32;

Query Match 87.5%; Score 14; DB 4; Length 97;  
Best Local Similarity 100.0%; Pred. No. 2.2e-09;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 EFRHDSGYEVHHQK 16  
Db 1 EFRHDSGYEVHHQK 14  
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RESULT 8  
O57394 PRELIMINARY; PRT; 699 AA.  
AC O57394;  
DT 01-JUN-1998 (TREMELrel. 06, Created)  
DT 01-JUN-1998 (TREMELrel. 06, Last sequence update)  
DT 01-NOV-1999 (TREMELrel. 12, Last annotation update)  
DE EL AMYLOID PRECURSOR PROTEIN 699.  
GN EL APP699.  
OS Narke japonica (Electric ray).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
OC Elasmobranchii; Rajiformes; Narke.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-ELECTRIC LOBE;  
RA IJIMA K., LEE D., OKUTSU J., TOMITA S., HIRASHIMA N., KIRINO Y.,  
RA SUZUKI T.;  
RL Biochem. J. 0:0-0(1998).  
DR EMBL; AB005544; BAA24230.1; -.  
DR PROSITE; PS00319; A4\_EXTRA; 1.  
DR PROSITE; PS00320; A4\_INTRA; 1.  
DR PRINTS; PR00203; AMYLOIDA4.  
DR PRINTS; PR00204; BETAAMYLOID.  
SQ SEQUENCE 699 AA; 78879 MW; 11604C05 CRC32;

Query Match 62.5%; Score 10; DB 13; Length 699;  
Best Local Similarity 100.0%; Pred. No. 0.00047;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 DSGYEVHHQK 16  
Db 607 DSGYEVHHQK 616  
|||||

RESULT 9  
Q91963 PRELIMINARY; PRT; 747 AA.  
AC Q91963;  
DT 01-NOV-1996 (TREMELrel. 01, Created)  
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)  
DT 01-NOV-1999 (TREMELrel. 12, Last annotation update)  
DE APP747.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;  
OC Batrachia; Anura; Mesobatrachia; Pipidae; Xenopodinae;  
OC Xenopus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 93129227.  
RA OKADO H., OKAMOTO H.;  
RT "A Xenopus homologue of the human beta-amyloid precursor protein:  
RT developmental regulation of its gene expression.";  
RL Biochem. Biophys. Res. Commun. 189:1561-1568(1992).  
DR EMBL; S52417; AAB24853.1; -.  
DR PROSITE; PS00320; A4\_INTRA; 1.  
DR PROSITE; PS00280; BPTL\_KUNITZ; 1.  
DR PROSITE; PS00319; A4\_EXTRA; 1.  
DR PFAM; PF00014; Kunitz\_BPTI; 1.  
DR PRINTS; PR00203; AMYLOIDA4.  
DR PRINTS; PR00204; BETAAMYLOID.  
DR PRINTS; PR00759; BASICTPASE.  
KW Serine protease inhibitor.  
SQ SEQUENCE 747 AA; 84892 MW; A7580143 CRC32;

Query Match 43.8%; Score 7; DB 13; Length 747;  
Best Local Similarity 100.0%; Pred. No. 1.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 10 YEVHHQK 16  
Db 658 YEVHHQK 664  
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Wed Sep 13 08:11:37 2000

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RESULT 10
Q85276 PRELIMINARY; PRT; 780 AA.
ID Q85276
AC Q85276;
DT 01-NOV-1996 (TREMELrel. 07, Created)
DT 01-AUG-1998 (TREMELrel. 07, Last sequence update)
DT 01-NOV-1996 (TREMELrel. 07, Last sequence update)
DE POLYPROTEIN (FRAGMENT).
OS Potato virus Y.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
RN [1]
RP SEQUENCE FROM N.A.
RA GRIFFIN J.D., SHIEL P.S., BERGER P.H., THORNBURY D.W.;
RL Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.
DR EMBL; M81435; AAA47185.1; -.
DR PFAM; PF00767; Poty_coat; 1.
KW Polyprotein. 1 1
FT NON_TER 1 25 NIB.
FT CHAIN 26 292 COAT PROTEIN.
SQ SEQUENCE 292 AA; 32945 MW; 8CB34E72 CRC32;

Query Match 37.5%; Score 6; DB 12; Length 292;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 YEVHHQ 15
Db 20 YEVHHQ 25

RESULT 13
Q85108 PRELIMINARY; PRT; 298 AA.
ID Q85108
AC Q85108;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMELrel. 08, Last annotation update)
DE CAPSID PROTEIN (FRAGMENT).
OS Potato virus Y.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
RN [1]
RP SEQUENCE FROM N.A.
RA D'AQUINO L., DALWAY T., BURGYN J., RAGOZZINO A., SCALA F.;
RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U10378; AAA19172.1; -.
DR PFAM; PF00767; Poty_coat; 1.
FT NON_TER 1 298
FT NON_TER 298 298
SQ SEQUENCE 298 AA; 33459 MW; 93324303 CRC32;

Query Match 37.5%; Score 6; DB 12; Length 298;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 YEVHHQ 15
Db 27 YEVHHQ 32

RESULT 14
Q85259 PRELIMINARY; PRT; 313 AA.
ID Q85259
AC Q85259;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-JAN-1999 (TREMELrel. 09, Last annotation update)

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DE ORF (FRAGMENT).  
 OS Potato virus Y.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;  
 OC Potyvirus.  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN-NECROTIC (PVY-T);  
 RC HIDAKA M.;  
 RA Submitted (NOV-1991) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; D12570; BAA02120.1; -  
 DR PFAM; PF00767; Poty\_coat; 1.  
 KW Coat protein. 1 1  
 FT NON\_TER 47 313 COAT PROTEIN.  
 FT CHAIN 47 313  
 SQ SEQUENCE 313 AA; 35372 MW; 453E75C2 CRC32;

Query Match 37.5%; Score 6; DB 12; Length 313;  
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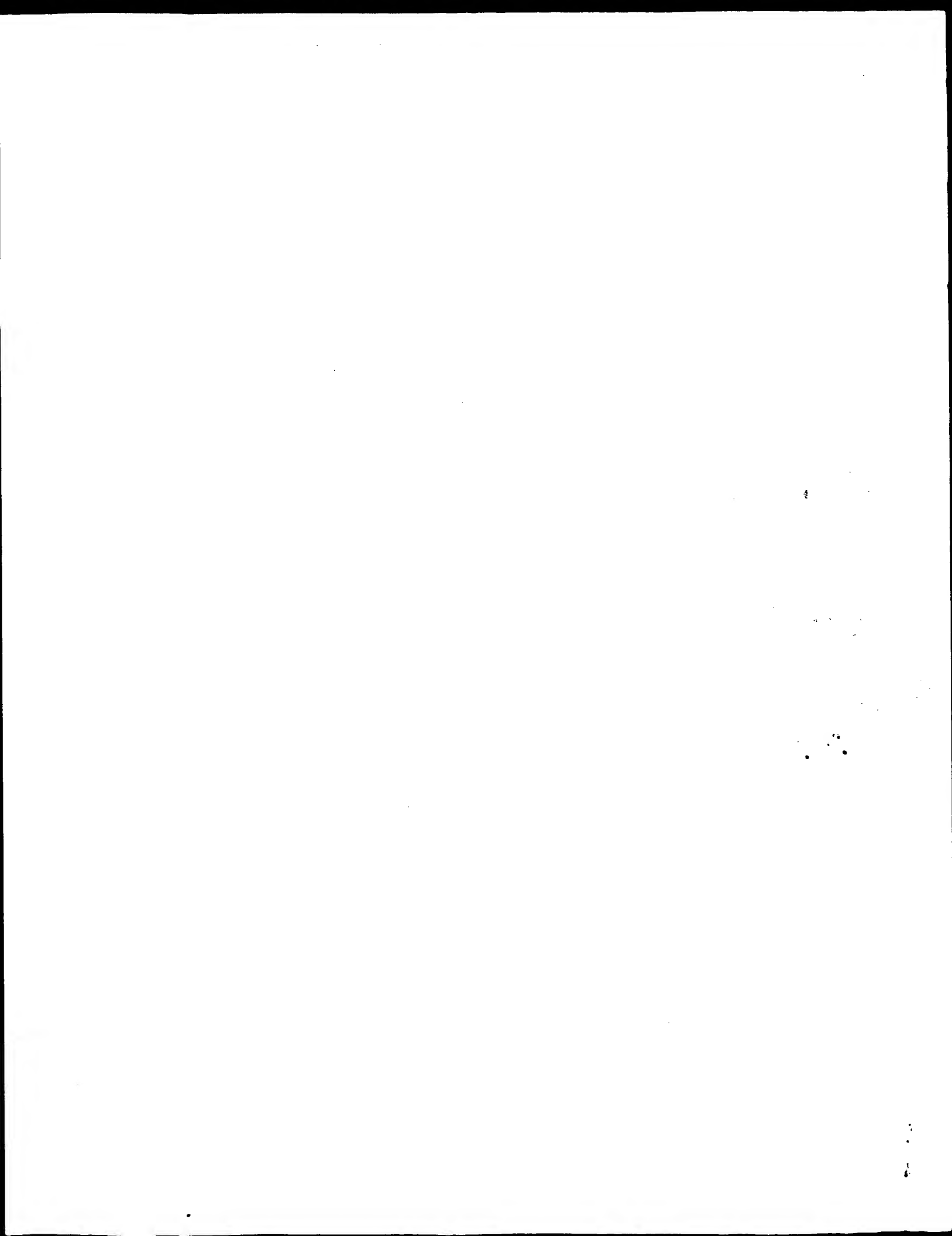
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 Db 41 YEYVHHQ 46

RESULT 15  
 Q9WG05 PRELIMINARY; PRT; 365 AA.  
 AC Q9WG05;  
 DT 01-NOV-1999 (TREMELREL. 12, Created)  
 DT 01-NOV-1999 (TREMELREL. 12, Last sequence update)  
 DT 01-NOV-1999 (TREMELREL. 12, Last annotation update)  
 DE POLYPROTEIN (FRAGMENT).  
 OS Potato virus Y.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;  
 OC Potyvirus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-ORDINARY, O;  
 RA BHAT A.I., VARMA A., PAPPU H.R., RAJAMANNAR M., JAIN R.K., PRAVEEN S.;  
 RT "N-terminal serology and sequence relationships indicate that a  
 RT potyvirus from eggplant, Solanum melongena L., is a strain of potato  
 RT virus Y.";  
 RT Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AF118153; AAD24563.1; -  
 KW Polyprotein. 1 1  
 FT NON\_TER 1 1  
 SQ SEQUENCE 365 AA; 41418 MW; F3CF9EBD CRC32;

Query Match 37.5%; Score 6; DB 12; Length 365;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 YEYVHHQ 15  
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 Db 93 YEYVHHQ 98

Search completed: September 13, 2000, 02:27:32  
 Job time: 174 sec



OM of: US-09-155-076-2 to: EST:\* out\_format : pfs  
 Date: Sep 13, 2000 3:35 AM  
 About: Results were produced by the GenCore software, version 4.5,  
 Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:  
 -MODE=frame-p2n.model  
 -O=/cgn2.1/USPTO.spool/US09155076/runat\_29082000\_092538\_16898/app\_query.fasta\_1.144  
 -DB=EST -OEWT=fastap -SUFFIX=rst -GAPOP=4.500 -GAPEXT=0.050  
 -MINMATCH=0.100 -LOOPEXT=0.000 -LOOPEXT=0.000 -GAPOP=4.500  
 -GAPEXT=0.050 -GAPOP=60.000 -GAPEXT=60.000 -GAPOP=6.000  
 -GAPEXT=7.000 -GAPOP=60.000 -GAPEXT=60.000 -DELOP=6.000  
 -DELEXT=7.000 -START=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45  
 -DOCALIGN=200 -THR\_SCORE=quality -THR\_MIN=1 -ALIGN=15  
 -MODE=LOCAL -OUTEWT=pfs -NORM=est -MINLEN=0 -MAXLEN=1000000  
 -USER=US09155076 -CGN1\_1.1327 -NCPU=6 -ICPU=3 -LONGLOG -NO\_XLPXY  
 -WAIT -THREADS=1

## Search information block:

Query: US-09-155-076-2

Query length: 16

Database: EST\*

Database sequences: 5247842

Database length: -2090053206

Search time (sec): 889.020000

WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPOP=XGAPOP=60.000  
 WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=XGAPEXT=60.000

## score\_list:

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gb_est4:AA379017	-	16.00	339.24	4.6e-10	277	AA379017 RC3-HT0230-241099-012
gb_est27:AA390276	-	16.00	339.22	4.6e-10	278	AA390276 QW-BT202-070599-188 BT
gb_est5:AA303751	+	16.00	338.85	4.8e-10	297	AA303751 EST16434 Aorta endothel
gb_est47:AF06018	+	16.00	338.70	4.9e-10	305	F06018 HSC00A101 normalized inf
gb_est44:AA580695	-	16.00	338.68	4.9e-10	306	AA580695 RC4-LT0011-100100-012
gb_est26:AA1902528	-	16.00	338.17	5.2e-10	335	AA1902528 QW-BT009-101198-075 BT
gb_est5:AA322074	-	16.00	338.12	5.3e-10	338	AA322074 EST24653 Cerebellum II
gb_est5:AA304003	+	16.00	338.12	5.3e-10	338	AA304003 QW-BT009-101198-074 BT
gb_est52:TA49906	+	16.00	337.86	5.4e-10	354	AA304003 EST16883 Aorta endothel
gb_est51:AA19709	+	16.00	337.42	5.8e-10	383	TA49906 ya99b06.r1 Stratagene pl
gb_est2:AA134479	-	16.00	337.19	5.9e-10	399	R19709 yg35f04.r1 Soares infant
gb_est16:AA112471	-	16.00	336.95	6.1e-10	417	AA134479 zol0c04.r1 Stratagene
gb_est44:AW601576	+	16.00	336.39	6.6e-10	461	AA124771 am61h12.x1 Johnston fi
gb_est51:R25913	+	16.00	336.29	6.7e-10	469	AW601576 QV3-BT0381-270100-073
gb_est4:AA218652	+	16.00	336.10	6.8e-10	485	R25913 yg56c07.r1 Soares infant
gb_est44:AW602193	+	16.00	335.81	7.1e-10	511	AA218652 zq14d12.s1 Stratagene
gb_est45:AW673480	+	16.00	335.48	7.4e-10	542	AW602193 PM2-BT0546-210100-004
gb_est2:AA082598	+	16.00	334.86	8.0e-10	606	AW673480 ba54e09.v3 NIH MGC_10
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gb_est44:AW581403	+	16.00	334.45	8.4e-10	652	AA1980795 pat.pk0033.f8.f1 chick
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gb_est1:AA032972	+	14.00	297.03	1.0e-07	286	AW607890 RC0-HT0505-180100-011
gb_est1:AA034297	+	14.00	296.98	1.0e-07	289	AA032972 zk07c09.r1 Soares pres
gb_est41:AW608486	+	14.00	294.62	1.4e-07	440	AA034297 zk20a06.r1 Soares pres
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gb_est54:W26339	-	13.00	276.47	1.4e-06	264	AA362065 PM2-CT0265-281099-004
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gb_est44:AW581394	-	12.00	253.41	2.8e-05	351	AA299326 EST11904 Uterus tumor
gb_est44:AW608448	+	12.00	250.42	4.0e-05	650	AW581394 RC0-LT0070-070100-011
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gb_est44:AW608455	+	11.00	231.22	0.0005	470	W26191 22B11 Human retina cdna
gb_est44:DS1546	+	11.00	229.84	0.0006	602	AW608455 RC0-LT0070-170100-031
gb_est53:TS6402	+	10.00	211.31	0.0061	386	DS1546 HU042F12B Clontech huma
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gb_est54:W27250	-	10.00	210.15	0.0071	475	AA393653 RC5-ST0317-161299-011
gb_est54:W27250	-	10.00	209.64	0.0076	520	W27250 24G5 Human retina cdna
gb_est54:W26650	-	10.00	206.48	0.0113	915	W26650 34C4 Human retina cdna

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 gb\_est54:W27265 + 9.00 187.71 0.1258 613 ! W27265 24f1 Human retina cdn  
 gb\_est54:W27702 + 9.00 187.59 0.1277 626 ! W27702 36g11 Human retina cd  
 gb\_est44:AW607850 + 9.00 187.58 0.1280 628 ! AW607850 RC0-HT0505-010200-0  
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seq\_documentation\_block:

LOCUS AA385402 246 bp mRNA EST 21-APR-1997  
 DEFINITION EST99048 Thyroid Homo sapiens CDNA 5' end similar to amyloid, A4  
 beta subunit, mRNA sequence.  
 ACCESSION AA385402  
 VERSION AA385402.1 GI:2037720  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 246)

## REFERENCE

## AUTHORS

Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,  
 Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,  
 White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,  
 Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fink,L.D.,  
 Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,  
 Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,  
 Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,  
 Moreno-Palancas,R.F., McDonald,L.A., Nguyen,D.T., Peilgrino,S.M.,  
 Phillips,C.A., Ryder,S.E., Scott,J.L., Sayde,D.M., Shirley,R.,  
 Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,  
 Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,  
 Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,  
 He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,  
 Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,  
 Raymond,L., Wei,Y.F., Wang,J., Xu,C., Yu,G.L., Ruben,S.M.,  
 Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,  
 Fraser,C.M. and Venter,J.C.  
 Initial assessment of human gene diversity and expression patterns  
 based upon 83 million nucleotides of CDNA sequence  
 Nature 377 (6547 Suppl), 3-174 (1995)

## JOURNAL

## MEDLINE

## COMMENT

Other ESTs: TRC172078

Contact: Kerlavage, AR

Bioinformatics

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850 USA

Tel: 3018699036

Fax: 3018699423

Email: arkerlav@tigr.org

For clone availability, additional sequence and expression

information related to this EST, please check the TIGR Human Gene

Index (<http://www.tigr.org/tadb/hgi/hgi.html>)

Seq primer: M3 Reverse.

Location/Qualifiers

1. 246

/organism="Homo sapiens"

/db\_xref="ATCC (inhost):189572"

/db\_xref="taxon:9606"

/clone\_lib="Thyroid"

/dev\_stage="adult"

/note="Organ: thyroid gland; Vector: pBluescript SK-;

Site\_1: EcoRI; Site\_2: XhoI"

BASE COUNT 70 a 48 c 68 g 58 t 2 others

## ORIGIN

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Ratio: 1.000 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

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US-09-155-076-2 x AA385402  ..
Align seg 1/1 to: AA385402 from: 1 to: 246

1 AspaLaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
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116 GATGCAGAAATCCGACATGACTCAGGATATGAGTTCATCATCAAAA 163

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seq_documentation_block:
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DEFINITION RC3-HT0230-241099-012-c12 HT0230 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW379017
VERSION AW379017.1 GI:6883676
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 277)
HCGP http://www.ludwig.org.br/ORESTES.
AUTHORS The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT On Apr 7, 1998 this sequence version replaced gi:3036339.
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC3&t2=RC3-HT0230-
241099-012-c12&t3=1999-10-24&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 277.

FEATURES
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/db_xref="taxon:9606"
/clone_lib="HT0230"
/dev_stage="Adult"
/note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 70 a 79 c 51 g 77 t
ORIGIN

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Quality: 16.00 Length: 16
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-2 x AW379017/rev ..
Align seg 1/1 to reverse of: AW379017 from: 1 to: 277

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220 GATGCAGAAATCCGACATGACTCAGGATATGAGTTCATCATCAAAA 173

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seq_documentation_block:
LOCUS AW379017 297 bp mRNA EST 18-APR-1997
DEFINITION EST16434 Aorta endothelial cells, TNF alpha-treated homo sapiens
cDNA 5' end similar to amyloid, A4 beta subunit, mRNA sequence.
ACCESSION AA303751
VERSION AA303751.1 GI:1956103

US-09-155-076-2 x AA385402  ..
Align seg 1/1 to: AA385402 from: 1 to: 246

1 AspaLaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
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seq_documentation_block:
LOCUS AW379017 277 bp mRNA EST 04-FEB-2000
DEFINITION RC3-HT0230-241099-012-c12 HT0230 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW379017
VERSION AW379017.1 GI:6883676
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 277)
HCGP http://www.ludwig.org.br/ORESTES.
AUTHORS The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT On Apr 7, 1998 this sequence version replaced gi:3036339.
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC3&t2=RC3-HT0230-
241099-012-c12&t3=1999-10-24&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 277.

FEATURES
source
1..277
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0230"
/dev_stage="Adult"
/note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 70 a 79 c 51 g 77 t
ORIGIN

alignment_scores:
Quality: 16.00 Length: 16
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-2 x AW379017/rev ..
Align seg 1/1 to reverse of: AW379017 from: 1 to: 277

1 AspaLaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
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220 GATGCAGAAATCCGACATGACTCAGGATATGAGTTCATCATCAAAA 173

seq_name: gb_est27:AI909276
seq_documentation_block:
LOCUS AW379017 297 bp mRNA EST 18-APR-1997
DEFINITION EST16434 Aorta endothelial cells, TNF alpha-treated homo sapiens
cDNA 5' end similar to amyloid, A4 beta subunit, mRNA sequence.
ACCESSION AA303751
VERSION AA303751.1 GI:1956103

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**KEYWORDS**  
**SOURCE** EST.  
**ORGANISM** Homo sapiens  
**REFERENCE** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
**AUTHORS** Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 297)  
 Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,  
 Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,  
 White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,  
 Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,  
 Fitzgerald,L.M., Fitchugh,W.M., Fritchman,J.L., Geoghegan,N.S.,  
 Glodak,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,  
 Kelley,J.M., Keiley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,  
 Moreno-Palancas,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,  
 Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,  
 Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,  
 Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,  
 Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,  
 He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,  
 Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,  
 Raymond,L., Wei,Y.F., Wang,J., Xu,C., Yu,G.L., Ruben,S.M.,  
 Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,  
 Fraser,C.M. and Venter,J.C.  
**TITLE** Initial assessment of human gene diversity and expression patterns  
 based upon 83 million nucleotides of cDNA sequence  
**JOURNAL** Nature 377 (6547 Suppl), 3-174 (1995)  
**MEDLINE** 12140200  
**COMMENT** On Sep 29, 1997 this sequence version replaced gi:1520591.  
 Other\_ESTs: TNC172078  
 Contact: Kerlavage, AR  
 Bioinformatics  
 The Institute for Genomic Research  
 9712 Medical Center Drive, Rockville, MD 20850 USA  
 Tel: 3018699056  
 Fax: 3018699423  
 Email: arkerl@tigr.org  
 For clone availability, additional sequence and expression  
 information related to this EST, please check the TIGR Human Gene  
 Index (<http://www.tigr.org/tdb/hgi/hgi.html>)  
 Seq primer: M3 Reverse.

**FEATURES**  
 source  
 1..297  
 /organism="Homo sapiens"  
 /db\_xref="ATCC (inhost):115367"  
 /db\_xref="taxon:9606"  
 /clone\_lib="Aorta endothelial cells, TNF alpha-treated"  
 /cell\_type="endothelial cell"  
 /dev\_stage="adult"  
 /note="organ: aorta; Vector: pBluescript SK-; Site\_1:  
 EcoRI; Site\_2: XhoI"  
 BASE COUNT 79 a 71 c 79 g 67 t 1 others  
 ORIGIN

alignment\_scores:  
 Quality: 16.00 Length: 16  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000  
 alignment\_block:  
 US-09-155-076-2 x AA303751 ..  
 Align seg 1/1 to: AA303751 from: 1 to: 297

1 AspAlaCluPheargHisAspSerGlyTyrGluValHisGlnLys 16  
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 217 GATGCAGAAATCCGACATGACTCAGGATATGAAGTTCATCATCAAAA 264  
 seq\_name: gb\_est47:F06018  
 seq\_documentation\_block:  
 LOCUS F06018 305 bp mRNA EST 19-FEB-1995  
 DEFINITION HSCOUA101 normalized infant brain cDNA Homo sapiens cdna clone

**ACCESSION**  
**VERSION** F06018.1 GI:669834  
**KEYWORDS** EST.  
**SOURCE** human.  
**ORGANISM** Homo sapiens  
**REFERENCE** 1 (bases 1 to 305)  
**AUTHORS** Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Eukaryota; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C.,  
 Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B.,  
 Lorenzo,F., Mitcheil,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,  
 Sebastiani,Kabatchis,C. and Tessier,A.  
**TITLE** IMAGE: molecular integration of the analysis of the human genome  
 and its expression  
**JOURNAL** C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)  
**MEDLINE** 95277534  
**COMMENT** On May 20, 1999 this sequence version replaced gi:4878117.  
 Contact: Genethon  
 Genexpress-Genethon  
 Genethon Centre de recherche sur le Genome Humain  
 1, rue de l'Internationale, Bp60 91002 EVRY Cedex, FRANCE  
 Tel: 33169472800  
 Fax: 33160778698  
 Email: genexpress@genethon.fr  
 Single read.  
 Genexpress.library.idt: C; Genexpress\_sequence\_idt: ylc-0ua10  
 Seq primer: (-21)M13\_universal.

**FEATURES**  
 source  
 1..305  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="c-0ua10"  
 /clone\_lib="normalized infant brain cDNA"  
 /sex="Female"  
 /tissue\_type="total brain"  
 /dev\_stage="3 months old"  
 /note="organ: brain; Vector: lafmid BA; Site\_1: HindIII;  
 Site\_2: NotI; sex:Female; dev stage=3 months old;  
 isolate:muscular atrophy patient; tissue\_type=total  
 brain; total mRNA was oligo-(dt) primed and directionally  
 cloned 5' -> 3' into the HindIII -> NotI sites of the  
 lafmid BA vector. Clone library from B.Soaes, Psychiatry  
 Dept. Columbia University, USA. Normalization\_method:  
 Bento Soares, P.N.A.S in press"  
 BASE COUNT 88 a 65 c 80 g 71 t 1 others  
 ORIGIN

alignment\_scores:  
 Quality: 16.00 Length: 16  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000  
 alignment\_block:  
 US-09-155-076-2 x F06018 ..  
 Align seg 1/1 to: F06018 from: 1 to: 305

1 AspAlaCluPheargHisAspSerGlyTyrGluValHisGlnLys 16  
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 3 GATGCAGAAATCCGACATGACTCAGGATATGAAGTTCATCATCAAAA 50  
 seq\_name: gb\_est44:AW580695  
 seq\_documentation\_block:  
 LOCUS AW580695 306 bp mRNA EST 16-MAR-2000  
 DEFINITION RC4-LT0011-100100-012-cl1 LT0011 Homo sapiens cdna, mRNA sequence.  
 ACCESSION AW580695  
 VERSION AW580695.1 GI:7255744  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens

Eukaryota, Metazoa: Chordata; Craniala; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 306)  
1 (bases 1 to 306)  
HCGF <http://www.ludwig.org.br/ORESTES>.  
THE FAPESP/LICR Human Cancer Genome Project  
Unpublished (1999)  
On Jan 6, 2000 this sequence version replaced gi:5676947.

Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
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Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel.: +55-11-2704922  
Fax: +55-11-2707001  
Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?l1-RC4&t2-RC4-LT0011-100100-012-cl1&t3-2000-01-10&t4-1>)  
Seq primer: puc 18 forward  
High quality sequence start: 6  
High quality sequence stop: 306.

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		/organism="Homo sapiens"
		/db_xref="taxon:9606"
		/clone_lib="LT0011"
		/dev_stage="Adult"
		/note="Organ: leiomios; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT	72 a	80 c 65 g 89 t
ORIGIN		

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alignment_scores:
  Quality: 16.00      Length: 16
  Ratio: 1.000       Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
  US-09-155-076-2 x AW580695/rev ..
  Align seg 1/1 to reverse of: AW580695 from: 1 to: 306

1 AspaLaclupheaRgHisaspSerGlyTyrGluValHisHisGlnLys 16
188 GATGCAGAAATTCGACATGACTCAGGATGATGAAGTTTCATCATCAAAA 141

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seq_name: gb_est26:AI902528

seq_documentation_block:
LOCUS   AI902528             335 bp      mRNA
DEFINITION  QV-BT009-101198-075 BT009 Homo sapiens cDNA, mRNA sequence.
ACCESSION  AI902528
VERSION    AI902528.1      GI:6492915
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 335)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S. Briones,M.R.,

```

**TITLE** Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags  
 PROC. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 On May 19, 1998 this sequence version replaced gi:3138510.  
 Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

**FEATURES**

	source
	1. .335
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/clone_lib="BT009"
	/sex="female"

Seq primer: puc.18 forward.

Location/Qualifiers

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/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_lib="BT009"

/sex="female"

Seq primer: puc.18 forward.

Location/Qualifiers

1. .335

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_lib="BT009"

/sex="female"

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/dev_stage="Adult"
/notes="Organ: breast; Vector: puc18; Site1: SmaI; Site2:
SmaI; A mini-library was made by cloning products derived
from ORNSTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
77 a 89 c 76 g 93 t
BASE COUNT
ORIGIN
alignment_scores:
Quality: 16.00 Length: 16
Ratio: 1.000 Gaps: 0

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Percent Similarity: 100.000    Percent Identity: 100.000  
alignment_block:  
US-09-155-076-2 x AI902528/rev ..  
  
Align seg 1/1 to reverse of: AI902528 from: 1 to: 335  
  
1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16  
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|||  
312 GATGCAGAAATTCGACATGCTCAGCATATCAACTTCATCATCAA 265  
  
seq_name: gb_est5:AA322074  
  
seq_documentation_block:  
LOCUS AA322074      338 bp   mRNA          EST              19-APR-1997
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DEFINITION	SEQUENCE	REFERENCE
ESR274653 Cerebellum II Homo sapiens cDNA 3' end similar to amyloid precursor protein	AA322074	Adams, N.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstein, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man, Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Gish, W.B., Gruber, C.P., et al. 1991
A4 beta subunit, mRNA sequence.	AA322074.1 GI:1974399	
EST.		
KEYWORDS		
SOURCE	human.	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.	
	1 (bases 1 to 338)	

Globeck, A., Gnehm, C.L., Hanna, M.C., Neubronn, E., Ninkner, F.S.O., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palancques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, F., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,



**TITLE**  
JOURNAL  
MEDLINE  
COMMENT

Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wang,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.  
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence  
Nature 377 (6547 Suppl.), 3-174 (1995)

**Other\_ESTS**: THCL172078  
Nature 377 (6547 Suppl.), 3-174 (1995)  
Contact: Kerlavage, AR  
Bioinformatics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850 USA  
Tel: 3018699056  
Fax: 3018699423  
Email: arkerlav@tigr.org

For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi/hgi.html>)  
Seq primer: M13 Reverse

# FEATURES

source  
1..338  
/organism="Homo sapiens"  
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/clone.lib="Cerebellum II"  
/tissue\_type="cerebellum"  
/dev\_stage="adult"  
/note="Organ: brain; Vector: pBluescript SK-; Site\_1: EcoRI; Site\_2: XhoI"  
BASE COUNT 86 a 78 c 95 g 79 t  
ORIGIN

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Quality: 16.00 Length: 16  
Ratio: 1.000 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

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US-09-155-076-2 x AA322074 ..  
Align seg 1/1 to: AA322074 from: 1 to: 338

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210 GATCGAGATTCGACATGCTCAGGATGATGAGTTTCATCATCAAAA 257

seq\_name: gb\_est26:AI902529

**seq\_documentation\_block:**  
LOCUS AI902529 338 bp mRNA EST 30-MAR-2000  
DEFINITION OV-BT009-101198-074 BT009 Homo sapiens cDNA, mRNA sequence.  
ACCESSION AI902529  
VERSION AI902529.1 GI:6492916  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

**REFERENCE**  
AUTHORS  
Dias Neto,E., Garcia Correa,R., Verjovsky-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunsteig,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.Y. and Simpson,A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
On Oct 30, 1998 this sequence version replaced gi:3814489.

Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/seq/gethtml.pl?tl=QV&t2=QV-BT009-074.html>)  
Seq primer: puc 18 forward.

# FEATURES

source  
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/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone.lib="BT009"  
/sex="female"  
/dev\_stage="Adult"  
/note="Organ: breast; Vector: puc18; Site\_1: SmaI; Site\_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."  
BASE COUNT 78 a 89 c 76 g 95 t  
ORIGIN

**alignment\_scores:**  
Quality: 16.00 Length: 16  
Ratio: 1.000 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

# alignment\_block:

US-09-155-076-2 x AI902529/rev ..  
Align seg 1/1 to reverse of: AI902529 from: 1 to: 338  
1 AspalagluPheArgHisAspSerGlyTyrGluValHisHisGlnIlys 16  
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315 GATCGAGATTCGACATGCTCAGGATGATGAGTTTCATCATCAAAA 268

seq\_name: gb\_est5:AA304003

**seq\_documentation\_block:**  
LOCUS AA304003 354 bp mRNA EST 18-APR-1997  
DEFINITION EST16883 Aorta endothelial cells, TNF alpha-treated Homo sapiens cDNA 5' end similar to amyloid, A4 beta subunit, mRNA sequence.  
ACCESSION AA304003  
VERSION AA304003.1 GI:1956491  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

**REFERENCE**  
AUTHORS  
Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstein,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Frichman,J.L., Georghagen,N.S., Glocke,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Metrick,J.M., Moren-Palancas,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Staudk,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dinkes,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H.,

Wed Sep 13 08:11:37 2000

On Nov 2, 1998 this sequence version replaced gi:3828645.

## COMMENT

Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,  
 Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,  
 Fraser, C.M., and Venter, J.C.  
 Initial assessment of human gene diversity and expression patterns  
 based upon 83 million nucleotides of cDNA sequence  
 Nature 377 (6547 Suppl), 3-174 (1995)  
 12140200

On Jan 17, 1998 this sequence version replaced gi:1900069.

## OTHER\_ESTS

Other\_ESTS: THCL172078  
 Contact: Kerlavage, AR  
 Bioinformatics  
 The Institute for Genomic Research  
 9712 Medical Center Drive, Rockville, MD 20850 USA  
 Tel: 3018699056  
 Fax: 3018699423

Email: arkerlav@tigr.org  
 For clone availability, additional sequence and expression  
 information related to this EST, please check the TIGR Human Gene  
 Index (<http://www.tigr.org/tdb/hgi/hgi.html>)  
 Seq primer: M13 Reverse.

## FEATURES

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 /organism="Homo sapiens"  
 /db\_xref="ATCC (inhost):115766"  
 /db\_xref="taxon:9606"  
 /clone\_lib="Aorta endothelial cells, TNF alpha-treated"  
 /cell\_type="endothelial cell"  
 /dev\_stage="adult"  
 /note="Organ: aorta; Vector: pBluescript SK-; Site\_1:  
 EcoRI; Site\_2: XhoI"

BASE COUNT 102 a 80 c 92 g 78 t 2 others  
 ORIGIN

alignment\_scores:  
 Quality: 16.00 Length: 16  
 Ratio: 1.000 Gaps: 0  
 Percent Smilarity: 100.000 Percent Identity: 100.000

alignment\_block:  
 US-09-155-076-2 x AA304003 ..

Align seg 1/1 to: AA304003 from: 1 to: 354

1 AspAlaGluPheargHisaspSerGlyTyrGluValHisGlnLys 16  
 10 GATGCAGATTCCGACATGACTCAGGATATGAAAGTTTCATCAAAAA 57

seq\_name: gb\_est52:T49906

seq\_documentation\_block:  
 LOCUS T49906 383 bp mRNA EST 06-FEB-1995  
 DEFINITION ya99b06.r1 stragene placenta (#937225) Homo sapiens cDNA clone  
 IMAGE:69779 5' similar to gb:X06989.rnal ALZHEIMER'S  
 DISEASE AMYLOID A4 PROTEIN PRECURSOR (HUMAN), mRNA sequence.

ACCESSION T49906  
 VERSION T49906.1 GI:651766  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,  
 Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W.,  
 Hawkins, S., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,  
 Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,  
 Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,  
 Trevisan, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R.  
 and Marra, M.

TITLE Generation and analysis of 280,000 human expressed sequence tags  
 JOURNAL Genome Res. 6 (9), 807-828 (1996)  
 MEDLINE 97044478

Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 Source: IMAGE Consortium, LLNL  
 This clone is available royalty-free through LLNL; contact the  
 IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
 Seq primer: M13RP1  
 High quality sequence stop: 384.

## FEATURES

Source  
 1..383  
 /organism="Homo sapiens"  
 /db\_xref="GDB:490676"  
 /db\_xref="taxon:9606"  
 /clone\_lib="IMAGE:69779"  
 /clone\_lib="Stratagene placenta (#937225)"  
 /sex="male"  
 /lab\_host="SOLR cells (kanamycin resistant)"  
 /note="Organ: placenta; Vector: pBluescript SK-; Site\_1:  
 EcoRI; Site\_2: XhoI; Cloned unidirectionally. Primer:  
 Oligo dt. Caucasian. Average insert size: 1.2 kb; Uni-ZAP  
 XR Vector; -5' adaptor sequence: 5' GAATTCGCGACGAG 3' -3'  
 adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"

BASE COUNT 113 a 81 c 103 g 86 t  
 ORIGIN

alignment\_scores:  
 Quality: 16.00 Length: 16  
 Ratio: 1.000 Gaps: 0  
 Percent Smilarity: 100.000 Percent Identity: 100.000

alignment\_block:  
 US-09-155-076-2 x T49906 ..

Align seg 1/1 to: T49906 from: 1 to: 383

1 AspAlaGluPheargHisaspSerGlyTyrGluValHisGlnLys 16  
 61 GATGCAGATTCCGACATGACTCAGGATATGAAAGTTTCATCAAAAA 108

seq\_name: gb\_est51:R19709

seq\_documentation\_block:  
 LOCUS R19709 399 bp mRNA EST 17-APR-1995  
 DEFINITION Y933f04.r1 Soares infant brain INIB Homo sapiens cDNA clone  
 IMAGE:34389 5' similar to gb:X06989.rnal ALZHEIMER'S DISEASE  
 AMYLOID A4 PROTEIN PRECURSOR (HUMAN);, mRNA sequence.

ACCESSION R19709  
 VERSION R19709.1 GI:774343  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
 Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
 Trevisan, E., Waterston, R., Williamson, A., Wohlmann, P. and  
 Wilson, R.

TITLE The WashU-Merck EST Project  
 JOURNAL Unpublished (1995)  
 COMMENT On Jan 19, 1998 this sequence version replaced gi:2284625.  
 Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu

Insert Size: 1369  
 High quality sequence stops: 214 Source: IMAGE Consortium, LNL  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.lnl.gov) for further information.  
 Insert Length: 1369 Std Error: 0.00  
 Seq primer: M13RP1  
 High quality sequence stop: 214.

# FEATURES

Location/Qualifiers  
 1..399  
 /organism="Homo sapiens"  
 /db\_xref="GDB:406736"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:34389"  
 /clone.lib="Soares infant brain LNB"  
 /sex="female"  
 /dev.stage="73 days post natal"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /note="Organ: whole brain; Vector: Lfamid BA; Site.1: Not  
 I; Site.2: Hind III; 1st strand cDNA was primed with a Not  
 I - oligo(GT) primer [5'  
 AACGGAAGATTCGCGCCGACGAGATTTTATTTT 3'];  
 double-stranded cDNA was ligated to Hind III adaptors  
 (Pharmacia), digested with Not I and directionally cloned  
 into the Not I and Hind III sites of the Lfamid BA vector.  
 Library went through one round of normalization. Library  
 constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 104 a 85 c 106 g 94 t 10 others  
 ORIGIN

alignment\_scores:  
 Quality: 16.00 Length: 16  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

# alignment\_block:

US-09-155-076-2 x R19709 ..

Align seg 1/1 to: R19709 from: 1 to: 399

1 AspAlaGluPheArgHisaspSerGlyTyrGluValHisHisGlnLys 16

|||||  
 219 GATGCAGATTCGACATGACTCAGGATATGAAGTTCATCATCAAAA 266

seq\_name: gb\_est2:AA134479

seq\_documentation\_block:  
 LOCUS AA134479 417 bp mRNA EST 23-DEC-1997  
 DEFINITION z010904.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens  
 cDNA clone IMAGE:567318 5' similar to gb:X06989\_rnal ALZHEIMER'S  
 DISEASE AMYLOID A4 PROTEIN PRECURSOR (HUMAN);, mRNA sequence.

ACCESSION AA134479  
 VERSION AA134479.1 GI:1692245

# KEYWORDS

EST.

# SOURCE

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 417)

# REFERENCE

## AUTHORS

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,  
 Chissole, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W.,  
 Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, N.,  
 Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,  
 Rohlfing, T., Scheinberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,  
 Trevas, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R.  
 and Marra, M.

Generation and analysis of 289,000 human expressed sequence tags

Genome Res. 6 (9), 807-828 (1996)

9704478

# MEDLINE

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

WARNING: there is evidence that suggests that the 384-well parent  
 plate of this clone contains both human and mouse derived clones.  
 Thus, the origin of this clone is uncertain. This caution should be  
 kept in mind should you use this clone.

This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.lnl.gov) for further information.  
 Insert Length: 1384 Std Error: 0.00  
 Seq primer: -28M13 rev2 from Amersham  
 High quality sequence stop: 394.

# FEATURES

## source

Location/Qualifiers  
 1..417  
 /organism="Homo sapiens"  
 /db\_xref="GDB:459171"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:567318"  
 /clone.lib="Stratagene neuroepithelium NT2RAMI 937234"  
 /dev.stage="Ntera-2/RA+MI neuroepithelial cells"  
 /lab\_host="SOLR (kanamycin resistant)"  
 /note="Vector: pBluescript SK-; Site.1: EcoRI; Site.2:  
 XhoI; Cloned unidirectionally. Primer: Oligo dT. NT2  
 (Ntera-2/ci.D1) precursor cells induced with Retinoic  
 Acid for 1 week, followed by 3 weeks in mitotic inhibitors  
 (Replate #2). Average insert size: 1.1 kb; Uni-ZAP XR  
 Vector; -5' adaptor sequence: 5' GAATTCGACGAG 3' -3'  
 adaptor sequence: 5' CTCGAGTTTTTTTTTTT 3' ..

BASE COUNT 110 a 93 c 117 g 95 t 2 others  
 ORIGIN

alignment\_scores:  
 Quality: 16.00 Length: 16  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

# alignment\_block:

US-09-155-076-2 x AA134479 ..

Align seg 1/1 to: AA134479 from: 1 to: 417

1 AspAlaGluPheArgHisaspSerGlyTyrGluValHisHisGlnLys 16

|||||  
 159 GATGCAGATTCGACATGACTCAGGATATGAAGTTCATCATCAAAA 206

seq\_name: gb\_est16:AA124771

seq\_documentation\_block:  
 LOCUS AA124771 461 bp mRNA EST 11-SEP-1998  
 DEFINITION am1h12.x1 Johnston frontal cortex Homo sapiens cDNA clone  
 IMAGE:1540103 3' similar to gb:X06989\_rnal ALZHEIMER'S DISEASE  
 AMYLOID A4 PROTEIN PRECURSOR (HUMAN);, mRNA sequence.

ACCESSION AA124771

VERSION AA124771.1 GI:3593285

# KEYWORDS

EST.

# SOURCE

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 461)

# REFERENCE

## AUTHORS

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,  
 Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,  
 Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,  
 Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.

WashU-NCI human EST Project

Unpublished (1997)

Contact: Wilson RK

Washington University School of Medicine

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Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information.  
Seq primer: -40m13 fwd. ET from Anersham  
High quality sequence stop: 423.

FEATURES  
source

Location/Qualifiers  
1. .461  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1540103"  
/clone\_lib="Johnston frontal cortex"  
/sex="male"  
/tissue\_type="pooled frontal lobe"  
/dev\_stage="adult"  
/lab\_host="SOLR (kanamycin resistant)"  
/note="Organ: brain; Vector: Bluescript SK-; Site:1:  
ECORI; Stanley Neuropathology Consortium  
(www.stanleylab.org) brains S-58, S-65, S-67, S-78.  
Random + oligo-dT primed into EcoRI site of 2AP II Vector.  
Mass excised. Avg insert length 1.9kb. Custom library  
provided by Dr. Nancy Johnston [(410) 614-3918,  
njewelchlink.welch.jhu.edu]."  
1 others

BASE COUNT 101 a 123 c 110 g 126 t  
ORIGIN

alignment\_scores:  
Quality: 16.00 Length: 16  
Ratio: 1.000 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
US-09-155-076-2 x A1124771/rev ..  
Align seg 1/1 to reverse of: A1124771 from: 1 to: 461  
1 AspalagluPheArgHisAspSerGlyTyrGluValHisGlnLys 16  
|||||  
314 GATGAGAATTCGACATGACTCAGATATGAGATTTCATCATCAAAAA 267

seq\_name: gb\_est44:AW601576

seq\_documentation\_block:  
LOCUS AW601576 469 bp mRNA EST 23-MAR-2000  
DEFINITION QV3-BT0381-270100-073-f06 BT0381 Homo sapiens cDNA, mRNA sequence.  
ACCESSION AW601576  
VERSION AW601576.1 GI:7306315  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
AUTHORS HCGP http://www.ludwig.org.br/ORESTES.  
TITLE The FAPESP/LICR Human Cancer Genome Project  
JOURNAL Unpublished (1999)  
COMMENT On Jan 6, 2000 this sequence version replaced gi:6677550.  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV3st2=QV3-BT0381-  
270100-073-f06st3=2000-01-27st4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 111  
High quality sequence stop: 469.

FEATURES  
source

Location/Qualifiers  
1. .469

/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="BT0381"  
/dev\_stage="Adult"  
/note="Organ: breast; Vector: puc18; Site\_1: SmaI; Site\_2:  
SmaI; A mini-library was made by cloning products derived  
from ORESTES PCR (U.S. Letters Patent application No.  
136,716 - Ludwig Institute for Cancer Research) profiles  
into the pUC 18 vector. Reverse transcription of tissue  
mRNA and cDNA amplification were performed under low  
stringency conditions."  
BASE COUNT 128 a 120 c 117 g 104 t  
ORIGIN

alignment\_scores:  
Quality: 16.00 Length: 16  
Ratio: 1.000 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
US-09-155-076-2 x AW601576 ..  
Align seg 1/1 to: AW601576 from: 1 to: 469  
1 AspalagluPheArgHisAspSerGlyTyrGluValHisGlnLys 16  
|||||  
422 GATGAGAATTCGACATGACTCAGATATGAGATTTCATCATCAAAAA 469

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 13, 2000, 02:21:36 ; Search time 17.65 seconds  
(without alignments)  
21.472 Million cell updates/sec

Title: US-09-155-076-2  
Perfect score: 92  
Sequence: 1 DAEFRHDSGYEVHHQK 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0  
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_36.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	92	100.0	16	1 R60371	Beta-amyloid (1-16)
2	92	100.0	16	1 W35344	Human beta-amyloid
3	92	100.0	21	1 W08361	Beta-secretase sub
4	92	100.0	22	1 R07753	Beta-amyloid prot
5	92	100.0	28	1 P90381	Synthetic A4 amylo
6	92	100.0	28	1 R54702	Beta-amyloid fragm
7	92	100.0	28	1 R60368	Beta-amyloid (1-28
8	92	100.0	28	1 W01413	Beta/A4-amyloid pe
9	92	100.0	28	1 W01414	Beta/A4-amyloid pe
10	92	100.0	28	1 R64170	A4-O(1-28) a parti
11	92	100.0	28	1 R64172	A4-B(1-28) a parti
12	92	100.0	28	1 W81467	Synthetic amyloid
13	92	100.0	30	1 W81468	Synthetic amyloid
14	92	100.0	33	1 W08359	Beta-secretase sub
15	92	100.0	33	1 W81469	Synthetic amyloid
16	92	100.0	33	1 W98002	Amyloid precursor
17	92	100.0	35	1 W02335	Beta-amyloid pepti
18	92	100.0	35	1 W47228	Beta-amyloid pepti
19	92	100.0	35	1 W89355	Beta-amyloid pepti
20	92	100.0	35	1 W89359	Beta-amyloid pepti
21	92	100.0	36	1 W81471	Synthetic amyloid
22	92	100.0	38	1 R60362	Beta-amyloid (1-38
23	92	100.0	38	1 W92722	Human tachykinin a
24	92	100.0	39	1 R60363	Beta-amyloid (1-39
25	92	100.0	39	1 W81472	Synthetic amyloid
26	92	100.0	40	1 R33191	Beta-amyloid pepti
27	92	100.0	40	1 R60364	Beta-amyloid (1-40
28	92	100.0	40	1 W23335	Amyloid beta pepti
29	92	100.0	40	1 W37507	Amyloid beta prote
30	92	100.0	40	1 W47232	Beta-amyloid pepti
31	92	100.0	40	1 W47226	Beta-amyloid pepti
32	92	100.0	40	1 W81473	Synthetic amyloid
33	92	100.0	40	1 W92723	Human tachykinin a

34	92	100.0	40	1 W99584	Wild type aggregat
35	92	100.0	41	1 R22206	Alzheimer's amyloi
36	92	100.0	41	1 R60365	Beta-amyloid (1-41
37	92	100.0	41	1 R65283	Beta amyloid pepti
38	92	100.0	42	1 R20330	Sequence of A99 (b
39	92	100.0	42	1 R33192	Beta-amyloid pepti
40	92	100.0	42	1 R60366	Beta-amyloid (1-42
41	92	100.0	42	1 R65285	Beta amyloid pepti
42	92	100.0	42	1 R65286	Beta amyloid pepti
43	92	100.0	42	1 R65287	Beta amyloid pepti
44	92	100.0	42	1 R65288	Beta amyloid pepti
45	92	100.0	42	1 R94591	Alzheimer amyloid

## ALIGNMENTS

### RESULT 1

R60371 ID R60371 standard; peptide; 16 AA.  
AC R60371; 1995 (first entry)  
DT 15-MAR-1995  
DE Beta-amyloid (1-16).  
KW Amyloid precursor protein; APP; Alzheimer's disease; beta-amyloid;  
KW anti-beta-amyloid antibody; diagnosis; immunogen; antigen; epitope.  
OS Homo sapiens.  
PN W09417197-A.  
PD 04-AUG-1994.  
PF 24-JAN-1994; J00089.  
PR 25-JAN-1993; JP-010132.  
PR 05-FEB-1993; JP-019035.  
PR 16-NOV-1993; JP-286985.  
PR 28-DEC-1993; JP-334773.  
PA (TAKE ) TAKEDA CHEM IND LTD.  
PI Kitada C, Odaoka A, Suzuki N;  
DR WPI; 94-264110/32.  
PT Antibodies recognising specific parts of beta-amyloid - can be used for diagnosis of diseases implicating beta-amyloid, such as Alzheimer's disease  
PT Claim 7; Page 85; 116pp; Japanese.  
CC Antibodies which recognise specific subfragments of the beta-amyloid protein are claimed. Specifically, the antibodies (which are pref. monoclonal) recognise residues 1-16 and/or 1-28 from the N-terminal portion of beta-amyloid or they recognise residues 25-35 or 35-43 from the C-terminal portion. The antibodies are useful for assaying beta-amyloid and its derivatives for diagnosis of Alzheimer's disease.  
CC Sequence 16 AA;

Query Match 100.0%; Score 92; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 5.6e-09;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16  
|||||

Db 1 DAEFRHDSGYEVHHQK 16  
|||||

### RESULT 2

W35344 ID W35344 standard; peptide; 16 AA.  
AC W35344;  
DT 17-APR-1998 (first entry)  
DE Human beta-amyloid precursor 16-mer peptide.  
KW Beta-amyloid precursor polypeptide; acetylcholinesterase; AChE;  
KW neuronal degeneration; Parkinson's disease; Alzheimer's disease;  
KW stroke; cancer; calcium channel modulator; antibody; inhibitor.  
OS Homo sapiens.  
PN W09735962-AI.  
PD 02-OCT-1997.  
PF 21-MAR-1997; G00796.  
PR 22-MAR-1996; GB-006040.

PA (ISIS-) ISIS INNOVATION LTD.  
PI Greenfield SA, Vaux DJ;  
DR WPI; 97-489626/45.  
PT Peptide(s) from acetylcholine esterase which open calcium channels -  
PT used for treating disorders of the central nervous system, cancer  
PT and stroke  
PS Claim 3; Page 20; 27pp; English.  
CC This 16-mer peptide is present in a region of the beta-amyloid precursor  
CC polypeptide. This region lies at the amino acid terminus of the 42  
CC residue peptide which accumulates in Alzheimer's disease. The 16-mer  
CC has at least 70% homology with the beta-amyloid precursor. This peptide  
CC is known to act alone or in synergism with a fragment of  
CC acetylcholinesterase (W35340-W35343) to contribute to neuronal  
CC degeneration. Compounds that inhibit the biological activity of the  
CC novel peptides, and antibodies, can be used to control cytoplasmic  
CC calcium ion currents in vivo, and are useful for treating disorders of  
CC the central nervous system (e.g. Parkinson's and Alzheimer's diseases),  
CC stroke and cancer.  
SQ Sequence 16 AA;  
  
Query Match 100.0%; Score 92; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 5.6e-09;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DAEFRHDSGYEVHHQK 16  
DB 1 DAEFRHDSGYEVHHQK 16  
| | | | | | | | | | | | | | | | | |  
RESULT 3  
ID W08361 standard; peptide; 21 AA.  
AC W08361;  
DT 05-SEP-1997 (first entry)  
DE Beta-secretase substrate #3.  
KW Beta-cleavage site; beta amyloid precursor protein; APP; beta-secretase;  
KW alpha-secretase; proteolytic cleavage; inhibitor; Alzheimer's disease.  
OS Synthetic.  
PN W09640885-A2.  
PD 19-DEC-1996.  
PF 07-JUN-1995; US-485152.  
PR 07-JUN-1995; US-480498.  
PA (ATHE-) ATHENA NEUROSCIENCES INC.  
PI Anderson JP, Chrysler SMS, Jacobson-croak KL, Keim PS;  
PI Mcconlogue LC, Sinha S, Tan H;  
DR WPI; 97-052304/05.  
PT Beta-secretase which specifically cleaves beta-amyloid precursor  
PT protein - useful to screen for inhibitors useful in treatment of  
PT Alzheimer's disease  
PS Disclosure; page 45; 92pp; English.  
CC W08359-W08362 represent substrates for the enzyme of the invention. The  
CC enzyme of the invention is beta-secretase, and specifically cleaves  
CC beta-amyloid precursor protein (beta-APP). Normal processing of beta-APP  
CC is thought to occur via cleavage between residues 16 and 17 of the  
CC beta-amyloid peptide region by an alpha-secretase. Pathogenic processing  
CC is thought to occur by beta-secretase cleavage of beta-APP.  
CC Beta-secretase activity can be detected and measured using a method of  
CC the invention, which detects at least one of the beta-secretase cleavage  
CC products formed on cleavage. The method can be used to determine whether  
CC a test substance inhibits proteolytic cleavage, by beta-secretase, of  
CC beta-APP. Compounds effective to at least partially inhibit  
CC beta-secretase activity can be used to inhibit cleavage of beta-APP in  
CC cells or mammalian hosts. Isolation and purification of beta-secretase  
CC will permit chemical modelling of a critical event in the pathology of  
CC Alzheimer's disease.  
SQ Sequence 21 AA;  
  
Query Match 100.0%; Score 92; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 7.6e-09;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16  
DB 6 DAEFRHDSGYEVHHQK 21  
| | | | | | | | | | | | | | | | | |  
RESULT 4  
ID R07753 standard; protein; 22 AA.  
AC R07753;  
DT 22-FEB-1991 (first entry)  
DE Beta-amyloid protein, SCVAP2.  
KW Monoclonal antibody SV17-6E10; Down's syndrome; Alzheimer's disease;  
KW beta-amyloid precursor; amyloid plaques.  
OS synthetic.  
PN W09012871-A.  
PD 01-NOV-1990.  
PF 13-APR-1989; US-338983.  
PR 14-APR-1989; US-338983.  
PA (REME-) RES FOUND MENTAL HY.  
PI Kim KS, Wisniewski HM, Wen GY, Chen CMJ, Sapienza VJ;  
PI WPI; 90-348474/46.  
DR Cerebrovascular amyloid protein-specific monoclonal antibody  
PT SV17-6E10 - for immunoassay of peptide whose levels are raised in  
PT Down's syndrome or Alzheimer's disease patients  
PS Example 4; page 11; 24pp; English.  
CC This peptide is used in a "Double Ab Sandwich Immunoassay" to  
CC detect beta-amyloid protein. SV17-6E10 MAb(capture Ab) is used  
CC to coat microtitre plate wells. The plate is then washed (dist-  
CCilled water), coated with PBS(rgb) and this (SCVAP2) protein is  
CC added. The plate is washed and a 2nd Ab (detection Ab), MAB 468-  
CC This double Ab sandwich ELISA test is a highly sensitive and  
CC accurate detection system for the beta-amyloid protein.  
CC See also R07752.  
SQ Sequence 22 AA;  
  
Query Match 100.0%; Score 92; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 8e-09;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DAEFRHDSGYEVHHQK 16  
DB 1 DAEFRHDSGYEVHHQK 16  
| | | | | | | | | | | | | | | | | |  
RESULT 5  
ID P90381 standard; protein; 28 AA.  
AC P90381;  
DT 1-NOV-1989 (first entry)  
DE Synthetic A4 amyloid peptide  
KW Synthetic; A4 amyloid polypeptide; Alzheimer's disease;  
KW immunoassays; antibodies.  
OS Synthetic  
PN W08906242-A.  
PD 13-JUL-1989.  
PF 11-OCT-1988; U03590.  
PR 08-OCT-1987; US-105751.  
PA (MCLE) McLean Hospital Corp; (UYRO) University of Rochester.  
PI Majocha R, Marotta CA, Zain S;  
PI WPI; 89-220551/30.  
DR Antibodies to A4 amyloid polypeptide  
PT - used in immunoassays and for imaging of A4 amyloid  
PT in Alzheimer's diseased patients.  
PS Claim 1; page 27; 30pp; English.  
CC Synthetic A4 amyloid polypeptide (see also P90382, P90383).  
CC Used as immunogen, (un)coupled, or to produce antibodies. used in  
CC immunoassays and for imaging of A4 amyloid in Alzheimer's disease.  
SQ Sequence 28 AA;  
  
Query Match 100.0%; Score 92; DB 1; Length 28;

Best Local Similarity 100.0%; Pred. No. 1e-08; Mismatches 0; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16  
| | | | | | | | | | | | | | | |  
DB 1 DAEFRHDSGYEVHHQK 16

RESULT 6  
R54702  
ID R54702 standard; peptide; 28 AA.  
AC R54702;  
DT 15-DEC-1994 (first entry)  
DE Beta-amyloid fragment (1-28).  
KW Beta-amyloid protein; BAP; Alzheimer's disease; diagnosis.  
OS Homo sapiens.  
PN W09409364-A.  
PD 28-APR-1994.  
PF 13-OCT-1993; U09772.  
PR 13-OCT-1992; US-959251.  
PA (UYDU-) UNIV DUKE.  
PI Strittmatter WJ;  
DR WPI: 94-151484/16;  
PT Immobilised beta-amyloid protein or fragments - used in assays for obtaining prods for use in the diagnosis and treatment of PT disorders such as Alzheimer's disease.  
PS Claim 4; Page 28; 49pp; English.  
CC A construct comprising a beta-amyloid protein (BAP) or fragment (esp. the peptides given in R54702-03) immobilised on a solid support can be used to detect cpds. which bind to BAP. Binding of proteins in CC human cerebrospinal fluid proteins were shown to bind to beta-amyloid peptides 1-28 and 12-28. Hydropathic mimic peptide (12-28) CC was used as control.  
SQ Sequence 28 AA;

Query Match 100.0%; Score 92; DB 1; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16  
| | | | | | | | | | | | | | | |  
DB 1 DAEFRHDSGYEVHHQK 16

RESULT 7  
R60368  
ID R60368 standard; peptide; 28 AA.  
AC R60368;  
DT 15-MAR-1995 (first entry)  
DE Beta-amyloid (1-28).  
KW Amyloid precursor protein; APP; Alzheimer's disease; beta-amyloid; anti-beta-amyloid antibody; diagnosis; immunogen; antigen; epitope.  
OS Homo sapiens.  
PN W09417197-A.  
PD 04-AUG-1994.  
PF 24-JAN-1994; J00089.  
PR 25-JAN-1993; JP-010132.  
PR 05-FEB-1993; JP-019035.  
PR 16-NOV-1993; JP-286985.  
PR 28-DEC-1993; JP-334773.  
PA (TAKE ) TAKEDA CHEM IND LTD.  
PI Kitada C, Odaka A, Suzuki N;  
DR WPI: 94-264110/32;  
PT Antibodies recognising specific parts of beta-amyloid - can be used for diagnosis of diseases implicating beta-amyloid, such as PT Alzheimer's disease  
PS Claim 7; Page 84; 116pp; Japanese.  
CC Antibodies which recognise specific subfragments of the beta-amyloid protein are claimed. Specifically, the antibodies (which are pref. CC monoclonal) recognise residues 1-16 and/or 1-28 from the N-terminal CC portion of beta-amyloid or they recognise residues 25-35 or 35-43 CC from the C-terminal portion. The antibodies are useful for assaying

CC beta-amyloid and its derivatives for diagnosis of Alzheimer's  
CC disease.  
SQ Sequence 28 AA;

Query Match 100.0%; Score 92; DB 1; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16  
| | | | | | | | | | | | | | | |  
DB 1 DAEFRHDSGYEVHHQK 16

RESULT 8  
W01413  
ID W01413 standard; Protein; 28 AA.  
AC W01413;  
DT 20-JAN-1997 (first entry)  
DE Beta/A4-amyloid peptide residues 1-28.  
KW Beta/A4-amyloid peptide; tissue plasminogen activator;  
KW Alzheimer's disease; stimulation; investigation; pathogenesis;  
KW hereditary cerebral haemorrhage with amyloidosis-Dutch type;  
KW control; cerebral amyloid angiopathy; cerebral; haemorrhage;  
KW homo sapiens.  
OS Homo sapiens.  
PN W09615799-A1.  
PD 30-MAY-1996.  
PF 22-NOV-1995; U15007.  
PR 22-NOV-1994; US-347144.  
PA (RUTF ) UNIV RUTGERS STATE NEW JERSEY.  
PI Anderson S;  
DR WPI: 96-268332/27;  
PT Use of agents which bind beta-amyloid peptide - for diagnosis, PT prevention and treatment of vascular damage caused by amyloid PT deposits, partic. in haemorrhaging and Alzheimer's disease  
PS Example 1; Fig 1; 52pp; English.  
CC To investigate the effects of beta-amyloid peptide (BAP) on CC tissue plasminogen activator (t-PA) 3 synthetic peptides were used. CC One peptide contained 42 amino acids and corresp. to the full CC length BAP (R95248). The other 2 peptides (R95249 and 50) contained CC the 28 N-terminal residues of the BAP found in Alzheimer's disease CC and hereditary cerebral haemorrhage with amyloidosis-Dutch type CC (HCHWA-D), respectively. In an assay to determine the effect of CC the peptides on t-PA activation, each peptide (R95248, 49 and 50) CC gave 1st order rate constant of activation (k<sub>app</sub>) values of CC 13.4, 13.9 and 14.5, respectively, compared to 1.7 and 7.8 for null CC and fibrinogen controls. The results demonstrate that the BAP are CC able to stimulate t-PA activity in vitro, which is significant in CC that it provides a means for investigating and controlling the CC pathogenesis of Alzheimer's disease, HCHWA-D and cerebral amyloid CC angiopathy related cerebral haemorrhage.  
SQ Sequence 28 AA;

Query Match 100.0%; Score 92; DB 1; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16  
| | | | | | | | | | | | | | | |  
DB 1 DAEFRHDSGYEVHHQK 16

RESULT 9  
W01414  
ID W01414 standard; Protein; 28 AA.  
AC W01414;  
DT 20-JAN-1997 (first entry)  
DE Beta/A4-amyloid peptide residues 1-28 Dutch.  
KW Beta/A4-amyloid peptide; tissue plasminogen activator; Dutch;  
KW Alzheimer's disease; stimulation; investigation; pathogenesis;  
KW hereditary cerebral haemorrhage with amyloidosis-Dutch type;

KW control: cerebral amyloid angiopathy; cerebral; haemorrhage;  
KW hemorrhage.

OS Homo sapiens.

FH Key Location/Qualifiers

FT misc\_difference 22

FT /note= "wild type Glu substd. with Gln"

PN WO9615799-A1.

PD 30-MAY-1996.

PF 22-NOV-1995; US-347144.

PR (RUTF ) UNIV RUTGERS STATE NEW JERSEY.

PA Anderson S;

PI WPI: 96-268332/27.

PT Use of agents which bind beta-amyloid peptide - for diagnosis,

PT prevention and treatment of vascular damage caused by amyloid

PT deposits, partic. in haemorrhaging and Alzheimer's disease

PS Example 1; Fig 1; 52pp; English.

CC To investigate the effects of beta-amyloid peptide (BAP) on

CC tissue plasminogen activator (t-PA) 3 synthetic peptides were used.

CC One peptide contained 42 amino acids and corresp. to the full

CC length BAP (R95248). The other 2 peptides (R95249 and 50) contained

CC the 28 N-terminal residues of the BAP found in Alzheimer's disease

CC and hereditary cerebral haemorrhage with amyloidosis-Dutch type

CC (HCHWA-D), respectively. In an assay to determine the effect of

CC the peptides on t-PA activation, each peptide (R95248, 49 and 50)

CC gave 1st order rate constant of activation (k(app)) values of

CC 13.4, 13.9 and 14.5, respectively, compared to 1.7 and 7.8 for null

CC and fibrinogen controls. The results demonstrate that the BAP are

CC able to stimulate t-PA activity in vitro, which is significant in

CC that it provides a means for investigating and controlling the

CC pathogenesis of Alzheimer's disease, HCHWA-D and cerebral amyloid

CC angiopathy related cerebral haemorrhage.

CC Sequence 28 AA;

SQ

Query Match 100.0%; Score 92; DB 1; Length 28;

Best Local Similarity 100.0%; Pred. No. 1e-08;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQK 16

DB 1 DAEFRHDSGYEVHHQK 16

RESULT 10

R64170

ID R64170 standard; peptide; 28 AA.

AC R64170;

DT 03-AUG-1995 (first entry)

DE A4-O(1-28) a partial beta amyloid peptide.

KW beta amyloid protein; mutant; variant; detection; amyloid deposition;

KW diagnosis; amyloidosis associated disease; Alzheimer's disease;

KW Down's syndrome; A4-O(1-28).

KW Synthetic.

OS WO9428412-A.

PN 08-DEC-1994.

PF 27-MAY-1994; US-05809.

PR 28-MAY-1993; US-065010.

PA (MIRI-) MIRIAM HOSPITAL.

PI Majocha RE, Marotta CA;

DR WPI: 95-023013/03.

PT Amyloid binding composition comprising labelled amyloid protein

PT and carrier - useful for in vivo imaging of amyloid deposits, for

PT diagnosing Alzheimer's disease and Down's Syndrome.

PS Example 1; Page 23; 58pp; English.

CC R64170, the A4-O(1-28) polypeptide is the first 28 amino acids of the

CC 4.2 kb peptide deriv. from senile plaque cores of an AD (Alzheimer's

CC disease) brain, known as beta amyloid. A4-O has strong aggregation

CC properties, and binds to itself strongly. This peptide is used to obtain

CC and select beta amyloid proteins that can be used for in vivo imaging

CC of amyloid deposits and hence diagnosis of an amyloidosis-associated

CC disease, such as AD or Down's syndrome. R64165 shows the generic sequence

CC of the amyloid protein for generation of variants.

CC

SQ Sequence 28 AA;

Query Match 100.0%; Score 92; DB 1; Length 28;

Best Local Similarity 100.0%; Pred. No. 1e-08; 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQK 16

DB 1 DAEFRHDSGYEVHHQK 16

RESULT 11

R64172

ID R64172 standard; peptide; 28 AA.

AC R64172;

DT 03-AUG-1995 (first entry)

DE A4-B(1-28) a partial beta amyloid peptide.

KW beta amyloid protein; mutant; variant; detection; amyloid deposition;

KW diagnosis; amyloidosis associated disease; Alzheimer's disease;

KW Down's syndrome; A4-B(1-28).

KW Synthetic.

OS WO9428412-A.

PN 08-DEC-1994.

PF 27-MAY-1994; US-05809.

PR 28-MAY-1993; US-065010.

PA (MIRI-) MIRIAM HOSPITAL.

PI Majocha RE, Marotta CA;

DR WPI: 95-023013/03.

PT Amyloid binding composition comprising labelled amyloid protein

PT and carrier - useful for in vivo imaging of amyloid deposits, for

PT diagnosing Alzheimer's disease and Down's Syndrome.

PS Example 3; Page 23; 58pp; English.

CC R64172, the A4-B(1-28) polypeptide is deriv. from vascular amyloid of the

CC AD (Alzheimer's disease) brain and a Down Syndrome brain. Three of the

CC 28 amino acids are different from the A4-O(1-28) peptide shown in R64170.

CC A4-O has strong aggregation properties, and binds to itself strongly. It

CC is used to obtain and select beta amyloid proteins that can be used for

CC in vivo imaging of amyloid deposits and hence diagnosis of an

CC amyloidosis-associated disease, such as AD or Down's syndrome. R64165

CC shows the generic sequence of the amyloid protein for generation of

CC variants. 28 AA;

SQ Sequence 28 AA;

Query Match

Best Local Similarity 100.0%; Score 92; DB 1; Length 28;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQK 16

DB 1 DAEFRHDSGYEVHHQK 16

RESULT 12

W81467

ID W81467 standard; peptide; 28 AA.

AC W81467;

DT 28-JAN-1999 (first entry)

DE Synthetic amyloid beta (Abeta) peptide 2 (residues 1-28).

KW Amyloid beta; Abeta; deoxygenated solvent; evaporative deposition;

KW research; neurotoxicity; free-radical; glutamine synthetase.

OS Synthetic.

PN US5840838-A.

PD 24-NOV-1998.

PF 29-FEB-1996; 609090.

PR 29-FEB-1996; US-609090.

PA (KENT ) UNIV KENTUCKY RES FOUND.

PI Aksenov M, Butterfield DA, Carney JM, Hensley K;

DR WPI: 99-034120/03.

PT Process for treating synthetic amyloid beta peptides - by organic

PT solvent treatment, useful for studying neurotoxicity

PS Claim 5; Columns 9-10; 14pp; English.



CC Sequences W81466 to W81476 represent synthetic amyloid beta (Abeta) peptides. The invention provides a process for treating a synthetic Abeta peptide that comprises dissolving the peptide in a deoxygenated solvent selected from trifluoroethanol, hexafluorocyclohexane, dimethyl sulfoxide, morpholinopropanesulphonic acid, dimethylformamide and acetonitrile to a concentration of 0.01-10 mg/ml, incubating the solution at 20-65 deg. C for 0.5-4 hour, and removing the solvent by 'evaporative deposition' in 5-10 minutes. Synthetic amyloid beta peptides are useful as research tools for studying neurotoxicity resulting from Abeta peptide - enhanced free-radical production. The treatment increases the activity of the synthetic Abeta peptides in tests to determine free-radical generating capacity and glutamine synthetase inactivation.

Query Match 100.0%; Score 92; DB 1; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16  
|||||  
DB 1 DAEFRHDSGYEVHHQK 16

## RESULT 13

ID W81468 standard; peptide; 30 AA.  
AC W81468;  
DT 28-JAN-1999 (first entry)  
DE Synthetic amyloid beta (Abeta) peptide 3 (residues 1-30).  
KW Amyloid beta; Abeta; deoxygenated solvent; evaporative deposition;  
KW research; neurotoxicity; free-radical; glutamine synthetase.  
OS Synthetic.  
PN US5840838-A.  
PD 24-NOV-1998.  
PF 29-FEB-1996; US-609090.  
PR 29-FEB-1996; US-609090.  
PA (KENT ) UNIV KENTUCKY RES FOUND.  
PI Aksenov M, Butterfield DA, Carney JM, Hensley K;  
DR WPI; 99-034120/03.  
PT Process for treating synthetic amyloid beta peptides - by organic solvent treatment, useful for studying neurotoxicity

PS Claim 5; Columns 9-10; 14pp; English.  
CC Sequences W81466 to W81476 represent synthetic amyloid beta (Abeta) peptides. The invention provides a process for treating a synthetic Abeta peptide that comprises dissolving the peptide in a deoxygenated solvent selected from trifluoroethanol, hexafluorocyclohexane, dimethyl sulfoxide, morpholinopropanesulphonic acid, dimethylformamide and acetonitrile to a concentration of 0.01-10 mg/ml, incubating the solution at 20-65 deg. C for 0.5-4 hour, and removing the solvent by 'evaporative deposition' in 5-10 minutes. Synthetic amyloid beta peptides are useful as research tools for studying neurotoxicity resulting from Abeta peptide - enhanced free-radical production. The treatment increases the activity of the synthetic Abeta peptides in tests to determine free-radical generating capacity and glutamine synthetase inactivation.

Query Match 100.0%; Score 92; DB 1; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.1e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16  
|||||  
DB 1 DAEFRHDSGYEVHHQK 16

## RESULT 14

W81468  
ID W81468 standard; peptide; 33 AA.  
AC W81468;  
DT 05-SEP-1997 (first entry)  
DE Beta-secretase substrate #1.

KW Beta-cleavage site; beta amyloid precursor protein; APP; beta-secretase;  
KW alpha-secretase; proteolytic cleavage; inhibitor; Alzheimer's disease.  
OS Synthetic.

PN WO9640885-A2.  
PD 19-DEC-1996.  
PF 07-JUN-1996; US-485152.  
PR 07-JUN-1995; US-485152.  
PR 07-JUN-1995; US-480498.  
PA (ATHE-) ATHENA NEUROSCIENCES INC.  
PI Anderson JP, Chrysler SMS, Jacobson-croak KL, Keim PS;  
PI McConlogue LC, Sinha S, Tan H;  
DR WPI; 97-052304/05.

PT Beta-secretase which specifically cleaves beta-amyloid precursor protein - useful to screen for inhibitors useful in treatment of Alzheimer's disease

PT Alzheimer's disease  
PS Disclosure; Page 44; 92pp; English.  
CC W81468 standard; peptide; 30 AA.  
CC W8359-W8362 represent substrates for the enzyme of the invention. The enzyme of the invention is beta-secretase, and specifically cleaves beta-amyloid precursor protein (beta-APP). Normal processing of beta-APP is thought to occur via cleavage between residues 16 and 17 of the beta-amyloid peptide region by an alpha-secretase. Pathogenic processing is thought to occur by beta-secretase cleavage of beta-APP.  
CC Beta-secretase activity can be detected and measured using a method of the invention, which detects at least one of the beta-secretase cleavage products formed on cleavage. The method can be used to determine whether a test substance inhibits proteolytic cleavage, by beta-secretase, of beta-APP. Compounds effective to at least partially inhibit beta-secretase activity can be used to inhibit cleavage of beta-APP in cells or mammalian hosts. Isolation and purification of beta-secretase will permit chemical modelling of a critical event in the pathology of Alzheimer's disease.

SQ Sequence 33 AA;

Query Match 100.0%; Score 92; DB 1; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.3e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16  
|||||  
DB 18 DAEFRHDSGYEVHHQK 33

## RESULT 15

W81469  
ID W81469 standard; peptide; 33 AA.  
AC W81469;  
DT 28-JAN-1999 (first entry)  
DE Synthetic amyloid beta (Abeta) peptide 4 (residues 1-33).  
KW Amyloid beta; Abeta; deoxygenated solvent; evaporative deposition;  
KW research; neurotoxicity; free-radical; glutamine synthetase.  
OS Synthetic.  
PN US5840838-A.  
PD 24-NOV-1998.  
PF 29-FEB-1996; US-609090.  
PR 29-FEB-1996; US-609090.  
PA (KENT ) UNIV KENTUCKY RES FOUND.  
PI Aksenov M, Butterfield DA, Carney JM, Hensley K;  
DR WPI; 99-034120/03.  
PT Process for treating synthetic amyloid beta peptides - by organic solvent treatment, useful for studying neurotoxicity

PS Claim 5; Columns 9-10; 14pp; English.  
CC Sequences W81466 to W81476 represent synthetic amyloid beta (Abeta) peptides. The invention provides a process for treating a synthetic Abeta peptide that comprises dissolving the peptide in a deoxygenated solvent selected from trifluoroethanol, hexafluorocyclohexane, dimethyl sulfoxide, morpholinopropanesulphonic acid, dimethylformamide and acetonitrile to a concentration of 0.01-10 mg/ml, incubating the solution at 20-65 deg. C for 0.5-4 hour, and removing the solvent by 'evaporative deposition' in 5-10 minutes. Synthetic amyloid beta peptides are useful as research tools for studying neurotoxicity resulting from Abeta peptide - enhanced free-radical production. The treatment increases the activity of the synthetic Abeta peptides in tests to determine free-radical



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OM protein - protein search, using sw model

Run on: September 13, 2000, 02:22:01 ; Search time 14.59 Seconds  
(without alignments)  
16.811 Million cell updates/sec

Title: US-09-155-076-2

Perfect score: 92  
Sequence: 1 DAEFRHDSGYEVHQQ 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 152396 seqs, 15329161 residues

Total number of hits satisfying chosen parameters: 152396

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA.\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	92	100.0	16	1	US-08-302-808-10
2	92	100.0	16	2	US-08-986-948-10
3	92	100.0	21	2	US-08-659-984A-18
4	92	100.0	27	1	US-08-141-324-11
5	92	100.0	27	1	US-08-141-324-12
6	92	100.0	27	1	US-08-541-902-11
7	92	100.0	27	1	US-08-541-902-12
8	92	100.0	28	1	US-08-346-849-4
9	92	100.0	28	1	US-08-302-808-7
10	92	100.0	28	2	US-08-609-090-2
11	92	100.0	28	2	US-08-986-948-7
12	92	100.0	28	2	US-08-293-284A-4
13	92	100.0	28	2	US-08-461-216-2
14	92	100.0	30	2	US-08-609-090-3
15	92	100.0	33	2	US-08-609-090-4
16	92	100.0	33	2	US-08-659-984A-16
17	92	100.0	35	1	US-08-304-585-6
18	92	100.0	35	2	US-08-612-785B-15
19	92	100.0	35	2	US-08-612-785B-38
20	92	100.0	36	2	US-08-609-090-6
21	92	100.0	38	1	US-08-302-808-1
22	92	100.0	38	2	US-07-737-371E-68
23	92	100.0	38	2	US-08-986-948-1
24	92	100.0	39	1	US-08-302-808-2
25	92	100.0	39	1	US-08-609-090-7
26	92	100.0	39	2	US-08-682-245A-1
27	92	100.0	39	2	US-08-986-948-2
28	92	100.0	40	1	US-07-744-767A-1

29 92 100.0 40 1 US-08-235-400-2 Sequence 2, Appli  
30 92 100.0 40 1 US-08-476-464A-2 Sequence 2, Appli  
31 92 100.0 40 1 US-08-304-585-1 Sequence 1, Appli  
32 92 100.0 40 1 US-08-304-585-8 Sequence 8, Appli  
33 92 100.0 40 1 US-08-302-808-3 Sequence 3, Appli  
34 92 100.0 40 2 US-08-433-734-1 Sequence 1, Appli  
35 92 100.0 40 2 US-08-609-090-8 Sequence 69, Appli  
36 92 100.0 40 2 US-07-737-371E-69 Sequence 2, Appli  
37 92 100.0 40 2 US-08-682-245A-2 Sequence 3, Appli  
38 92 100.0 40 2 US-08-986-948-3 Sequence 1, Appli  
39 92 100.0 40 4 US-08-461-216-1 Sequence 1, Appli  
40 92 100.0 41 1 PCT-US92-06700-1 Sequence 1, Appli  
41 92 100.0 41 1 US-07-819-361-1 Sequence 4, Appli  
42 92 100.0 41 1 US-08-302-808-4 Sequence 3, Appli  
43 92 100.0 41 2 US-08-682-245A-3 Sequence 4, Appli  
44 92 100.0 41 2 US-08-986-948-4 Sequence 2, Appli  
45 92 100.0 42 1 US-07-744-767A-2 Sequence 2, Appli

#### ALIGNMENTS

RESULT 1  
US-08-302-808-10  
; Sequence 10, Application US/08302808  
; Patent No. 5750349  
; GENERAL INFORMATION:  
; APPLICANT: SUZUKI, No. 5750349uhiro  
; APPLICANT: ODAKA, Asano  
; APPLICANT: KITADA, Chieko  
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR  
; DERIVATIVES AND USE THEREOF  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
; STREET: 130 WATER STREET  
; CITY: BOSTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02019  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA: US/08/302,808  
; FILING DATE: 15-SEP-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA: PCT/JP94/00089  
; FILING DATE: 24-JAN-1994  
; APPLICATION NUMBER: 010132/1993  
; FILING DATE: 25-JAN-1993  
; APPLICATION NUMBER: 019035/1993  
; FILING DATE: 05-FEB-1993  
; APPLICATION NUMBER: 286985/1993  
; FILING DATE: 16-NOV-1993  
; APPLICATION NUMBER: 334773/1993  
; FILING DATE: 28-DEC-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DAVID, RESNICK S  
; REGISTRATION NUMBER: 34,235  
; REFERENCE/DOCKET NUMBER: 44631  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-523-3400  
; TELEFAX: 617-523-6440  
; TELEX: 200291 STR  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single

Wed Sep 13 08:11:39 2000

;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; HYPOTHETICAL: NO  
;; ANTI-SENSE: NO  
;; FRAGMENT TYPE: N-terminal  
;; ORIGINAL SOURCE:  
US-08-302-808-10

Query Match 100.0%; Score 92; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.1e-09;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16  
| | | | | | | | | | | | | | | |  
Db 1 DAEFRHDSGYEVHHQK 16

RESULT 2  
US-08-986-948-10  
; Sequence 10, Application US/08986948  
; Patent No. 5955317  
; GENERAL INFORMATION:  
; APPLICANT: SUZUKI, No. 5955317uhiro  
; APPLICANT: OKADA, Asano  
; APPLICANT: KITADA, Chieko  
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR  
; DERIVATIVES AND USE THEREOF  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
; STREET: 130 WATER STREET  
; CITY: BOSTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02019  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/986,948  
; FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/302,808  
FILING DATE: 15-SEP-1994  
APPLICATION NUMBER: PCT/JP94/00089  
FILING DATE: 24-JAN-1994  
APPLICATION NUMBER: 010132/1993  
FILING DATE: 25-JAN-1993  
APPLICATION NUMBER: 019035/1993  
FILING DATE: 05-FEB-1993  
APPLICATION NUMBER: 286985/1993  
FILING DATE: 16-NOV-1993  
APPLICATION NUMBER: 334773/1993  
FILING DATE: 28-DEC-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: DAVID, RESNICK S  
REGISTRATION NUMBER: 34,235  
REFERENCE/DOCKET NUMBER: 44631  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
TELEX: 200291 STRE  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

;; HYPOTHETICAL: NO  
;; ANTI-SENSE: NO  
;; FRAGMENT TYPE: N-terminal  
;; ORIGINAL SOURCE:  
US-08-986-948-10

Query Match 100.0%; Score 92; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.1e-09;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16  
| | | | | | | | | | | | | | | |  
Db 1 DAEFRHDSGYEVHHQK 16

RESULT 3  
US-08-659-984A-18  
; Sequence 18, Application US/08659984A  
; Patent No. 5942400  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, John P.  
; APPLICANT: Sinha, Sukanto  
; APPLICANT: Jacobson-Croak, Kirsten L.  
; TITLE OF INVENTION: Assays for Detecting Beta-Secretase  
; TITLE OF INVENTION: Inhibition  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Ctr., 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/659,984A  
; FILING DATE: 07-JUN-1996  
; CLASSIFICATION: 436  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/485,152  
; FILING DATE: 07-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Heslin, James M.  
; REGISTRATION NUMBER: 29,541  
; REFERENCE/DOCKET NUMBER: 15270-002810US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 21 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-659-984A-18

Query Match 100.0%; Score 92; DB 2; Length 21;  
Best Local Similarity 100.0%; Pred. No. 4.2e-09;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16  
| | | | | | | | | | | | | | | |  
Db 6 DAEFRHDSGYEVHHQK 21

RESULT 4

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STATE: CO
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/141,324
FILING DATE: 21-OCT-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 44-93
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-499-8080
TELEFAX: 303-499-8089
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-141-324-12

Query Match 100.0%; Score 92; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 5.5e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0

QY 1 DAEFRHDSGYEVHHQK 16
      |||
Db 9 DAEFRHDSGYEVHHQK 24

RESULT 6
US-08-541-902-11
Sequence 11, Application US/08541902
Patent No. 5707620
GENERAL INFORMATION:
APPLICANT: Travis, James
APPLICANT: Potempa, Jan S.
APPLICANT: Barr, Philip J.
APPLICANT: Pavloff, Nadine
APPLICANT: Pike, Robert N.
TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee and Winner, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: CO
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/541,902
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/141,324
FILING DATE: 21-OCT-1993
ATTORNEY/AGENT INFORMATION:

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us-09-155-076-2\_1.rai

Wed Sep 13 08:11:39 2000

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; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 44-93
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-499-8080
; TELEFAX: 303-499-8089
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-541-902-11

Query Match 100.0%; Score 92; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 5.5e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
Db 9 DAEFRHDSGYEVHHQK 24

; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-541-902-12

Query Match 100.0%; Score 92; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 5.5e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
Db 9 DAEFRHDSGYEVHHQK 24

RESULT 8
US-08-346-849-4
; Sequence 4, Application US/08346849
; Patent No. 5670483
; GENERAL INFORMATION:
; APPLICANT: Zhang, Shuguang
; APPLICANT: Lockshin, Curtis
; APPLICANT: Rich, Alexander
; APPLICANT: Holmes, Todd
; TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
; TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
; TITLE OF INVENTION: THEREFOR
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/346,849
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/973,326
; FILING DATE: 28 DECEMBER 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: MIT-6008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-346-849-4

Query Match 100.0%; Score 92; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.7e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
Db 1 DAEFRHDSGYEVHHQK 16

RESULT 9
US-08-302-808-7
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; Sequence 7, Application US/08302808  
; Patent No. 5750349  
; GENERAL INFORMATION:  
; APPLICANT: SUZUKI, No. 5750349uh1ro  
; APPLICANT: ODAKA, Asano  
; APPLICANT: KITADA, Chieko  
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR  
; DERIVATIVES AND USE THEREOF  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
; STREET: 130 WATER STREET  
; CITY: BOSTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02019  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/302,808  
; FILING DATE: 15-SEP-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/JP94/00089  
; FILING DATE: 24-JAN-1994  
; APPLICATION NUMBER: 010132/1993  
; FILING DATE: 25-JAN-1993  
; APPLICATION NUMBER: 019035/1993  
; FILING DATE: 05-FEB-1993  
; APPLICATION NUMBER: 286985/1993  
; FILING DATE: 16-NOV-1993  
; APPLICATION NUMBER: 334773/1993  
; FILING DATE: 28-DEC-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DAVID, RESNICK S  
; REGISTRATION NUMBER: 34,235  
; REFERENCE/DOCKET NUMBER: 44631  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-523-3400  
; TELEFAX: 617-523-6440  
; TELEX: 200291 STRE  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 28 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:  
US-08-302-808-7

Query Match 100.0%; Score 92; DB 1; Length 28;  
Best Local Similarity 100.0%; Pred. No. 5.7e-09;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16  
| | | | | | | | | | | | | | | | | |  
DB 1 DAEFRHDSGYEVHHQK 16

RESULT 10  
US-08-609-090-2  
; Sequence 2, Application US/08609090  
; Patent No. 5840838  
; GENERAL INFORMATION:  
; APPLICANT: HENSLEY, Kenneth

; APPLICANT: BUTTERFIELD, D. A.  
; APPLICANT: CARNEY, John M.  
; APPLICANT: AKSENOV, Michael  
; TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF  
; AN OLIGOPEPTIDE OR POLYPEPTIDES  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LOWE PRICE LEBLANC & BECKER  
; STREET: 99 Canal Center Plaza, Suite 300  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/609,090  
; FILING DATE: 29-FEB-1996  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kraus, Eric J.  
; REGISTRATION NUMBER: 36,190  
; REFERENCE/DOCKET NUMBER: 434-059  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-684-1111  
; TELEFAX: 703-684-1124  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 28 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-609-090-2

Query Match 100.0%; Score 92; DB 2; Length 28;  
Best Local Similarity 100.0%; Pred. No. 5.7e-09;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16  
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DB 1 DAEFRHDSGYEVHHQK 16

RESULT 11  
US-08-986-948-7  
; Sequence 7, Application US/08986948  
; Patent No. 5955317  
; GENERAL INFORMATION:  
; APPLICANT: SUZUKI, No. 5955317uh1ro  
; APPLICANT: ODAKA, Asano  
; APPLICANT: KITADA, Chieko  
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR  
; DERIVATIVES AND USE THEREOF  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
; STREET: 130 WATER STREET  
; CITY: BOSTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02019  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/986.948

NAME: Broderick, Thomas F.  
REGISTRATION NUMBER: 31,332  
REFERENCE/DOCKET NUMBER: UOFW-1-6707  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 1-206-682-8100; 1-206-224-0709 (direct)  
TELEFAX: 1-206-224-0779  
TELEX: 4938023  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28 amino acids  
TYPE: amino acid  
STRANDEDNESS: single

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
 STREET: Two Militia Drive  
 CITY: Lexington  
 STATE: Massachusetts  
 COUNTRY: U.S.A.  
 ZIP: 02173-4799  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25



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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; DESCRIPTION: {SYMBOL"/A4(1-28)}
; DESCRIPTION: page 83, line 31
US-08-461-216-2
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Query Match 100.0%; Score 92; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.7e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 DAEFRHDSGYEVHHQK 16
Db 1 DAEFRHDSGYEVHHQK 16
|||||
```

```
RESULT 14
US-08-609-090-3
; Sequence 3, Application US/08609090
; Patent No. 5840838
; GENERAL INFORMATION:
; APPLICANT: HENSLEY, Kenneth
; APPLICANT: BUTTERFIELD, D. A.
; APPLICANT: CARNEY, John M.
; APPLICANT: AKSENOV, Michael
; TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF
; AN OLIGOPEPTIDE OR POLYPEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LOWE PRICE LEBLANC & BECKER
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
```

```
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,090
; FILING DATE: 29-FEB-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kraus, Eric J.
; REGISTRATION NUMBER: 36,190
; REFERENCE/DOCKET NUMBER: 434-059
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-684-1111
; TELEFAX: 703-684-1124
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-609-090-3
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Query Match 100.0%; Score 92; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 6.1e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 DAEFRHDSGYEVHHQK 16
Db 1 DAEFRHDSGYEVHHQK 16
|||||
```

```
RESULT 15
US-08-609-090-4
; Sequence 4, Application US/08609090
```

```
; Patent No. 5840838
; GENERAL INFORMATION:
; APPLICANT: HENSLEY, Kenneth
; APPLICANT: BUTTERFIELD, D. A.
; APPLICANT: CARNEY, John M.
; APPLICANT: AKSENOV, Michael
; TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF
; AN OLIGOPEPTIDE OR POLYPEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LOWE PRICE LEBLANC & BECKER
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,090
; FILING DATE: 29-FEB-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kraus, Eric J.
; REGISTRATION NUMBER: 36,190
; REFERENCE/DOCKET NUMBER: 434-059
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-684-1111
; TELEFAX: 703-684-1124
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-609-090-4
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Query Match 100.0%; Score 92; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 6.8e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 DAEFRHDSGYEVHHQK 16
Db 1 DAEFRHDSGYEVHHQK 16
|||||
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Search completed: September 13, 2000, 02:22:02
Job time: 140 sec
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OM of: US-09-155-076-2 to: GenEmbl:\* out\_format : pfs

Date: Sep 13, 2000 2:56 AM

About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

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-Q/cgn2\_1/USP10\_spool/US09155076/runat\_29082000\_092505\_15746/app\_query.fasta\_1.144  
-DB-GenEmbl -QMT-fastcap -SUFFIX=rge -GAPOP=12.000 -GAPEXT=4.000  
-MINMATCH=0.100 -LOOPEXT=0.000 -LOOPEXT=0.000 -GAPOP=4.500  
-MINMATCH=0.050 -GAPOP=10.000 -GAPEXT=0.500 -GAPOP=6.000  
-GAPEXT=7.000 -GAPOP=10.000 -GAPEXT=0.500 -DELOP=6.000  
-DELEXT=7.000 -START=1 -NATRI-X-biosome62 -TRANS-human40.cdi  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0  
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0  
-MAXLEN=100000 -USER=US09155076 -CGN1\_1\_3119 -NCPU=6 -ICPU=3  
-LONGLOG -NO\_XLPXY -WAIT -THREADS=1

Search information block:

Query: US-09-155-076-2

Query length: 16

Database: GenEmbl.\*

Database sequences: 972840

Database length: 892348106

Search time (sec): 757.400000

score\_list:

Sequence	Strd	Orig	ZScore	Escore	Len	Documentation
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gb_pat:AR016774	+	92.00	296.89	1.9e-08	85	A49528 Sequence 10 from Patent W
gb_pat:AR016774	+	92.00	291.45	3.9e-08	156	A69920 Sequence 15 from Patent W
gb_pat:AR016774	+	92.00	290.42	4.4e-08	175	X56127 S.scrofa mRNA for amyloid
gb_pat:AR016774	+	92.00	290.42	4.4e-08	175	X56128 U.maritimus mRNA for amyloid
gb_pat:AR016774	+	92.00	290.37	4.5e-08	176	X56125 C.familialis mRNA for amyloid
gb_pat:AR016774	+	92.00	290.37	4.5e-08	176	X56129 Oryctolagus sp. mRNA for amyloid
gb_pat:AR016774	+	92.00	290.32	4.5e-08	177	X56126 Cavia sp. mRNA for amyloid
gb_pat:AR016774	+	92.00	290.27	4.5e-08	178	X56124 B.taurus mRNA for amyloid
gb_pat:AR016774	+	92.00	289.74	4.8e-08	189	X56130 Ovis sp. mRNA for amyloid
gb_pat:AR016774	+	92.00	287.52	6.4e-08	242	M29269 Human amyloid-beta protein gene
gb_pat:AR016774	+	92.00	287.38	6.6e-08	246	M37895 Human amyloid-beta protein gene
gb_pat:AR016774	+	92.00	287.38	6.6e-08	246	S60721 beta-amyloid peptide precursor
gb_pat:AR016774	+	92.00	287.38	6.6e-08	246	S61380 beta-amyloid peptide precursor
gb_pat:AR016774	+	92.00	286.38	7.4e-08	275	S61383 beta-amyloid peptide precursor
gb_pat:AR016774	+	92.00	285.60	8.2e-08	300	X13479 Human PreA4 gene for Alzheimer's
gb_pat:AR016774	+	92.00	285.60	8.2e-08	300	I08767 Sequence 14 from Patent W
gb_pat:AR016774	+	92.00	284.12	9.9e-08	354	A69499 Sequence 2 from Patent W
gb_pat:AR016774	+	92.00	284.12	9.9e-08	354	A69501 Sequence 4 from Patent W
gb_pat:AR016774	+	92.00	284.12	9.9e-08	354	A69503 Sequence 6 from Patent W
gb_pat:AR016774	+	92.00	284.12	9.9e-08	354	A69505 Sequence 8 from Patent W
gb_pat:AR016774	+	92.00	284.12	9.9e-08	354	A69507 Sequence 10 from Patent W
gb_pat:AR016774	+	92.00	284.12	9.9e-08	354	A72176 Sequence 2 from Patent W
gb_pat:AR016774	+	92.00	284.12	9.9e-08	354	A72178 Sequence 4 from Patent W
gb_pat:AR016774	+	92.00	284.12	9.9e-08	354	A72180 Sequence 6 from Patent W
gb_pat:AR016774	+	92.00	284.12	9.9e-08	354	A72182 Sequence 8 from Patent W
gb_pat:AR016774	+	92.00	284.12	9.9e-08	354	A72184 Sequence 10 from Patent W
gb_pat:AR016774	+	92.00	284.12	9.9e-08	354	AR066418 Sequence 2 from Patent W
gb_pat:AR016774	+	92.00	283.97	1.0e-07	360	A69509 Sequence 12 from Patent W
gb_pat:AR016774	+	92.00	283.97	1.0e-07	360	A72186 Sequence 12 from Patent W
gb_pat:AR016774	+	92.00	281.28	1.4e-07	486	I06120 Sequence 10 from Patent W
gb_pat:AR016774	+	92.00	281.28	1.4e-07	486	I08764 Sequence 8 from Patent W
gb_pat:AR016774	+	92.00	280.67	1.5e-07	520	A47565 Sequence 9 from Patent W
gb_pat:AR016774	+	92.00	280.12	1.7e-07	553	AR007224 Sequence 9 from Patent W
gb_pat:AR016774	+	92.00	271.46	5.0e-07	1455	X63471 O.cuniculus APP gene for Alzheimer's
gb_pat:AR016774	+	92.00	271.46	5.0e-07	1503	M83558 Rabbit Olf1 and amyloid
gb_pat:AR016774	+	92.00	271.06	5.3e-07	1521	AR003651 Sequence 3 from Patent W
gb_pat:AR016774	+	92.00	270.81	5.5e-07	1564	I09366 Sequence 1 from Patent W
gb_pat:AR016774	+	92.00	270.81	5.5e-07	1564	I09368 Sequence 1 from Patent W

gb\_pat:I24950 + 92.00 270.81 5.5e-07 1564 ! I24950 Sequence 4 from pate  
gb\_pat:I24950 + 92.00 270.81 5.5e-07 1564 ! M18734 Human beta-amyloid A  
gb\_pat:I24950 + 92.00 269.89 6.2e-07 1733 ! M16765 Human cerebrovascula  
gb\_pat:I24950 + 92.00 268.24 7.6e-07 2085 ! I29797 Sequence 9 from pate

seq\_name: gb\_pat:AR016774

seq\_documentation\_block:

LOCUS AR016774 58 bp DNA PAT 05-DEC-1998  
DEFINITION Sequence 15 from patent US 5777194.  
ACCESSION AR016774  
VERSION AR016774.1 GI:3973051

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 58)

AUTHORS Scott, R.W., Reaume, A.G., Trusko, S.P. and Siman, R.

TITLE Gene-targeted mice with humanized A.beta. sequence and Swedish FAD

MUTATION mutation

JOURNAL Patent: US 5777194-A 15 07-JUL-1998;

FEATURES Location/Qualifiers

1..58 /organism="unknown"

BASE COUNT 23 a 11 c 11 g 13 t

ORIGIN

alignment\_scores:

Quality: 92.00 Length: 16  
Ratio: 5.750 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-155-076-2 x AR016774 ..

Align seg 1/1 to: AR016774 from: 1 to: 58

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisHisGlnLys 16

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8 GATCAGAAATTCAGACATGATTGAGGATATGAAGTCCACCATCAAAAA 55

seq\_name: gb\_pat:AR016774

seq\_documentation\_block:

LOCUS AR016774 85 bp DNA PAT 07-MAR-1997

DEFINITION Sequence 10 from Patent WO9608561.

ACCESSION AR016774

VERSION AR016774.1 GI:2302985

KEYWORDS unidentified.

SOURCE unidentified.

ORGANISM unclassified.

REFERENCE 1 (bases 1 to 85)

AUTHORS Chaudhuri, B. and Stephan, C.

TITLE METHOD FOR DETECTION OF MALFOLDED PROTEIN

JOURNAL Patent: WO 9608561-A 10 21-MAR-1996;

COMMENT CIBA GEIGY AG (CH)

FEATURES Other publication AU 3521595 960329.

1..85 Location/Qualifiers

/organism="unidentified"

/db\_xref="taxon:32644"

BASE COUNT 22 a 18 c 21 g 24 t

ORIGIN

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Quality: 92.00 Length: 16  
Ratio: 5.750 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

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US-09-155-076-2 x A49528 ..
Align seg 1/1 to: A49528 from: 1 to: 85

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisHisGlnLys 16
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11 GAGCGTGAATTAGACAGACTCTGGTTACGAAGTTCACCACCAAG 58

seq_name: gb_pat:A69920

seq_documentation_block: 156 bp DNA PAT 07-MAY-1999
LOCUS A69920
DEFINITION Sequence 15 from Patent WO9807850.
ACCESSION A69920
VERSION A69920.1 GI:4774427
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
1 (bases 1 to 156)
AUTHORS
Preddie,E.R. and Bergmann,J.E.
TITLE
AGENTS FOR PRE-SYMPTOMATIC DETECTION AND THERAPEUTIC TARGETING OF
ALZHEIMER'S DISEASE AND DOWN SYNDROME IN HUMANS
JOURNAL
PATENT: WO 9807850-A 26-FEB-1998;
PREDDIE ENRIQUE R (CA)
FEATURES
Location/Qualifiers
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1..156
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cclone="ALZAS1"
BASE COUNT 54 a 29 c 25 g 48 t
ORIGIN

alignment_scores:
Quality: 92.00 Length: 16
Ratio: 5.750 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-2 x A69920 ..
Align seg 1/1 to: A69920 from: 1 to: 156

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisHisGlnLys 16
|||||
4 GATGCAGAAATTCGACATGACTCAGGATATGAAGTTCATCAAAAA 51

seq_name: gb_on:SSAPPMR

seq_documentation_block: 175 bp mRNA MAM 14-JUL-1992
LOCUS SSAPPMR
DEFINITION S.scrofa mRNA for amyloid precursor protein.
ACCESSION X56127
VERSION X56127.1 GI:1895
KEYWORDS
amyloid polypeptide.
SOURCE
p1g.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Artiodactyla; Suiformes; Suina; Suidae; Sus.
REFERENCE
1 (bases 1 to 175)
AUTHORS
Johnstone,E.M.
Direct Submission
TITLE
Submitted (24-SEP-1990) E.M. Johnstone, ELI LILLY AND COMPANY,
LILLY CORPORATE CENTER 0424, INDIANAPOLIS IN 46285, USA
JOURNAL
REFERENCE
2 (bases 1 to 175)
AUTHORS
Johnstone,E.M., Chaney,M.O., Norris,F.H., Pascual,R. and
Little,S.P.
TITLE
Conservation of the sequence of the Alzheimer's disease amyloid
peptide in dog, polar bear and five other mammals by cross-species
polymerase chain reaction analysis
JOURNAL
Brain Res. Mol. Brain Res. 10 (4), 299-305 (1991)
MEDLINE
92017079
FEATURES
Location/Qualifiers
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<1..>175
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/submitted_id="CAA39593.1"
/db_xref="GI:2166"
/db_xref="SWISS-PROT:Q29149"
/translation="SEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGV
VIATVIVITLVM"
BASE COUNT 45 a 34 c 50 g 46 t
ORIGIN

seq_documentation_block: 175 bp mRNA MAM 14-JUL-1992
LOCUS UMAPPMR
DEFINITION U.maritimus mRNA for amyloid precursor protein (APP) (partial).
ACCESSION X56128
VERSION X56128.1 GI:2165
KEYWORDS
amyloid polypeptide.
SOURCE
polar bear.
ORGANISM Thalarchos maritimus
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Carnivora; Fissipedia; Ursidae; Thalarchos.
REFERENCE
1 (bases 1 to 175)
AUTHORS
Johnstone,E.M.
Direct Submission
TITLE
Submitted (24-SEP-1990) E.M. Johnstone, ELI LILLY AND COMPANY,
LILLY CORPORATE CENTER 0424, INDIANAPOLIS IN 46285, USA
JOURNAL
REFERENCE
2 (bases 1 to 175)
AUTHORS
Johnstone,E.M., Chaney,M.O., Norris,F.H., Pascual,R. and
Little,S.P.
TITLE
Conservation of the sequence of the Alzheimer's disease amyloid
peptide in dog, polar bear and five other mammals by cross-species
polymerase chain reaction analysis
JOURNAL
Brain Res. Mol. Brain Res. 10 (4), 299-305 (1991)
MEDLINE
92017079
FEATURES
Location/Qualifiers
source
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/organism="Thalarchos maritimus"
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<1..>175
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/db_xref="SWISS-PROT:Q29149"
/translation="SEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGV
VIATVIVITLVM"
BASE COUNT 45 a 34 c 50 g 46 t
ORIGIN
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seq_documentation_block:	seq_documentation_block:	seq_documentation_block:	seq_documentation_block:
<p>LOCUS ORAPPMR 176 bp mRNA 14-JUL-1992</p> <p>DEFINITION Oryctolagus sp. mRNA for amyloid precursor protein (APP) (partial).</p> <p>ACCESSION X56129</p> <p>VERSION X56129.1 GI:1817</p> <p>KEYWORDS amyloid polypeptide.</p> <p>SOURCE Oryctolagus cuniculus.</p> <p>ORGANISM Oryctolagus cuniculus</p> <p>REFERENCE 1 (bases 1 to 176)</p> <p>AUTHORS Johnstone,E.M.</p> <p>TITLE Direct Submission</p> <p>JOURNAL Submitted (24-SEP-1990) E.M. Johnstone, ELI LILLY AND COMPANY, LILLY CORPORATE CENTER 0424, INDIANAPOLIS IN 46285, USA</p> <p>REFERENCE 2 (bases 1 to 176)</p> <p>AUTHORS Johnstone,E.M., Chaney,M.O., Norris,F.H., Pascual,R. and Little,S.P.</p> <p>TITLE Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis</p> <p>JOURNAL Brain Res. Mol. Brain Res. 10 (4), 299-305 (1991)</p> <p>MEDLINE 92017079</p> <p>FEATURES</p> <p>Location/Qualifiers</p> <p>1..176</p> <p>/organism="Oryctolagus cuniculus"</p> <p>/db_xref="taxon:9986"</p> <p>/tissue_type="brain"</p> <p>&lt;1..&gt;176</p> <p>/codon_start=3</p> <p>/product="amyloid precursor protein"</p> <p>/protein_id="CAA39594.1"</p> <p>/db_xref="GI:1818"</p> <p>/db_xref="SWISS-PROT:Q28748"</p> <p>/translation="SEVKMDAEPHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIATVITVITLMLK"</p> <p>BASE COUNT 44 a 28 c 52 g 52 t</p> <p>ORIGIN</p>	<p>LOCUS CSAPPMR 176 bp mRNA 14-JUL-1992</p> <p>DEFINITION Cavia sp. mRNA for amyloid precursor protein (APP) (partial).</p> <p>ACCESSION X56126</p> <p>VERSION X56126.1 GI:49569</p> <p>KEYWORDS amyloid polypeptide.</p> <p>SOURCE Cavia sp.</p> <p>ORGANISM Cavia sp.</p> <p>REFERENCE 1 (bases 1 to 176)</p> <p>AUTHORS Johnstone,E.M.</p> <p>TITLE Direct Submission</p> <p>JOURNAL Submitted (24-SEP-1990) E.M. Johnstone, ELI LILLY AND COMPANY, LILLY CORPORATE CENTER 0424, INDIANAPOLIS IN 46285, USA</p> <p>REFERENCE 2 (bases 1 to 176)</p> <p>AUTHORS Johnstone,E.M., Chaney,M.O., Norris,F.H., Pascual,R. and Little,S.P.</p> <p>TITLE Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis</p> <p>JOURNAL Brain Res. Mol. Brain Res. 10 (4), 299-305 (1991)</p> <p>MEDLINE 92017079</p> <p>FEATURES</p> <p>Location/Qualifiers</p> <p>1..176</p> <p>/organism="Cavia familiaris"</p> <p>/db_xref="taxon:9615"</p> <p>/tissue_type="kidney"</p> <p>&lt;1..&gt;176</p> <p>/codon_start=1</p> <p>/product="amyloid precursor protein"</p> <p>/protein_id="CAA39590.1"</p> <p>/db_xref="GI:873"</p> <p>/db_xref="SWISS-PROT:Q28280"</p> <p>/translation="ISEVKMDAEPHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIATVITVITLMLK"</p> <p>BASE COUNT 47 a 32 c 49 g 48 t</p> <p>ORIGIN</p>	<p>LOCUS CSAPPMR 176 bp mRNA 14-JUL-1992</p> <p>DEFINITION Cavia sp. mRNA for amyloid precursor protein (APP) (partial).</p> <p>ACCESSION X56126</p> <p>VERSION X56126.1 GI:49569</p> <p>KEYWORDS amyloid polypeptide.</p> <p>SOURCE Cavia sp.</p> <p>ORGANISM Cavia sp.</p> <p>REFERENCE 1 (bases 1 to 176)</p> <p>AUTHORS Johnstone,E.M.</p> <p>TITLE Direct Submission</p> <p>JOURNAL Submitted (24-SEP-1990) E.M. Johnstone, ELI LILLY AND COMPANY, LILLY CORPORATE CENTER 0424, INDIANAPOLIS IN 46285, USA</p> <p>REFERENCE 2 (bases 1 to 176)</p> <p>AUTHORS Johnstone,E.M., Chaney,M.O., Norris,F.H., Pascual,R. and Little,S.P.</p> <p>TITLE Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis</p> <p>JOURNAL Brain Res. Mol. Brain Res. 10 (4), 299-305 (1991)</p> <p>MEDLINE 92017079</p> <p>FEATURES</p> <p>Location/Qualifiers</p> <p>1..176</p> <p>/organism="Canis familiaris"</p> <p>/db_xref="taxon:9615"</p> <p>/tissue_type="kidney"</p> <p>&lt;1..&gt;176</p> <p>/codon_start=1</p> <p>/product="amyloid precursor protein"</p> <p>/protein_id="CAA39590.1"</p> <p>/db_xref="GI:873"</p> <p>/db_xref="SWISS-PROT:Q28280"</p> <p>/translation="ISEVKMDAEPHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIATVITVITLMLK"</p> <p>BASE COUNT 47 a 32 c 49 g 48 t</p> <p>ORIGIN</p>	<p>LOCUS CSAPPMR 176 bp mRNA 14-JUL-1992</p> <p>DEFINITION Cavia sp. mRNA for amyloid precursor protein (APP) (partial).</p> <p>ACCESSION X56126</p> <p>VERSION X56126.1 GI:49569</p> <p>KEYWORDS amyloid polypeptide.</p> <p>SOURCE Cavia sp.</p> <p>ORGANISM Cavia sp.</p> <p>REFERENCE 1 (bases 1 to 176)</p> <p>AUTHORS Johnstone,E.M.</p> <p>TITLE Direct Submission</p> <p>JOURNAL Submitted (24-SEP-1990) E.M. Johnstone, ELI LILLY AND COMPANY, LILLY CORPORATE CENTER 0424, INDIANAPOLIS IN 46285, USA</p> <p>REFERENCE 2 (bases 1 to 176)</p> <p>AUTHORS Johnstone,E.M., Chaney,M.O., Norris,F.H., Pascual,R. and Little,S.P.</p> <p>TITLE Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis</p> <p>JOURNAL Brain Res. Mol. Brain Res. 10 (4), 299-305 (1991)</p> <p>MEDLINE 92017079</p> <p>FEATURES</p> <p>Location/Qualifiers</p> <p>1..176</p> <p>/organism="Canis familiaris"</p> <p>/db_xref="taxon:9615"</p> <p>/tissue_type="kidney"</p> <p>&lt;1..&gt;176</p> <p>/codon_start=1</p> <p>/product="amyloid precursor protein"</p> <p>/protein_id="CAA39590.1"</p> <p>/db_xref="GI:873"</p> <p>/db_xref="SWISS-PROT:Q28280"</p> <p>/translation="ISEVKMDAEPHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIATVITVITLMLK"</p> <p>BASE COUNT 47 a 32 c 49 g 48 t</p> <p>ORIGIN</p>

Wed Sep 13 08:11:40 2000

us-09-155-076-2\_1.rge

Little,S.P.  
Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis

JOURNAL  
MEDLINE  
FEATURES  
92017079

source  
Location/Qualifiers  
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/tissue\_type="brain"  
<1. >176

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/protein\_id="CAA39591.1"  
/db\_xref="GI:49570"  
/translation="ISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGG  
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BASE COUNT 52 a 30 c 46 g 48 t

ORIGIN

alignment\_scores:  
Quality: 92.00 Length: 16  
Ratio: 5.750 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
US-09-155-076-2 x CSAPPMR ..

Align seg 1/1 to: CSAPPMR from: 1 to: 176

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisHisGlnLys 16  
19 GATGCAGAAATTCGACATGACTCAGGATATGAGTCCATCATCAAAAA 66

seq\_name: gb\_om:BTAPPMR

seq\_documentation\_block:  
LOCUS BTAPPMR 177 bp mRNA 14-JUL-1992  
DEFINITION B.taurus mRNA for amyloid precursor protein (APP) (partial).  
ACCESSION X56124  
VERSION X56124.1 GI:82  
KEYWORDS amyloid polypeptide.  
SOURCE Bos taurus.  
ORGANISM Bos taurus.  
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Artiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

REFERENCE  
1 (bases 1 to 177)  
AUTHORS Johnstone,E.M., Chaney,M.O., Norris,F.H., Pascual,R. and Little,S.P.  
TITLE Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis  
JOURNAL Brain Res. Mol. Brain Res. 10 (4), 299-305 (1991)

FEATURES  
source  
1. 177  
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/protein\_id="CAA39589.1"  
/db\_xref="GI:83"  
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BASE COUNT 49 a 30 c 49 g 49 t

ORIGIN

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Quality: 92.00 Length: 16  
Ratio: 5.750 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
US-09-155-076-2 x BTAPPMR ..

Align seg 1/1 to: BTAPPMR from: 1 to: 177

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisHisGlnLys 16  
19 GATGCAGAAATTCGACATGACTCAGGATATGAGTCCATCATCAAAAA 66

seq\_name: gb\_om:OVAPPMR

seq\_documentation\_block:  
LOCUS OVAPPMR 178 bp mRNA 14-JUL-1992  
DEFINITION Ovis sp. mRNA for amyloid precursor protein (APP) (partial).  
ACCESSION X56130  
VERSION X56130.1 GI:1829  
KEYWORDS amyloid polypeptide.  
SOURCE Ovis sp.  
ORGANISM Ovis sp.  
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Artiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Ovis.

REFERENCE  
1 (bases 1 to 178)  
AUTHORS Johnstone,E.M.  
TITLE Direct Submission  
JOURNAL Submitted (24-SEP-1990) E.M. Johnstone, ELI LILLY AND COMPANY, LILLY CORPORATE CENTER 0424, INDIANAPOLIS IN 46285, USA

REFERENCE  
2 (bases 1 to 178)  
AUTHORS Johnstone,E.M., Chaney,M.O., Norris,F.H., Pascual,R. and Little,S.P.  
TITLE Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis  
JOURNAL Brain Res. Mol. Brain Res. 10 (4), 299-305 (1991)

FEATURES  
Location/Qualifiers  
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BASE COUNT 48 a 31 c 49 g 50 t

ORIGIN

alignment\_scores:  
Quality: 92.00 Length: 16  
Ratio: 5.750 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
US-09-155-076-2 x OVAPPMR ..

Align seg 1/1 to: OVAPPMR from: 1 to: 178

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisHisGlnLys 16

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MEDLINE      90260663
FEATURES
source
    Location/Qualifiers
      1..242
      /organism="Homo sapiens"
      /isolate="hereditary cerebral hemorrhage with amyloidosis
      of Dutch type patient"
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      /map="21q21.2"
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      exon
      104..204
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      /note="G00-119-692"
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      BASE COUNT
      ORIGIN

alignment_scores:
  Quality: 92.00      Length: 16
  Ratio: 5.750      Gaps: 0
  Percent Similarity: 100.000      Percent Identity: 100.000

alignment_block:
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seq_name: gb_pr2:S60721

seq_documentation_block:
  LOCUS      S60721      246 bp      mRNA      PRI      23-JUL-1993
  DEFINITION  beta-amyloid peptide precursor {clone 1} [human, mRNA Partial
  Mutant, 246 nt].
  ACCESSION  S60721
  VERSION    S60721.1  GI:299644
  KEYWORDS
  SOURCE
  ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
    Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 246)
  Denman,R.B., Rosenzweig,R. and Miller,D.L.
  A system for studying the effect(s) of familial Alzheimer disease
  mutations on the processing of the beta-amyloid peptide precursor
  Biochem. Biophys. Res. Commun. 192 (1), 96-103 (1993)
  93236601
  GenBank staff at the National Library of Medicine created this
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  This sequence comes from Fig. 1.
  Map location: 21.
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BASE COUNT 72 a 40 c 69 g 65 t  
ORIGIN

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Ratio: 5.750 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
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1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16  
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52 GATGCAGAAATCCGACATGACTCAGGATATGAAGTTCATCATCAAAAA 99

seq\_name: gb\_pr2:S61380

seq\_documentation\_block: 246 bp mRNA PRI 23-JUL-1993  
LOCUS S61380  
DEFINITION beta-amyloid peptide precursor (clone 2) [human, mRNA Partial  
Mutant, 246 nt].  
ACCESSION S61380  
VERSION S61380 GI:299646  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 246)  
AUTHORS Denman, R.B., Rosenczwaig, R. and Miller, D.L.  
TITLE A system for studying the effect(s) of familial Alzheimer disease  
mutations on the processing of the beta-amyloid peptide precursor  
JOURNAL Biochem. Biophys. Res. Commun. 192 (1), 96-103 (1993)  
MEDLINE 93236601  
REMARK GenBank staff at the National Library of Medicine created this  
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This sequence comes from Fig. 1.  
Map location: 21.

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BASE COUNT 73 a 40 c 69 g 64 t  
ORIGIN

alignment\_scores:  
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Ratio: 5.750 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
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seq\_name: gb\_pr2:S61383

seq\_documentation\_block: 246 bp mRNA PRI 23-JUL-1993  
LOCUS S61383  
DEFINITION beta-amyloid peptide precursor (clone 3) [human, mRNA Partial  
Mutant, 246 nt].  
ACCESSION S61383  
VERSION S61383 GI:299648  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 246)  
AUTHORS Denman, R.B., Rosenczwaig, R. and Miller, D.L.  
TITLE A system for studying the effect(s) of familial Alzheimer disease  
mutations on the processing of the beta-amyloid peptide precursor  
JOURNAL Biochem. Biophys. Res. Commun. 192 (1), 96-103 (1993)  
MEDLINE 93236601  
REMARK GenBank staff at the National Library of Medicine created this  
entry [NCBI gibbsq 132966] from the original journal article.  
This sequence comes from Fig. 1.  
Map location: 21.

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Align seg 1/1 to: S61380 from: 1 to: 246

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16  
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52 GATGCAGAAATCCGACATGACTCAGGATATGAAGTTCATCATCAAAAA 99

seq\_name: gb\_pr2:S61383

seq\_documentation\_block: 246 bp mRNA PRI 23-JUL-1993  
LOCUS S61383  
DEFINITION beta-amyloid peptide precursor (clone 3) [human, mRNA Partial  
Mutant, 246 nt].  
ACCESSION S61383  
VERSION S61383 GI:299648  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 246)  
AUTHORS Denman, R.B., Rosenczwaig, R. and Miller, D.L.  
TITLE A system for studying the effect(s) of familial Alzheimer disease  
mutations on the processing of the beta-amyloid peptide precursor  
JOURNAL Biochem. Biophys. Res. Commun. 192 (1), 96-103 (1993)  
MEDLINE 93236601  
REMARK GenBank staff at the National Library of Medicine created this  
entry [NCBI gibbsq 132966] from the original journal article.  
This sequence comes from Fig. 1.  
Map location: 21.

FEATURES  
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1..246  
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KGAIIGLMVGGVVIAIVITLVLMLKKQWTSIHGVE"

BASE COUNT 72 a 40 c 71 g 63 t  
ORIGIN

alignment\_scores:  
Quality: 92.00 Length: 16  
Ratio: 5.750 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
US-09-155-076-2 x S61383 ..  
Align seg 1/1 to: S61383 from: 1 to: 246

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16  
|||||  
52 GATGCAGAAATCCGACATGACTCAGGATATGAAGTTCATCATCAAAAA 99



OM of: US-09-155-076-2 to: N\_Geneseq\_36.\* out\_format : pfs

Date: Sep 13, 2000 2:58 AM

About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

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Search information block:

Query: US-09-155-076-2

Query length: 16

Database: N\_Geneseq\_36.\*

Database sequences: 311585

Database length: 125096042

Search time (sec): 75.680000

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N_Geneseq_36:N92266	+	92.00	285.75	2.6e-08	177	Region of pre-APP coding sequence
N_Geneseq_36:Q77992	+	92.00	285.15	2.8e-08	189	CDNA encoding the APP leader seq
N_Geneseq_36:V23754	+	92.00	282.15	4.1e-08	262	Alzasi coding sequence. Nucleid
N_Geneseq_36:Q88696	+	92.00	281.00	4.7e-08	297	Beta-amyloid precursor protein
N_Geneseq_36:Q88697	+	92.00	281.00	4.7e-08	297	Beta-amyloid precursor protein
N_Geneseq_36:Q88698	+	92.00	281.00	4.7e-08	297	Beta-amyloid precursor protein
N_Geneseq_36:Q10017	+	92.00	280.91	4.8e-08	300	Sequence encoding beta-amyloid
N_Geneseq_36:Q42655	+	92.00	280.91	4.8e-08	300	Full-length beta-amyloid protein
N_Geneseq_36:Q88699	+	92.00	280.64	5.0e-08	309	Beta-amyloid precursor protein
N_Geneseq_36:Q88700	+	92.00	280.64	5.0e-08	309	Beta-amyloid precursor protein
N_Geneseq_36:T18082	+	92.00	279.87	5.5e-08	336	Familial Alzheimer's disease AP
N_Geneseq_36:V20377	+	92.00	279.39	5.8e-08	354	DNA for APP C-terminal fragment
N_Geneseq_36:V20380	+	92.00	279.39	5.8e-08	354	DNA for APP C-terminal fragment
N_Geneseq_36:V20381	+	92.00	279.39	5.8e-08	354	DNA for APP C-terminal fragment
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N_Geneseq_36:V07188	+	92.00	279.39	5.8e-08	354	DNA for APP C-terminal fragment
N_Geneseq_36:X08982	+	92.00	279.39	5.8e-08	354	Flag-amyloid protein precursor
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N_Geneseq_36:N80605	+	92.00	276.48	8.5e-08	486	Lambda SM2 encoding first 18 am
N_Geneseq_36:Q10015	+	92.00	276.48	8.5e-08	486	Genomic clone including beta-am
N_Geneseq_36:Q42652	+	92.00	276.48	8.5e-08	486	Clone lambda SM2 encoding beta-am
N_Geneseq_36:Q82910	+	92.00	275.86	9.2e-08	520	Human beta amyloid fusion prote
N_Geneseq_36:V23753	+	92.00	275.86	9.2e-08	520	Alzas coding sequence. Nucleic
N_Geneseq_36:N90457	+	92.00	266.11	3.2e-07	1504	CDNA sequence of clone amy 37
N_Geneseq_36:V26456	+	92.00	266.01	3.2e-07	1521	Maltose binding protein-APP (S
N_Geneseq_36:N90397	+	92.00	265.77	3.3e-07	1562	CDNA sequence of amy 37 clone.
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N_Geneseq_36:Q69003	+	92.00	263.11	4.7e-07	2085	Mouse amyloid precursor protei
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N_Geneseq_36:N80604	+	92.00	262.39	5.2e-07	2256	Lambda APCP16844, amino acids 1
N_Geneseq_36:Q10014	+	92.00	262.39	5.2e-07	2256	Clone lambda APCP16814 of beta
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N_Geneseq_36:Q42661	+	92.00	262.39	5.2e-07	2256	Lambda clone APCP16814 encodes
N_Geneseq_36:Q27802	+	92.00	262.35	5.2e-07	2265	APP751. Polynucleotide probe c
N_Geneseq_36:X08983	+	92.00	262.35	5.2e-07	2265	Amyloid precursor protein (APP
N_Geneseq_36:V10322	+	92.00	262.17	5.3e-07	2310	Human APP770 cDNA. Identifying
N_Geneseq_36:Q48860	+	92.00	262.16	5.3e-07	2313	Mutated APP770 exon 17 DNA. Ne
N_Geneseq_36:Q74708	+	92.00	262.16	5.3e-07	2313	CDNA of APP 770 gene contig. mu

N\_Geneseq\_36:N91050 + 92.00 259.93 7.1e-07 2949 ! Sequence encoding novel amy  
N\_Geneseq\_36:Q05086 + 92.00 259.93 7.1e-07 2949 ! Sequence encodes NAP-2 gene  
N\_Geneseq\_36:N91049 + 92.00 259.76 7.2e-07 3006 ! Sequence encoding novel amy  
N\_Geneseq\_36:Q05085 + 92.00 259.76 7.2e-07 3006 ! Sequence encodes NAP gene a

seq\_name: N\_Geneseq\_36:T38687

seq\_documentation\_block:

ID T38687 standard; DNA; 58 BP.

AC T38687;

DT 21-JUL-1997 (first entry)

DE Mouse amyloid precursor protein exon 16 primer ST61.

KW Exon 16; murine; mouse; amyloid; precursor; protein; APP;

KW humanisation; homozygous; heterozygous; human; Abeta; Swedish;

KW familial; Alzheimer's; disease; FAD; mutation; tool; model;

KW elucidation; pathology; symptomatology; screen; inhibition;

KW transgenic; polymerase chain reaction; primer; PCR;

KW amplification; ss.

OS Synthetic.

PN N09634097-AL.

PD 31-OCT-1996.

PF 26-APR-1996; 005824.

PR 26-APR-1996; US-429207.

PR 23-APR-1996; US-636876.

PA (CEPH-) CEPHALON INC.

PI Hoffman EK. Reaume AG, Scott RW, Siman R, Trusko SP;

DR WPI; 96-497629/49.

PT Transgenic mice with humanised amyloid precursor protein gene -

PT having at least 1 Swedish FAD mutation, useful as tools or models to

PT elucidate role of human A-beta in Alzheimer's disease

PS Example 1; Page 75; 123pp; English.

CC The present sequence is a primer for the PCR amplification of exon

CC 16 of the mouse amyloid precursor protein (APP) gene, into which 6

CC humanising base pair changes was introduced. The exon was then used

CC in the preparation of mice homozygous or heterozygous for a

CC targeted APP encoding gene, comprising a human Abeta peptide

CC encoding sequence in place of the endogenous murine sequence, and

CC at least 1 Swedish Familial Alzheimer's Disease (FAD) mutation. The

CC mice can be used as tools, or models to elucidate the role of human

CC Abeta in AD pathology and symptomatology. They can also be used to

CC screen chemical compounds for the ability to inhibit in vivo

CC processing of APP, to yield the human Abeta peptide by

CC administering the chemical compounds to a mouse and measuring the

CC relative amounts of amyloidogenic and nonamyloidogenic processing

CC of APP in a sample from the mouse at an appropriate interval after

CC administration of the chemical compounds.

SQ Sequence 58 BP; 23 A; 11 C; 11 G; 13 T;

## alignment\_scores:

Quality: 92.00 Length: 16  
Ratio: 5.750 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

## alignment\_block:

US-09-155-076-2 x T38687

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8 GATGCAGAAATTCAGACATGATTCAGGATATGAGTCCACCATCAAAA 55

seq\_name: N\_Geneseq\_36:T14516

seq\_documentation\_block:

ID T14516 standard; DNA; 85 BP.

AC T14516;

DT 30-OCT-1996 (first entry)

DE Beta-amyloid4 peptide coding sequence.

DE Unfolded-protein-response element; UPR; BIP; expression cassette; p53;

KW reporter element; protein misfolding; prion; beta-amyloid peptide; plant;

KW host cell; animal; insect cell; fungal cell; saccharomyces cerevisiae;



58 GATCGAGAATTCGACATGACTCAGGATATGATGAAGTTCATCATCAAAAA 105

seq\_name: N\_Geneseq\_36.V23754

seq\_documentation\_block:

ID V23754 standard; DNA; 262 BP.

AC V23754;

DT 18-AUG-1998 (first entry)

DE Alz1s1 coding sequence.

KW Dsas; DSASP; alz1s; Down's syndrome; diagnosis; therapy; human;

KW Alzheimer's disease; ss.

OS Homo sapiens.

FH Key Location/Qualifiers

FT CDS 50..205

FT /\*tag= a

FT /product= ALZASpl

FT /note= "specifically claimed fragment"

FN WO9807850-A2.

PD 26-FEB-1998.

PF 22-AUG-1997; E04599.

PR 22-AUG-1996; CA-183901.

PA (BERG/) BERGMANN J E.

PA (PRED/) FREDDIE E R.

PI Bergmann JE, Freddie ER;

DR WPI: 98-169155/15.

DR P-PSDB: W53984.

PT Nucleic acid molecules dsas, and alz1s - used for detecting and

PT treating Down's syndrome and Alzheimer's disease

PS Claim 13; Fig 11; 96pp; English.

CC This sequence represents the human alz1s1 nucleic acid. The dsas

CC and alz1s DNA sequences are the nucleic acids of the invention. Reagents

CC specifically for DSASP can be used for the diagnosis of Down's syndrome

CC in humans and especially in pregnant women. Molecules that inhibit the

CC activity of the promoters (PDS1, PDS2, and PDS4) for dsas can be

CC used for treating Down's syndrome. The reagent capable of detecting

CC alz1s can be used for detecting Alzheimer's disease, especially in the

CC pre-symptomatic stage. Substances that inhibit the promoters for alz1s

CC can be used in treating Alzheimer's disease.

SQ Sequence 262 BP; 96 A; 43 C; 52 G; 71 T;

alignment\_scores:

Quality: 92.00 Length: 16

Ratio: 5.750 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-155-076-2 x V23754 ..

Align seg 1/1 to: V23754 from: 1 to: 262

1 ASPALGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16

|||||

53 GATCGAGAATTCGACATGACTCAGGATATGATGAAGTTCATCATCAAAAA 100

seq\_name: N\_Geneseq\_36.Q88696

seq\_documentation\_block:

ID Q88696 standard; cDNA to mRNA; 297 BP.

AC Q88696;

DT 11-NOV-1995 (first entry)

DE Beta-amyloid precursor protein C-terminal peptide gene.

KW Human; beta-amyloid precursor protein; C-terminal peptide;

KW gene transfer; transgenic animal; Alzheimer disease model;

KW gene therapy; ss.

OS Homo sapiens.

PN EP-653154-A.

PD 17-MAY-1995.

PF 07-NOV-1994; 117512.

PR 12-NOV-1993; JP-306026.

PA (FARH ) HOECHST JAPAN LTD.

PA (FARH ) HOECHST JAPAN KK.

PI Kawarabayashi T, Kobayashi T, Sato M, Shoji M, Tada N;

DR WPI: 95-180492/24.

DR P-PSDB: R74694.

PT Transgenic animal model for Alzheimer's disease - contains DNA encoding part of beta-amyloid precursor protein in a gene construct designed for over-expression in various cell types

PS Claim 2; Page 11; 32pp; English.

CC The sequence encodes a human brain beta-amyloid precursor protein (APP) C-terminal peptide. The DNA may be transferred along with an

CC APP signal peptide gene (e.g. Q88695) into somatic and germ cells of

CC a non-human mammal, and the resulting transgenic animal may be used

CC as a model for Alzheimer disease (AD). The animal model exhibits

CC symptoms similar to AD, producing large quantities of APP C-terminal

CC peptide, death of neuron cells in pyramidal cells at cerebral

CC amyloid regions, increases in glial cells and deposition of

CC abnormally phosphorylated tau protein. The animal model may be

CC used to develop new therapies for AD, including gene therapy

CC strategies.

SQ Sequence 297 BP; 86 A; 64 C; 78 G; 69 T;

alignment\_scores:

Quality: 92.00 Length: 16

Ratio: 5.750 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-155-076-2 x Q88696 ..

Align seg 1/1 to: Q88696 from: 1 to: 297

1 ASPALGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16

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1 GATCGAGAATTCGACATGACTCAGGATATGATGAAGTTCATCATCAAAAA 48

seq\_name: N\_Geneseq\_36.Q88697

seq\_documentation\_block:

ID Q88697 standard; cDNA to mRNA; 297 BP.

AC Q88697;

DT 11-NOV-1995 (first entry)

DE Beta-amyloid precursor protein C-terminal peptide mutant gene.

KW Human; beta-amyloid precursor protein mutant; C-terminal peptide;

KW gene transfer; transgenic animal; Alzheimer disease model;

KW gene therapy; ss.

OS Homo sapiens.

PN EP-653154-A.

PD 17-MAY-1995.

PF 07-NOV-1994; 117512.

PR 12-NOV-1993; JP-306026.

PA (FARH ) HOECHST JAPAN LTD.

PA (FARH ) HOECHST JAPAN KK.

PI Kawarabayashi T, Kobayashi T, Sato M, Shoji M, Tada N;

DR WPI: 95-180492/24.

DR P-PSDB: R74695.

PT Transgenic animal model for Alzheimer's disease - contains DNA encoding part of beta-amyloid precursor protein in a gene construct designed for over-expression in various cell types

PS Claim 2; Page 12-13; 32pp; English.

CC The sequence encodes a human brain beta-amyloid precursor protein

CC (APP) mutant C-terminal peptide, and differs from Q88696 by a Glu

CC to Gln conversion at codon-22. The DNA may be transferred along

CC with an APP signal peptide gene (e.g. Q88695) into somatic and germ

CC cells of a non-human mammal, and the resulting transgenic animal may

CC be used as a model for Alzheimer disease (AD). The animal model

CC exhibits symptoms similar to AD, producing large quantities of APP

CC C-terminal peptide, death of neuron cells in pyramidal cells at

CC cerebral amyloid regions, increases in glial cells and deposition

CC of abnormally phosphorylated tau protein. The animal model may

CC be used to develop new therapies for AD, including gene therapy

CC strategies.

SQ Sequence 297 BP; 86 A; 65 C; 77 G; 69 T;

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alignment_scores:
  Quality: 92.00      Length: 16
  Ratio: 5.750       Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
  US-09-155-076-2 x Q88697 ..
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  1 AsplaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
  |||||
  1 GATCGAGATTCGACGACTGAGTATGAGATTCATCATCAAAAA 48

seq_name: N_Geneseq_36:Q88698

seq_documentation_block:
  ID Q88698 standard; cDNA to mRNA; 297 BP.
  AC Q88698;
  DT 11-NOV-1995 (first entry)
  DE Beta-amyloid precursor protein C-terminal peptide mutant gene.
  KW Human; beta-amyloid precursor protein mutant; C-terminal peptide;
  KW gene transfer; transgenic animal; Alzheimer disease model;
  KW gene therapy; ss.
  OS Homo sapiens.
  PN EP-653154-A.
  PD 17-MAY-1995.
  PF 07-NOV-1994; 117512.
  PR 12-NOV-1993; JP-306026.
  PA (FARH ) HOECHST JAPAN LTD.
  PA (FARH ) HOECHST JAPAN KK.
  PI Kawarabayashi T, Kobayashi T, Sato M, Shoji M, Tada N;
  DR WPI; 95-180492/24.
  DE Transgenic animal model for Alzheimer's disease - contains DNA encoding
  part of beta-amyloid precursor protein in a gene construct designed for
  over-expression in various cell types
  Claim 2; Page 13-14; 32pp; English.
  CC The sequence encodes a human brain beta-amyloid precursor protein
  (APP) mutant C-terminal peptide, and differs from Q88696 by
  conversion of Val to Ile at codon-46. The DNA may be transferred
  along with an APP signal peptide gene (e.g. Q88695) into somatic and
  germ cells of a non-human mammal, and the resulting transgenic animal
  may be used as a model for Alzheimer disease (AD). The animal model
  exhibits symptoms similar to AD, producing large quantities of APP
  C-terminal peptide, death of neuron cells in pyramidal cells at
  cerebral amyloid regions, increases in glial cells and deposition
  of abnormally phosphorylated tau protein. The animal model may
  be used to develop new therapies for AD, including gene therapy
  strategies.
  SQ Sequence 297 BP; 87 A; 64 C; 77 G; 69 T;

alignment_scores:
  Quality: 92.00      Length: 16
  Ratio: 5.750       Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
  US-09-155-076-2 x Q88698 ..
  Align seg 1/1 to: Q88698 from: 1 to: 297

  1 AsplaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
  |||||
  1 GATCGAGATTCGACGACTGAGTATGAGATTCATCATCAAAAA 48

seq_name: N_Geneseq_36:Q10017

seq_documentation_block:
  ID Q10017 standard; DNA; 300 BP.
  AC Q10017;
  DT 14-MAR-1991 (first entry)

```

```

DE Sequence encoding beta-amyloid-related protein.
KW Alzheimer's disease; AD; acute pancreatitis; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 1..300
FT /*tag= a
FN WO9014840-A.
PD 13-DEC-1990.
PF 04-JUN-1990; U03141.
PR 06-JUN-1989; US-361912.
PR 29-MAR-1990; US-502273.
PA (CALB-) CALIF BIOTECH INC.
PI Schilling JW, Ponte PA, Cordell B;
DR WPI; 91-006983/01.
DR R-PSDB; R10024.
DE DNA sequences, and protease inhibitors encoded by them and
PT antibodies - for diagnosis and treatment of alzhelmers disease
PS Disclosure; Fig 5; 96pp; English.
CC Sequence may be useful in prognosis and diagnosis of human
CC Alzheimer's disease (AD). Abs may be raised to the gene product, and
CC probes derived from the encoding sequence allowing diagnosis and
CC determination of genetic predisposition.
CC The gene product is a protease inhibitor and may also have utility
CC in treatment of acute pancreatitis.
SQ Sequence 300 BP; 87 A; 63 C; 80 G; 70 T;

alignment_scores:
  Quality: 92.00      Length: 16
  Ratio: 5.750       Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
  US-09-155-076-2 x Q10017 ..
  Align seg 1/1 to: Q10017 from: 1 to: 300

  1 AsplaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
  |||||
  4 GATCGAGATTCGACGACTGAGTATGAGTATCATCATCAAAAA 51

seq_name: N_Geneseq_36:Q42665

seq_documentation_block:
  ID Q42665 standard; cDNA; 300 BP.
  AC Q42665;
  DT 27-OCT-1993 (first entry)
  DE Full-length beta-amyloid protein coding region.
  KW Alzheimer's Disease; Amyloid Plaque Core Protein; APCP;
  KW neuritic plaque; ds.
  OS Homo sapiens.
  FH Key Location/Qualifiers
FT cds 1..300
FT /*tag= a
FT /product= beta-amyloid_protein
FT /note= "full-length coding sequence obtained by
FT combining overlapping clones SM2W3 and
FT SM2W4 (Q42664 and Q42663, respectively)"
FT misc_difference 160..162
FT /*tag= b
FT /codon= seq: AAC; aa: Lys
FT /note= "this codon is AAG in Q42664"
FN US5220013-A.
PD 15-JUN-1993.
PF 17-NOV-1986; 932193.
PR 17-NOV-1986; US-932193.
PR 31-DEC-1986; US-948376.
PR 30-JAN-1987; US-008810.
PR 18-AUG-1987; US-087002.
PR 30-NOV-1989; US-444118.
PA (SCIO-) SCIOS NOVA INC.
PI Cordell B, Ponte PA;
DR WPI; 93-205383/25.

```

DR P-PSDB: R37866.  
 PT DNA sequence useful for detection of Alzheimer's disease - for  
 PS encoding beta amyloid core protein  
 CC Disclosure; Fig 5; 40pp; English.  
 CC A clone was obtained from the genomic library described in Lawn et al.,  
 CC Cell, 15:1157-1174 (1978) which included a 57 base pair segment which  
 CC encodes amino acids 1-18 of the beta-amyloid protein. Immediately  
 CC preceded by a Methionine. A HindIII/RsaI fragment derived from the  
 CC genomic clone and containing the 57bp segment was used to isolate cDNA  
 CC fragments from a library prepared from temporal and parietal cortical  
 CC tissue from a normal human brain. Lambda clone SM2W3 (Q42664) contains  
 CC a 5' region segment which has a 6bp overlap with the 3' end of clone  
 CC SM2W4 (Q42663). The full-length beta-amyloid protein coding sequence  
 CC (Q42665), including an initiator Met residue which is probably  
 CC processed in vivo, was obtained by combining the sequences of the  
 CC two overlapping clones.  
 SQ Sequence 300 BP; 87 A; 65 C; 78 G; 70 T;

alignment\_scores:  
 Quality: 92.00 Length: 16  
 Ratio: 5.750 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

## alignment\_block:

US-09-155-076-2 x Q42665 ..

Align seg 1/1 to: Q42665 from: 1 to: 300

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16  
 4 GATGCAGAAATCCGACATGACTCAGGATATGAAGTTCATCATCAAAAA 51

seq\_name: N\_Geneseq\_36:Q88699

## seq\_documentation\_block:

ID Q88699 standard; cDNA to mRNA; 309 BP.

AC Q88699;  
 DT 11-NOV-1995 (first entry)  
 DE Beta-amyloid precursor protein C-terminal peptide gene.  
 KW Human; beta-amyloid precursor protein; C-terminal peptide;  
 KW gene transfer; transgenic animal; Alzheimer disease model;  
 KW gene therapy; ss.  
 OS Homo sapiens.  
 PN EP-653154-A.  
 PD 17-MAY-1995.  
 PF 07-NOV-1994; 117512.  
 PR 12-NOV-1993; JP-306026.  
 PA (FARH) HOECHST JAPAN LTD.  
 PA (FARH) HOECHST JAPAN KK.  
 PI Kawarabayashi T, Kobayashi T, Sato M, Shoji M, Tada N;  
 DR WPI: 95-180492/24.  
 DR P-PSDB: R74697.

PT Transgenic animal model for Alzheimer's disease - contains DNA encoding  
 PT part of beta-amyloid precursor protein in a gene construct designed for  
 PT over-expression in various cell types  
 PS Claim 2; Page 15; 32pp; English.

CC The sequence encodes a human brain beta-amyloid precursor protein  
 CC (APP) C-terminal peptide. The DNA may be transferred along with an  
 CC APP signal peptide gene (e.g. Q88695) into somatic and germ cells  
 CC of a non-human mammal, and the resulting transgenic animal may be  
 CC used as a model for Alzheimer disease (AD). The animal model  
 CC exhibits symptoms similar to AD, producing large quantities of APP  
 CC C-terminal peptide, death of neuron cells in pyramidal cells at  
 CC cerebral amyloid regions, increases in glial cells and deposition  
 CC of abnormally phosphorylated tau protein. The animal model may  
 CC be used to develop new therapies for AD, including gene therapy  
 CC strategies.

SQ Sequence 309 BP; 91 A; 64 C; 83 G; 71 T;

## alignment\_scores:

Quality: 92.00 Length: 16

Ratio: 5.750 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

## alignment\_block:

US-09-155-076-2 x Q88699 ..

Align seg 1/1 to: Q88699 from: 1 to: 309

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16  
 13 GATGCAGAAATCCGACATGACTCAGGATATGAAGTTCATCATCAAAAA 60

seq\_name: N\_Geneseq\_36:Q88700

## seq\_documentation\_block:

ID Q88700 standard; cDNA to mRNA; 309 BP.

AC Q88700;  
 DT 11-NOV-1995 (first entry)  
 DE Beta-amyloid precursor protein C-terminal peptide mutant gene.  
 KW Human; beta-amyloid precursor protein mutant; C-terminal peptide;  
 KW gene transfer; transgenic animal; Alzheimer disease model;  
 KW gene therapy; ss.  
 OS Homo sapiens.  
 PN EP-653154-A.  
 PD 17-MAY-1995.  
 PF 07-NOV-1994; 117512.  
 PR 12-NOV-1993; JP-306026.  
 PA (FARH) HOECHST JAPAN LTD.  
 PA (FARH) HOECHST JAPAN KK.  
 PI Kawarabayashi T, Kobayashi T, Sato M, Shoji M, Tada N;  
 DR WPI: 95-180492/24.  
 DR P-PSDB: R74698.

PT Transgenic animal model for Alzheimer's disease - contains DNA encoding  
 PT part of beta-amyloid precursor protein in a gene construct designed for  
 PT over-expression in various cell types  
 PS Claim 2; Page 16-17; 32pp; English.

CC The sequence encodes a human brain beta-amyloid precursor protein  
 CC (APP) mutant C-terminal peptide, and differs from Q88699 by  
 CC conversion of Lys to Asn at codon-3 and Met to Leu at codon-4. The  
 CC DNA may be transferred along with an APP signal peptide gene (e.g.  
 CC Q88695) into somatic and germ cells of a non-human mammal, and the  
 CC resulting transgenic animal may be used as a model for Alzheimer  
 CC disease (AD). The animal model exhibits symptoms similar to AD,  
 CC producing large quantities of APP C-terminal peptide, death of  
 CC neuron cells in pyramidal cells at cerebral amyloid regions,  
 CC increases in glial cells and deposition of abnormally  
 CC phosphorylated tau protein. The animal model may be used to develop  
 CC new therapies for AD, including gene therapy strategies.

SQ Sequence 309 BP; 90 A; 65 C; 82 G; 72 T;

## alignment\_scores:

Quality: 92.00 Length: 16

Ratio: 5.750 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

## alignment\_block:

US-09-155-076-2 x Q88700 ..

Align seg 1/1 to: Q88700 from: 1 to: 309

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16  
 13 GATGCAGAAATCCGACATGACTCAGGATATGAAGTTCATCATCAAAAA 60

seq\_name: N\_Geneseq\_36:T18082

## seq\_documentation\_block:

ID T18082 standard; DNA; 336 BP.

AC T18082;

DT 10-OCT-1996 (first entry)

DE Familial Alzheimer's disease APP isoform 751 gene fragment.  
 KW APP; amyloid precursor protein; isoform 751; inherent; familial;

Wed Sep 13 08:11:41 2000

us-09-155-076-2\_1.rng

KW Alzheimer's disease; mutation; diagnosis; transgenic model; study;  
 KW cognitive; beta A4 domain; exon 17; senility; ss.  
 OS Homo sapiens.

FH Key Location/Qualifiers  
 FT CDS 1..336  
 FT exon

FT FT /tag= a  
 FT FT /number= 17

FT FT /trans\_except= pos: 175-177, aa: ile  
 FT FT /note= "encodes amino acids 640-751 of full APP  
 FT FT isoform 751, the translation exception  
 FT FT at posn. 175-177 is the site of a Val to  
 FT FT ile mutation in isoform 751, bases 175-177  
 FT FT probably should be ATC and not TTC"  
 FT FT 43..168

FT FT misc\_feature  
 FT FT /tag= b  
 FT FT /note= "encodes the beta-A4 domain"

FT FT WO9606927-A1.

PD 07-MAR-1996.

PF 28-AUG-1995; U10920.

PR 01-SEP-1994; US-299872.

PA (MERL) MERCK & CO INC.

PI Chen HY, Heavens RP, Singh G, Sirinathsinghji DJS;

PI Smith DW, Trumbauer ME, Van Der Ploeg LHT, Vongs A;

PI Zheng H;

PI WPI; 96-160358/16.

DR P-PSDB; R93556.

DR Transgenic animal expressing familial form of human amyloid

PT precursor protein - used to evaluate compounds affecting

PT Alzheimer's disease and other cognitive disorders

PT Example 1; Fig 7; 32pp; English.

PS CC T18082 represents exon 17 of the amyloid precursor protein (APP)

CC isoform 751 gene from a patient diagnosed with familial Alzheimer's

CC disease (FAD). The sequence given corresponds to the coding sequence

CC for amino acids 640-751 of FAD APP 751. A feature of FAD is a Val to

CC Ile substitution at posn. 698 of the full APP (encoded by bases 175

CC to 177 of this sequence). DNA encoding this sequence was used to

CC construct expression vectors for the prodn. of transgenic animals (esp.

CC mice) carrying the FAD APP 751 mutation. The transgenic animals are

CC useful for the evaluation of test cpds. affecting Alzheimer's disease

CC and other cognitive disorders and for identification of new targets

CC in Alzheimer's disease since the progression of the disease can be

CC followed gradually.

CC N.B. the V-I mutation encoded at base 175-177, is given in the

CC specification as a TTC codon (most probably this should be ATC).

CC Sequence 336 BP; 102 A; 69 C; 88 G; 77 T;

SQ

alignment\_scores:

Quality: 92.00 Length: 16

Ratio: 5.750 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-155-076-2 x T18082 ..

Align seg 1/1 to: T18082 from: 1 to: 336

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisHisGlnLys 16

|||||

40 GATCGAGATTCCGACATGACTGACTGAGGATATGAGTTCATCATCAAAAA 87

seq\_name: N\_Geneseq\_36:V20377

seq\_documentation\_block:

ID V20377 standard; DNA; 354 BP.

AC V20377;

DT 26-JUN-1998 (first entry)

DE DNA for APP C-terminal fragment mutant SPA4CT Thr43Ser.

KW Human; amyloid precursor protein; APP; carboxy-terminal fragment;

KW A4CT; mutant SPA4CT Thr43Ser; disease model; treatment;

KW Alzheimer's disease; ss.

OS Homo sapiens.

OS Synthetic.

FH Key Location/Qualifiers

FT CDS 1..354

FT FT /tag= a

FT FT /note= "stop codon not given"

PN WO9803643-A2.

PD 29-JAN-1998.

PF 17-JUL-1997; E03960.

PR 08-MAY-1997; GB-009239.

PR 22-JUL-1996; GB-015351.

PR 09-SEP-1996; GB-018804.

PA (SMIK) SMITHKLINE BEECHAM AUSTRALIA PTY LTD.

PA (SMIK) SMITHKLINE BEECHAM PHARMA GMBH.

PI Beyreuther K, Lichtenthaler S, Masters CL, Prior P;

PI WPI; 98-120768/11.

DR P-PSDB; W50027.

DR Construct containing sequence for mutant form of amyloid precursor

PT protein - or its C-terminal fragment, and related transgenic animals

PT or transformed cells, used for identifying potential drugs for

PT Alzheimer's disease

PS Claim 10; Page 10; 15pp; English.

CC The present sequence encodes the human amyloid precursor protein

CC (APP) C-terminal fragment (A4CT) mutant SPA4CT Thr43Ser.

CC The mutation results in a higher ratio of beta A4 1-42 to beta A4

CC 1-40, useful in disease models to identify potential drugs for the

CC treatment of Alzheimer's disease.

CC Sequence 354 BP; 89 A; 83 C; 99 G; 83 T;

SQ

alignment\_scores:

Quality: 92.00 Length: 16

Ratio: 5.750 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-155-076-2 x V20377 ..

Align seg 1/1 to: V20377 from: 1 to: 354

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisHisGlnLys 16

|||||

58 GATCGAGATTCCGACATGACTGACTGAGGATATGAGTTCATCATCAAAAA 105

seq\_name: N\_Geneseq\_36:V20380

seq\_documentation\_block:

ID V20380 standard; DNA; 354 BP.

AC V20380;

DT 26-JUN-1998 (first entry)

DE DNA for APP C-terminal fragment mutant SPA4CT Thr43Ala/Val46Phe.

KW Human; amyloid precursor protein; APP; carboxy-terminal fragment;

KW A4CT; mutant SPA4CT Thr43Ala/Val46Phe; disease model; treatment;

KW Alzheimer's disease; ss.

OS Homo sapiens.

OS Synthetic.

FH Key Location/Qualifiers

FT CDS 1..354

FT FT /tag= a

FT FT /note= "stop codon not given"

PN WO9803643-A2.

PD 29-JAN-1998.

PF 17-JUL-1997; E03960.

PR 08-MAY-1997; GB-009239.

PR 22-JUL-1996; GB-015351.

PR 09-SEP-1996; GB-018804.

PA (SMIK) SMITHKLINE BEECHAM AUSTRALIA PTY LTD.

PA (SMIK) SMITHKLINE BEECHAM PHARMA GMBH.

PI Beyreuther K, Lichtenthaler S, Masters CL, Prior P;

PI WPI; 98-120768/11.

DR P-PSDB; W50030.

DR Construct containing sequence for mutant form of amyloid precursor

PT protein - or its C-terminal fragment, and related transgenic animals

PT or transformed cells, used for identifying potential drugs for

PT Alzheimer's disease

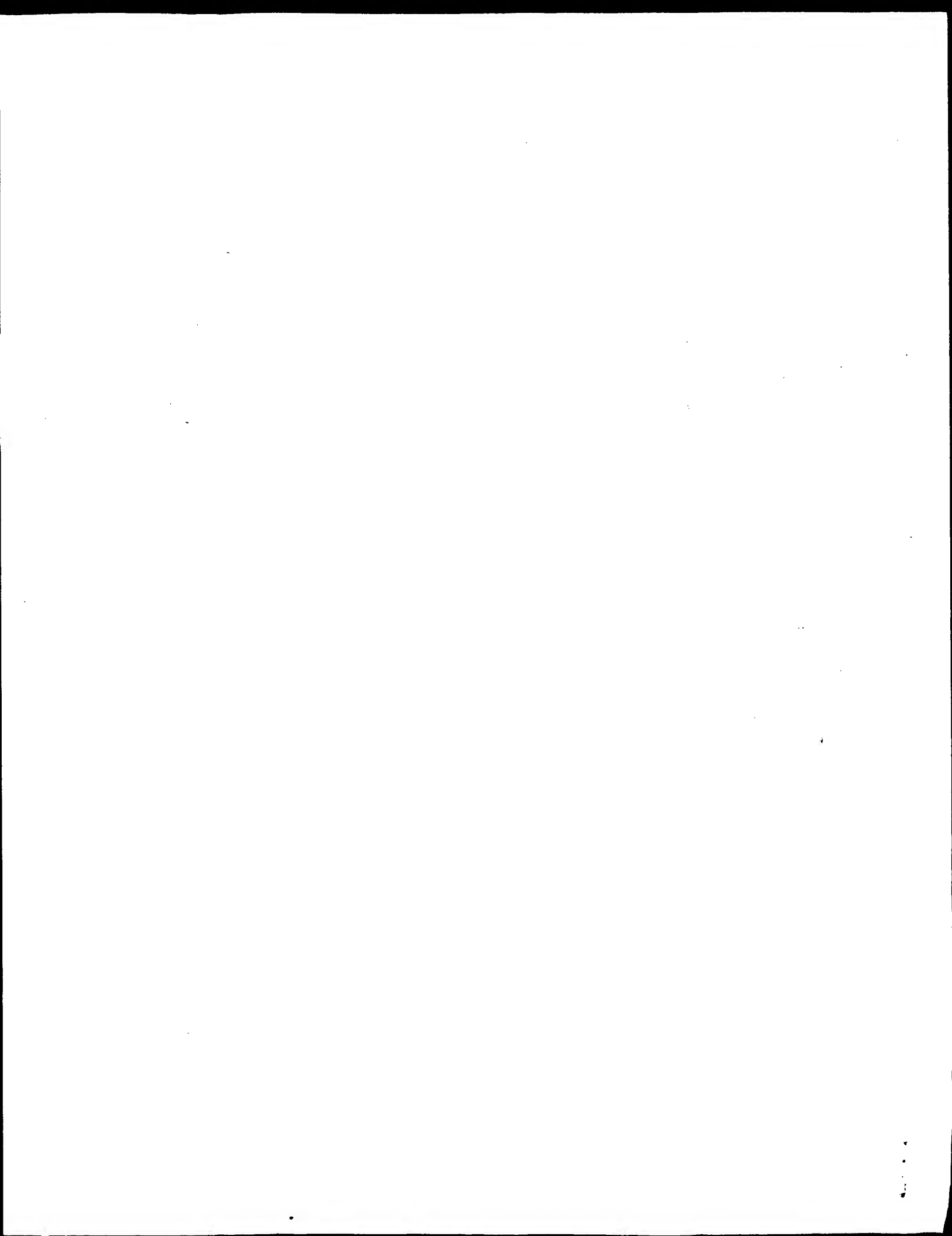
PS Claim 10: Page 11; 15pp; English.  
 CC The present sequence encodes the human amyloid precursor protein  
 CC (APP) C-terminal fragment (M4CT) mutant SP4ACT Thr43Ala/Val46Phe.  
 CC The mutation results in a higher ratio of beta A4 1-42 to beta A4  
 CC 1-40, useful in disease models to identify potential drugs for the  
 CC treatment of Alzheimer's disease.  
 SQ Sequence 354 BP; 91 A; 82 C; 98 G; 83 T;

alignment\_scores:  
 Quality: 92.00 Length: 16  
 Ratio: 5.750 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
 US-09-155-076-2 x V20380 ..

Align seg 1/1 to: V20380 from: 1 to: 354

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisHisGlnLys 16  
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 58 GATGCAGANTCCGACATGACTCAGGATATGAGTTTCATCATCAAAAA 105





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 About: Results were produced by the GenCore software, version 4.5.  
 Copyright (c) 1993-2000 CompuGen Ltd.

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/cgn2_6/ptodata/2/ina/5F_COMB.seq:US-08-422-333-3	+	92.00	285.70	2.0e-08	486
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/cgn2_6/ptodata/2/ina/5H_COMB.seq:US-08-422-333-5	+	92.00	274.88	8.1e-08	1521
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/cgn2_6/ptodata/2/ina/5Y_COMB.seq:US-08-422-333-22	+	92.00	260.01	5.4e-07	7298
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seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-636-876-15

seq_documentation_block:
; Sequence 15, Application US/08636876
; Patent No. 5777194
; GENERAL INFORMATION:
; APPLICANT: Scott, Richard W.
; APPLICANT: Reame, Andrew G.
; APPLICANT: Trusko, Stephen P.
; APPLICANT: Siman, Robert
; TITLE OF INVENTION: GENE-TARGETED NON-HUMAN MAMMAL WITH
; TITLE OF INVENTION: HUMANIZED AB SEQUENCE AND SWEDISH FAD MUTATIONS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street Suite 3100
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/636,876
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 02655/055001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-636-876-15

alignment_scores:
Quality: 92.00 Length: 16
Ratio: 5.750 Gaps: 0
Percent similarity: 100.000 Percent identity: 100.000

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8 GATGCAGAAATTCAGACATGATTCAGATATGAGTCCATCAAAA 55

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seq_documentation_block:
; Sequence 8, Application PC/TUS9404026
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Transgenic Animal Models for Alzheimer's Disease
; NUMBER OF SEQUENCES: 12

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CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower - 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-8402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04026
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Clough, Ph.D., David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 31188
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 189 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE: Human
ORGANISM: Human
PCT-US94-04026-8

alignment_scores:
Quality: 92.00 Length: 16
Ratio: 5.750 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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seq_documentation_block:
Sequence 3, Application US/08339708A
Patent No. 6037521
GENERAL INFORMATION:
APPLICANT: Sato, Masahiro
APPLICANT: Kobayashi, Takashi
APPLICANT: Tada, No. 6037521hiro
APPLICANT: Shoji, Mikio
APPLICANT: Kawarabayashi, Takeshi
TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR ALZHEIMER'S
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower - 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-8402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,708A
FILING DATE: 14-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 306026/93
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: SANDERCOCK, COLIN G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 026083/0159
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904135
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 297 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: homo sapiens
STRAIN: human brain
FEATURE:
NAME/KEY: CDS
LOCATION: 1..297
OTHER INFORMATION: /note= "1. human beta-amyloid
OTHER INFORMATION: precursor; 2. C-terminal peptide"
US-08-339-708A-3

alignment_scores:
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Ratio: 5.750 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
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seq_name: /cgn2_6/ptodata/2/ina/6_COMB.seq:US-08-339-708A-5

seq_documentation_block:
Sequence 5, Application US/08339708A
Patent No. 6037521
GENERAL INFORMATION:
APPLICANT: Sato, Masahiro
APPLICANT: Kobayashi, Takashi
APPLICANT: Tada, No. 6037521hiro
APPLICANT: Shoji, Mikio
APPLICANT: Kawarabayashi, Takeshi
TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR ALZHEIMER'S
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,708A
; FILING DATE: 14-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 306026/93
; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SANDERCOCK, COLIN G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 026083/0159
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 297 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: homo sapiens
; STRAIN: human brain
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..297
; OTHER INFORMATION: /note= "1. human beta-amyloid
; OTHER INFORMATION: precursor; 2. C-terminal peptide"
; US-08-339-708A-5

alignment_scores:
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1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisHisGlnLys 16
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1 GATGCAGAAATTCGACATGACTCAGGATATGAAAGTTTCATCATCAAAAA 48

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seq_documentation_block:
; Sequence 7, Application US/08339708A
; Patent No. 6037521
; GENERAL INFORMATION:
; APPLICANT: Sato, Masahiro
; APPLICANT: Takashi, Kobayashi
; APPLICANT: Tada, No. 6037521hiro
; APPLICANT: Shoji, Mikio
; APPLICANT: Kawarabayashi, Takeshi
; TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR ALZHEIMER'S
; TITLE OF INVENTION: DISEASE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,708A
; FILING DATE: 14-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 306026/93
; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SANDERCOCK, COLIN G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 026083/0159
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 297 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: homo sapiens
; STRAIN: human brain
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..297
; OTHER INFORMATION: /note= "1. human beta-amyloid
; OTHER INFORMATION: precursor; 2. C-terminal peptide"
; US-08-339-708A-7

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1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisHisGlnLys 16
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1 GATGCAGAAATTCGACATGACTCAGGATATGAAAGTTTCATCATCAAAAA 48

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seq_documentation_block:
; Patent No. 5220013
; APPLICANT: PONTE, PHYLLIS A.;CORDELL, BARBARA
; TITLE OF INVENTION: DNA SEQUENCE USEFUL FOR THE DETECTION
; OF ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/444,118
; FILING DATE: 30-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 87,002
; FILING DATE: 18-AUG-1987
; APPLICATION NUMBER: 8,810
; FILING DATE: 30-JAN-1987
; APPLICATION NUMBER: 948,376
; FILING DATE: 31-DEC-1986
; APPLICATION NUMBER: 932,193
; FILING DATE: 17-NOV-1986
; SEQ ID NO:9:

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; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,708A
; FILING DATE: 14-NOV-1994
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: JP 306026/93
; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SANDERCOCK, COLIN G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 026083/0159
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: homo sapiens
; STRAIN: human brain
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..309
; OTHER INFORMATION: /note= "1. human beta-amyloid
; precursor; 2. C-terminal peptide"
; US-08-339-708A-9

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  Ratio: 5.750 Gaps: 0
  Percent Similarity: 100.000 Percent Identity: 100.000

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seq_name: /cgn2_6/ptodata/2/ina/6_COMB.seq:US-08-339-708A-11

seq_documentation_block:
; Sequence 11, Application US/08339708A
; Patent No. 6037521
; GENERAL INFORMATION:
; APPLICANT: Sato, Masahiro
; APPLICANT: Takashi, Kobayashi
; APPLICANT: Tada, No. 6037521hiro
; APPLICANT: Shoji, Mikio
; APPLICANT: Kawarabayashi, Takeshi
; TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR ALZHEIMER'S DISEASE

; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,708A
; FILING DATE: 14-NOV-1994
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: JP 306026/93
; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SANDERCOCK, COLIN G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 026083/0159
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: homo sapiens
; STRAIN: human brain
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..309
; OTHER INFORMATION: /note= "1. human beta-amyloid
; precursor; 2. C-terminal peptide"
; US-08-339-708A-9

alignment_scores:
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  Percent Similarity: 100.000 Percent Identity: 100.000

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seq_name: /cgn2_6/ptodata/2/ina/6_COMB.seq:US-08-339-708A-9

seq_documentation_block:
; Sequence 9, Application US/08339708A
; Patent No. 6037521
; GENERAL INFORMATION:
; APPLICANT: Sato, Masahiro
; APPLICANT: Takashi, Kobayashi
; APPLICANT: Tada, No. 6037521hiro
; APPLICANT: Shoji, Mikio
; APPLICANT: Kawarabayashi, Takeshi
; TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR ALZHEIMER'S DISEASE

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;; TITLE OF INVENTION: DISEASE
;; NUMBER OF SEQUENCES: 23
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Foley & Lardner
;; STREET: 3000 K Street, N.W., suite 500
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20007-5109
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
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;; APPLICATION NUMBER: US/08-339,708A
;; FILING DATE: 14-NOV-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 306026/93
;; FILING DATE: 12-NOV-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: SANDERCOCK COLIN G.
;; REGISTRATION NUMBER: 31,298
;; REFERENCE/DOCKET NUMBER: 026083/0159
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202)672-5300
;; TELEFAX: (202)672-5399
;; TELEX: 904136
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 309 base pairs
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;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA to mRNA
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; ORGANISM: homo sapiens
;; STRAIN: human brain
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1..309
;; OTHER INFORMATION: /note= "1. human beta-amyloid
;; OTHER INFORMATION: precursor; 2. C-terminal peptide"
US-08-339-708A-11

alignment_scores:
  Quality: 92.00 Length: 16
  Ratio: 5.750 Gaps: 0
  Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-09-155-076-2 x US-08-339-708A-11
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seq_documentation_block:
; Sequence 2, Application US/08729345
; Patent No. 5849999
; GENERAL INFORMATION:
; APPLICANT: Neve, Rachael L.
; APPLICANT: Berger-Sweeney, Joanne
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMAL
; TITLE OF INVENTION: EXPRESSING FLAG-APP-C100 FUSION PROTEIN
; NUMBER OF SEQUENCES: 9
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;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Fish & Richardson P.C.
;; STREET: 225 Franklin Street
;; CITY: Boston
;; STATE: MA
;; COUNTRY: US
;; ZIP: 02110-2804
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/729,345
;; FILING DATE: 16-OCT-1996
;; CLASSIFICATION: 800
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Clark, Paul T
;; REGISTRATION NUMBER: 30,162
;; REFERENCE/DOCKET NUMBER: 04843/027001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-542-5070
;; TELEFAX: 617-542-8906
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 354 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
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US-08-729-345-2

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55 GATGAGAAATTCGACATGACTCAGGATATGAAGTTCATCATCAAAA 102
seq_name: /cgn2_6/ptodata/2/1na/backfiles1.seq:5187153-3
seq_documentation_block:
; Patent No. 5187153
; APPLICANT: CORDELL, BARBARA; SCHILLING, JAMES W.; KATUNUMA, NOBUHIKO
; TITLE OF INVENTION: METHODS OF TREATMENT USING ALZHEIMER'S
; AMYLOID POLYPEPTIDE DERIVATIVES
; NUMBER OF SEQUENCES: 33
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/502,273
; FILING DATE: 29-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 361,912
; FILING DATE: 06-JUN-1989
; APPLICATION NUMBER: 359,911
; FILING DATE: 12-MAY-1989
; APPLICATION NUMBER: 87,002
; FILING DATE: 18-AUG-1987
; APPLICATION NUMBER: 8,810
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us-09-155-076-2\_1.rni

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;
; FILING DATE: 30-JAN-1987
; APPLICATION NUMBER: 948,376
; FILING DATE: 31-DEC-1986
; APPLICATION NUMBER: 932,193
; FILING DATE: 17-NOV-1986
; SEQ ID NO:3:
5187153-3
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alignment_scores:
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    Percent Similarity: 100.000    Percent Identity: 100.000

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Align seg 1/1 to: 5187153-3 from: 1 to: 485
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seq_documentation_block:
; Patent No. 5220013
; APPLICANT: PONTE, PHYLLIS A.;CORDELL, BARBARA
; TITLE OF INVENTION: DNA SEQUENCE USEFUL FOR THE DETECTION
; OF ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 30
; CURRENT APPLICATION DATA:
; FILING DATE: 30-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 87,002
; FILING DATE: 18-AUG-1987
; APPLICATION NUMBER: 8,810
; FILING DATE: 30-JAN-1987
; APPLICATION NUMBER: 948,376
; FILING DATE: 31-DEC-1986
; APPLICATION NUMBER: 932,193
; FILING DATE: 17-NOV-1986
; SEQ ID NO:3:
5220013-3
    LENGTH: 486

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    Ratio: 5.750       Gaps: 0
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1 AspaLaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
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241 GATGCGAATTCGACATGACTCAGGATATGAAGTTCATCAAAAA 288
seq_name: /cgn2_6/ptodata/2/ina/backfiles1.seq:5223482-3

seq_documentation_block:
; Patent No. 5223482
; APPLICANT: SCHILLING, JAMES W.;PONTE, PHYLLIS A.;CORDELL,
; BARBARA
; TITLE OF INVENTION: RECOMBINANT ALZHEIMER'S PROTEASE
; INHIBITORY AMYLOID PROTEIN AND METHOD OF USE
; NUMBER OF SEQUENCES: 34
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 948,376
; FILING DATE: 31-DEC-1986
; APPLICATION NUMBER: 932,193
; FILING DATE: 17-NOV-1986
; SEQ ID NO:3:
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    LENGTH: 485

alignment_scores:
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    Ratio: 5.750       Gaps: 0
    Percent Similarity: 100.000    Percent Identity: 100.000

alignment_block:
US-09-155-076-2 x 5187153-3 ..
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1 AspaLaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
|||||
240 GATGCGAATTCGACATGACTCAGGATATGAAGTTCATCAAAAA 287
seq_name: /cgn2_6/ptodata/2/ina/backfiles1.seq:5220013-3

seq_documentation_block:
; Patent No. 5220013
; APPLICANT: PONTE, PHYLLIS A.;CORDELL, BARBARA
; TITLE OF INVENTION: DNA SEQUENCE USEFUL FOR THE DETECTION
; OF ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 30
; CURRENT APPLICATION DATA:
; FILING DATE: 30-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 87,002
; FILING DATE: 18-AUG-1987
; APPLICATION NUMBER: 8,810
; FILING DATE: 30-JAN-1987
; APPLICATION NUMBER: 948,376
; FILING DATE: 31-DEC-1986
; APPLICATION NUMBER: 932,193
; FILING DATE: 17-NOV-1986
; SEQ ID NO:3:
5220013-3
    LENGTH: 486

alignment_scores:
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    Ratio: 5.750       Gaps: 0
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US-09-155-076-2 x 5220013-3 ..
Align seg 1/1 to: 5220013-3 from: 1 to: 486
1 AspaLaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
|||||
241 GATGCGAATTCGACATGACTCAGGATATGAAGTTCATCAAAAA 288
seq_name: /cgn2_6/ptodata/2/ina/backfiles1.seq:5223482-3

seq_documentation_block:
; Patent No. 5223482
; APPLICANT: SCHILLING, JAMES W.;PONTE, PHYLLIS A.;CORDELL,
; BARBARA
; TITLE OF INVENTION: RECOMBINANT ALZHEIMER'S PROTEASE
; INHIBITORY AMYLOID PROTEIN AND METHOD OF USE
; NUMBER OF SEQUENCES: 34
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 948,376
; FILING DATE: 31-DEC-1986
; APPLICATION NUMBER: 932,193
; FILING DATE: 17-NOV-1986
; SEQ ID NO:3:
5223482-3
    LENGTH: 486

alignment_scores:
    Quality: 92.00      Length: 16
    Ratio: 5.750       Gaps: 0
    Percent Similarity: 100.000    Percent Identity: 100.000

alignment_block:
US-09-155-076-2 x 5223482-3 ..
Align seg 1/1 to: 5223482-3 from: 1 to: 486
1 AspaLaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
|||||
241 GATGCGAATTCGACATGACTCAGGATATGAAGTTCATCAAAAA 288
seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-268-348A-9

seq_documentation_block:
; Sequence 9, Application US/08268348A
; Patent No. 5750374
; GENERAL INFORMATION:
; APPLICANT: Dobeli, Heinz
; APPLICANT: Draeger, Nicholas
; APPLICANT: Trotman, Gerda H
; APPLICANT: Jakob, Peter
; APPLICANT: Stuber, Dietrich
; TITLE OF INVENTION: Process for Producing Hydrophobic
; TITLE OF INVENTION: Polypeptides and Proteins, and Fusion Proteins for Use in
; TITLE OF INVENTION: Producing Same
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/268,348A
; FILING DATE: 29-JUN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93110755.1
; FILING DATE: 06-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Parise, John P.
; REGISTRATION NUMBER: 34,403
; REFERENCE/DOCKET NUMBER: 4105/157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 235-6326
; TELEFAX: (201) 235-3500
```

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; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 520 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 115..516
;     OTHER INFORMATION: /product= "Amyloid Protein AA"
US-08-268-348A-9

alignment_scores:
  Quality: 92.00      Length: 16
  Ratio: 5.750       Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
US-09-155-076-2 x US-08-268-348A-9  ..
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1 AspalagluPheArghHisAspSerGlyTyrGluValHisGlnLys 16
|||||
388 GATCGGAGTTCGTCATGATTCAGGCTATGAAGTCCACCATCAAAAA 435

seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-480-498-3

seq_documentation_block:
; Sequence 3, Application US/08480498
; Patent No. 5744346
; GENERAL INFORMATION:
;   APPLICANT: Chrysler, Susanna M.S.
;   APPLICANT: Sinha, Sukanto
;   APPLICANT: Kelm, Pamela S.
;   APPLICANT: Anderson, John P.
;   TITLE OF INVENTION: Beta-Secretase
;   NUMBER OF SEQUENCES: 3
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend Kourie and Crew
;   STREET: One Market Plaza, Steuart Tower, Suite 2000
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94105
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/480,498
;   FILING DATE:
;   CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Heslin, James M.
;   REGISTRATION NUMBER: 29,541
;   REFERENCE/DOCKET NUMBER: 015270-002200
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-326-2400
;   TELEFAX: 415-326-2422
;   INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 1521 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;     MOLECULE TYPE: DNA (genomic)
US-08-480-498-3
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alignment_scores:
  Quality: 92.00      Length: 16
  Ratio: 5.750       Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
US-09-155-076-2 x US-08-480-498-3  ..
Align seg 1/1 to: US-08-480-498-3 from: 1 to: 1521

1 AspalagluPheArghHisAspSerGlyTyrGluValHisGlnLys 16
|||||
1222 GATCGAGAATTCGACATCATCAGGATATGAAGTTCATCAAAAA 1269
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us-09-155-076-2\_1.rni

Wed Sep 13 08:11:41 2000



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 13, 2000, 02:22:33 ; Search time 18.63 Seconds  
(without alignments)  
53.148 Million cell updates/sec

Title: US-09-155-076-2

Perfect score: 92  
Sequence: 1 DAEFRHDSGYEVHHQK 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 178050 seqs, 61884766 residues

Total number of hits satisfying chosen parameters: 178050

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_64.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	92	100.0	42	2	PN0512
2	92	100.0	57	2	E60045
3	92	100.0	57	2	F60045
4	92	100.0	57	2	G60045
5	92	100.0	57	2	D60045
6	92	100.0	57	2	A60045
7	92	100.0	57	2	B60045
8	92	100.0	82	2	P00438
9	92	100.0	695	1	A49795
10	92	100.0	770	1	QH0044
11	77	93.7	747	2	JH0773
12	73	79.3	33	2	S23094
13	73	79.3	695	2	A27485
14	73	79.3	695	2	S00550
15	50.5	54.9	284	2	S04723
16	50.5	54.9	327	2	S11435
17	50.5	54.9	519	2	PC1072
18	50.5	54.9	1555	2	JT0959
19	49.5	53.8	971	2	D70128
20	48.5	52.7	330	2	A26205
21	48.5	52.7	3063	2	JS0166
22	45.5	49.5	313	2	JT0960
23	45.5	49.5	427	2	JA0073
24	44	47.8	274	2	A64978
25	43	46.7	629	2	G60385
26	42.5	46.2	539	2	T39150
27	42	45.7	113	2	A64064
28	42	45.7	373	2	D64971
29	42	45.7	373	2	S28470

30 42 45.7 392 2 T19869  
31 42 45.7 667 2 S64915  
32 42 45.7 1240 2 S21086  
33 41 44.6 182 2 S33992  
34 41 44.6 213 2 S43723  
35 41 44.6 213 2 S43721  
36 41 44.6 213 2 S43722  
37 41 44.6 367 2 T39353  
38 41 44.6 494 2 C70940  
39 41 44.6 527 2 A43938  
40 41 44.6 672 2 S52673  
41 41 44.6 1918 2 S43719  
42 41 44.6 1920 2 S43720  
43 41 44.6 1926 2 S01169  
44 40.5 44.0 559 2 F71420  
45 40 43.5 155 2 T20945

#### ALIGNMENTS

##### RESULT 1

PN0512  
beta-amyloid protein - guinea pig (fragment)  
C:Species: Cavia porcellus (guinea pig)  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 17-Mar-1999  
C:Accession: PN0512  
R:Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno  
Biochem. Biophys. Res. Commun. 193, 624-630, 1993  
A:Title: Receptor-mediated specific biological activity of a beta-amyloid protein fra  
A:Reference number: PN0512; MUID:93290653  
A:Accession: PN0512  
A:Molecule type: protein  
A:Residues: 1-42 <SHI>  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas  
C:Keywords: alternative splicing; amyloid

Query Match 100.0%; Score 92; DB 2; Length 42;  
Best Local Similarity 100.0%; Pred. No. 1.5e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16  
|||||  
Db 1 DAEFRHDSGYEVHHQK 16

##### RESULT 2

E60045  
Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)  
C:Species: Ovis sp. (sheep)  
C:Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
C:Accession: E60045  
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d  
A:Reference number: A60045; MUID:92017079  
A:Accession: E60045  
A:Molecule type: mRNA  
A:Residues: 1-57 <JOH>  
A:Cross-references: EMBL:X56130  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas  
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 92; DB 2; Length 57;  
Best Local Similarity 100.0%; Pred. No. 2.1e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16  
|||||  
Db 6 DAEFRHDSGYEVHHQK 21

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Query Match      100.0%; Score 92; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
    |||
DB 6 DAEFRHDSGYEVHHQK 21
    |||

RESULT 6
A60045
Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: A60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079
A:Accession: A60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56125
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match      100.0%; Score 92; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
    |||
DB 6 DAEFRHDSGYEVHHQK 21
    |||

RESULT 7
B60045
Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)
C:Species: Ursus maritimus (polar bear)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C:Accession: B60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079
A:Accession: B60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56128; NID:92165; PIDN:CAA39593.1; PID:g2166
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match      100.0%; Score 92; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
    |||
DB 6 DAEFRHDSGYEVHHQK 21
    |||

RESULT 8
PQ0438
Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C:Accession: PQ0438; C60045
R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.
Biochem. Biophys. Res. Commun. 188, 905-911, 1992
A:Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precurs
A:Reference number: PQ0438; MUID:93075180

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A:Accession: PQ0438  
 A:Molecule type: DNA  
 A:Residues: 1-82 <DAV>  
 A:Cross-references: GB:M83558; GB:M83657  
 R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
 Brain Res. Mol. Brain Res. 10, 299-305, 1991  
 A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,  
 A:Reference number: A60045; MUID:92017079  
 A:Accession: C60045  
 A:Molecule type: mRNA  
 A:Residues: 12-68 <JOH>  
 A:Cross-references: EMBL:X56129  
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 100.0%; Score 92; DB 2; Length 82;  
 Best Local Similarity 100.0%; Pred. NO. 3.2e-08;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHOK 16  
 |||||  
 Db 17 DAEFRHDSGYEVHOK 32

RESULT 9  
 A49795  
 Alzheimer's disease amyloid beta protein precursor - crab-eating macaque  
 C:Species: Macaca fascicularis (crab-eating macaque)  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C:Accession: A49795  
 R:Podlisky, M.B.; Tolan, D.R.; Selkoe, D.J.  
 Am. J. Pathol. 138, 1423-1435, 1991  
 A:Title: Homology of the amyloid beta protein precursor in monkey and human supports a  
 A:Reference number: A49795; MUID:91273117  
 A:Accession: A49795  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-695 <POD>  
 A:Cross-references: GB:M56727; NID:g342062; PIDN:AAA36829.1; PID:g342063  
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
 C:Keywords: alternative splicing

Query Match 100.0%; Score 92; DB 1; Length 695;  
 Best Local Similarity 100.0%; Pred. NO. 3.1e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHOK 16  
 |||||  
 Db 597 DAEFRHDSGYEVHOK 612

RESULT 10  
 QRHUA  
 Alzheimer's disease amyloid beta protein precursor - human  
 N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor X1a inhibi  
 N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular  
 protein precursor splice form APP(770)  
 C:Species: Homo sapiens (man)  
 C:Date: 30-Jun-1987 #sequence\_revision 28-Jul-1995 #text\_change 24-Nov-1999  
 C:Accession: S02260; S05194; A32277; A33260; A35486; I39451; I39453; I39455; I39456; A44  
 468; A28583; A29302; A60805; J10038; S06121; A60355; A59011; A38384; S29076; S38252; S3  
 R:Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayne, R.M.; Unterbeck, A.; Bey  
 Nucleic Acids Res. 17, 517-522, 1989  
 A:Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded b  
 A:Reference number: S02260; MUID:89128427  
 A:Accession: S02260  
 A:Molecule type: DNA  
 A:Residues: 1-288, 'V', 365-770 <LEM>  
 A:Cross-references: EMBL:X13466  
 A:Note: alternative splice form APP(695)  
 R:Lemaire, H.G.

submitted to the EMBL Data Library, November 1988  
 A:Reference number: S05194  
 A:Accession: S05194  
 A:Molecule type: DNA  
 A:Residues: 1-14, 'VW', 17-288, 'V', 365-770 <LEM2>  
 A:Cross-references: EMBL:X13466; NID:g35598; PIDN:CAA31830.1; PID:g871360  
 A:Note: alternative splice form APP(695)  
 R:La Fauti, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.  
 Biochem. Biophys. Res. Commun. 159, 297-304, 1989  
 A:Title: Characterization of the 5'-end region and the first two exons of the beta-pr  
 A:Reference number: A32277; MUID:89165870  
 A:Accession: A32277  
 A:Molecule type: DNA  
 A:Residues: 1-75 <LAF>  
 A:Cross-references: GB:M24546; GB:M24547; NID:g341202; PIDN:AAC13654.1; PID:g516074  
 R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.  
 Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989  
 A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows simila  
 A:Reference number: A33260; MUID:89392030  
 A:Accession: A33260  
 A:Molecule type: DNA  
 A:Residues: 656-737 <JOH>  
 A:Cross-references: GB:M29270; NID:g178863; PIDN:AAA51768.1; PID:g178865  
 R:Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B  
 Biochem. Biophys. Res. Commun. 170, 301-307, 1990  
 A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid  
 A:Reference number: A35486; MUID:90321244  
 A:Accession: A35486  
 A:Molecule type: DNA  
 A:Residues: 672-710 <PRE1>  
 A:Note: 693-Gln was found in DNA isolated from HCHWA-D patients  
 R:Yoshikawa, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.  
 Gene 87, 257-263, 1990  
 A:Title: Genomic organization of the human amyloid beta-protein precursor gene.  
 A:Reference number: I39451; MUID:90236318  
 A:Accession: I39451  
 A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/  
 A:Molecule type: DNA  
 A:Residues: 1-770 <YOS1>  
 A:Cross-references: GB:M33112; NID:g178613; PIDN:AAB59502.1; PID:g178616  
 A:Accession: I39451  
 A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/  
 A:Molecule type: DNA  
 A:Residues: 1-530, 'QWLMPVTPAFWEAKVGR' <YOS2>  
 A:Cross-references: GB:M34875; NID:g178608; PIDN:AAB59501.1; PID:g178615  
 R:Yoshikawa, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.  
 Gene 102, 291-299, 1991  
 A:Reference number: A59020; MUID:91340168  
 A:Contents: annotation; erratum  
 A:Note: revised physical map for reference I39451  
 R:Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Du  
 Science 248, 1124-1126, 1990  
 A:Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemo  
 A:Reference number: I39453; MUID:90260663  
 A:Accession: I39453  
 A>Status: translated from GB/EMBL/DBDJ  
 A:Molecule type: DNA  
 A:Residues: 656-737 <LEF>  
 A:Cross-references: GB:M37896; NID:g178618; PIDN:AAA51727.1; PID:g178620  
 R:Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.  
 Science 254, 97-99, 1991  
 A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzhe  
 A:Reference number: I59562; MUID:92022553  
 A:Accession: I59562  
 A>Status: translated from GB/EMBL/DBDJ  
 A:Molecule type: DNA  
 A:Residues: 689-716, 'F', 718-737 <MUR>  
 A:Cross-references: GB:S57665; NID:g236720; PIDN:AAB19991.1; PID:g236721  
 R:Kamino, K.; Orr, H.T.; Payami, H.; Wijsman, E.M.; Alonso, M.E.; Pulst, S.M.; Anders  
 arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukula, W.; Larson, E.; Heston, L.L.; Mart  
 Am. J. Hum. Genet. 51, 998-1014, 1992  
 A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for t

A:Cross-references: GB:X06989; EMBL:Y00297; NID:g28720; PIDN:CAA30050.1; PID:g28721  
A:Accession: A44017; MUID:93035397  
A:Molecule type: DNA  
A:Residues: 687-718 <KAM1>  
A:Cross-references: GB:S4513; NID:g257377; PIDN:AA23645.1; PID:g257378  
A:Experimental source: familial Alzheimer disease family SB  
A:Note: sequence extracted from NCBI backbone (NCBIP:115374)  
A:Accession: B44017  
A:Molecule type: mRNA  
A:Residues: 687-718 <KAM2>  
A:Cross-references: GB:S45136; NID:g257379; PIDN:AA23646.1; PID:g257380  
A:Experimental source: familial Alzheimer disease family LIT  
A:Note: sequence extracted from NCBI backbone (NCBIP:115376)  
A:Note: this sequence has a silent mutation  
R:Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;  
Nature 325, 733-736, 1987  
A:Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface  
A:Reference number: A03134; MUID:87114572  
A:Accession: A03134  
A:Molecule type: mRNA  
A:Residues: 1-288, 'V', 365-770 <KAN>  
A:Cross-references: GB:Y00264; NID:g28525; PIDN:CAA68374.1; PID:g28526  
A:Note: alternative splice form APP(695)  
R:Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.  
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987  
A:Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular  
A:Reference number: A29030; MUID:87231971  
A:Accession: A29030  
A:Molecule type: mRNA  
A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>  
A:Cross-references: GB:M16765; NID:g178539; PIDN:AAA51722.1; PID:g178540  
A:Note: the authors translated the codon GAG for residue 647 as Asp  
R:Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.  
Science 235, 877-880, 1987  
A:Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid  
A:Reference number: A47584; MUID:87120328  
A:Accession: A47584  
A:Molecule type: mRNA  
A:Residues: 674-756, 'S', 758-770 <GOL>  
A:Cross-references: GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:g178707  
A:Experimental source: brain  
R:Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke  
Science 235, 880-884, 1987  
A:Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th  
A:Reference number: A47585; MUID:87120329  
A:Accession: A47585  
A:Molecule type: mRNA  
A:Residues: 674-703 <TANI>  
A:Cross-references: GB:M15532; NID:g177957; PIDN:AAA51564.1; PID:g177958  
R:Dyrks, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muelle  
EMBO J. 7, 949-957, 1988  
A:Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 prec  
A:Reference number: S02638; MUID:88296437  
A:Accession: S02638  
A:Molecule type: mRNA  
A:Residues: 675-678 <DYR>  
R:Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve  
Nature 331, 528-530, 1988  
A:Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat  
A:Reference number: S00707; MUID:88122640  
A:Accession: S00707  
A:Molecule type: mRNA  
A:Residues: 286-344, 'I', 365-366 <TAN2>  
A:Cross-references: EMBL:X06988; NID:g28817; PIDN:CAA30042.1; PID:g2929612  
A:Experimental source: promyelocytic leukemia cell line HL60  
A:Note: alternative splice form APP(751)  
R:Ponte, P.; Gonzalez-DeWhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Da  
Nature 331, 525-527, 1988  
A:Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibit  
A:Reference number: S00925; MUID:88122639  
A:Accession: S00925  
A:Molecule type: mRNA  
A:Residues: 1-344, 'I', 365-770 <PO2>





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OM protein - protein search, using sw model

Run on: September 13, 2000, 02:24:31 ; Search time 10.66 Seconds  
(without alignments)  
46.513 Million cell updates/sec

Title: US-09-155-076-2

Perfect score: 92

Sequence: 1 DAEFRHDSGYEVHHQK 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 85661 seqs, 30989116 residues

Total number of hits satisfying chosen parameters: 85661

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_38:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	92	100.0	57	1	A4_PIG	Q29023	sus scrofa
2	92	100.0	57	1	A4_URSUMA	Q29149	ursus marit
3	92	100.0	58	1	A4_CANFA	Q28280	canis famil
4	92	100.0	58	1	A4_RABIT	Q28748	oryctolagus
5	92	100.0	58	1	A4_SHEEP	Q28757	ovis aries
6	92	100.0	59	1	A4_BOVIN	Q28053	bos taurus
7	92	100.0	751	1	A4_SALSC	Q285241	saimiri sci
8	92	100.0	770	1	A4_HUMAN	P05067	homo sapien
9	73	79.3	770	1	A4_MOUSE	P12023	mus musculu
10	73	79.3	770	1	A4_RAT	P11897	rattus norv
11	50.5	54.9	284	1	POLG_PVYVO	P08592	potato viru
12	50.5	54.9	327	1	POLG_PVYCH	P21294	potato viru
13	49.5	53.8	971	1	V228_BORBU	OS1246	borrelia bu
14	48.5	52.7	330	1	COAT_PENV	P07993	pepper mott
15	48.5	52.7	3063	1	POLG_PVYN	P18247	p genome po
16	44	47.8	274	1	YOHM_ECOLI	P76425	escherichia
17	43	46.7	629	1	FRE7_YEAST	Q12333	saccharomyc
18	42	45.7	112	1	FER_HAEIN	P44428	haemophilus
19	42	45.7	315	1	HXB1_CYPCA	Q30346	cyprinus ca
20	42	45.7	373	1	HXB4_ECOLI	P32084	escherichia
21	42	45.7	667	1	EM70_YEAST	P32802	saccharomyc
22	42	45.7	1240	1	B3A2_HUMAN	P04920	homo sapien
23	41	44.6	494	1	COBQ_MYCTU	Q53677	mycobacteri
24	41	44.6	848	1	Z33A_HUMAN	Q06730	homo sapien
25	41	44.6	1926	1	LPH_RABIT	P09849	oryctolagus
26	40	43.5	403	1	NOF2_DROME	P15297	drosophila
27	40	43.5	418	1	MTML_WORSP	P11408	moraxella s
28	40	43.5	730	1	CATR_ASPPG	P35303	aspergillus
29	40	43.5	984	1	NOF_DROME	P16320	drosophila
30	39.5	42.9	3061	1	POLG_PVYHU	Q02963	p genome po
31	39	42.4	182	1	Y4YS_RHISN	P55727	rhibobium s
32	39	42.4	372	1	GM4D_YEREN	Q56872	yersinia en
33	38	41.3	260	1	RS4_YEAST	P05753	saccharomyc

34 38 41.3 372 1 GM4D\_VIBCH  
35 38 41.3 492 1 CAT1\_TOBAC  
36 38 41.3 630 1 HCYA\_EURCA  
37 38 41.3 955 1 VP2\_BT17  
38 38 41.3 1398 1 MEPI\_YEAST  
39 37.5 40.8 506 1 Z157\_HUMAN  
40 37.5 40.8 653 1 YDCP\_ECOLI  
41 37 40.2 131 1 DLX4\_ELECC  
42 37 40.2 208 1 YIMA\_STRCO  
43 37 40.2 351 1 NIFV\_FRAAL  
44 37 40.2 401 1 NIFV\_FRASP  
45 37 40.2 489 1 YEN5\_YEAST

Q56598 vibrio chol  
P49319 nicotiana t  
P14750 eurytelma c  
P05309 bluetongue  
P43638 saccharomyc  
P51786 homo sapien  
P76104 escherichia  
P87394 eleutheroda  
Q04296 streptomyce  
Q47884 frankia aln  
P54610 frankia sp.  
P39970 saccharomyc

## ALIGNMENTS

RESULT 1  
A4\_PIG STANDARD; PRT; 57 AA.  
AC Q29023;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID  
DE PROTEIN (BETA-APP)] (FRAGMENT).  
GN APP.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
RN [1]  
SEQUENCE FROM N.A.  
RP RP  
RC TISSUE-BRAIN.  
RX MEDLINE; 92017079.  
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;  
RT "Conservation of the sequence of the Alzheimer's disease amyloid  
RT peptide in dog, polar bear and five other mammals by cross-species  
RT polymerase chain reaction analysis.";  
RL Brain Res. Mol. Brain Res. 10:399-305(1991).  
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO  
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN  
CC G(O) (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.  
CC -----  
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CC -----  
CC EMBL; X56127; CAA39592.1; -.  
CC HSSP; P05067; IAML.  
DR PROSITE; PS00319; A4\_EXTRA; PARTIAL.  
DR PROSITE; PS00320; A4\_INTRA; PARTIAL.  
KW Glycoprotein; Amyloid; Neutrone; Transmembrane.  
FT CHAIN 1 1  
FT DOMAIN <1 33  
FT TRANSMEM 34 57  
FT NON\_TER 57 57  
SQ SEQUENCE 57 AA; 6172 MW; 84209D98E8A82DFA CRC64;

BETA-AMYLOID PROTEIN (POTENTIAL).  
EXTRACELLULAR (POTENTIAL).  
POTENTIAL.

Query Match 100.0%; Score 92; DB 1; Length 57;  
Best Local Similarity 100.0%; Pred. No. 1.8e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16

|||||

Db 6 DAEFRHDSGYEVHHQK 21

Wed Sep 13 08:11:42 2000

us-09-155-076-2\_1.rsp

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RESULT 2
A4_URMSA STANDARD; PRT; 57 AA.
AC Q29149;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID
DE PROTEIN (BETA-APP)] (FRAGMENT).
GN APP.
OS Ursus maritimus (Polar bear) (Thalarchos maritimus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Thalarchos.
[1]
RN SEQUENCE FROM N.A.
RP TISSUE-BRAIN;
RX MEDLINE; 92017079.
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
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CC -----
DR EMBL; X56125; CRA39590.1; -
DR HSP; P05067; IAML.
DR PROSITE; PS00319; A4 EXTRA; PARTIAL.
DR PROSITE; PS00320; A4 INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1
FT CHAIN 7 49 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 58 POTENTIAL.
FT NON_TER 58
FT SEQUENCE 57 AA; 6172 MW; 84209D88EBA82DFA CRC64;
SQ
Query Match 100.0%; Score 92; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAFFRHDGSEYVHHQK 16
DB 6 DAFFRHDGSEYVHHQK 21
| | | | | | | | | | | | | | | |
RESULT 3
A4_CANFA STANDARD; PRT; 58 AA.
AC Q28280;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID
DE PROTEIN (BETA-APP)] (FRAGMENT).
GN APP.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
[1]
RN SEQUENCE FROM N.A.
RP TISSUE-BRAIN;
RX MEDLINE; 92017079.
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
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CC -----
DR EMBL; X56128; CRA39593.1; -
DR HSP; P05067; IAML.
DR PROSITE; PS00319; A4 EXTRA; PARTIAL.
DR PROSITE; PS00320; A4 INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1
FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 57 POTENTIAL.
FT NON_TER 57
FT SEQUENCE 57 AA; 6172 MW; 84209D88EBA82DFA CRC64;
SQ
Query Match 100.0%; Score 92; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAFFRHDGSEYVHHQK 16
DB 6 DAFFRHDGSEYVHHQK 21
| | | | | | | | | | | | | | | |
RESULT 4
A4_RABIT STANDARD; PRT; 58 AA.
AC Q28748;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID
DE PROTEIN (BETA-APP)] (FRAGMENT).
GN APP.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
[1]
RN SEQUENCE FROM N.A.
RP TISSUE-BRAIN;
RX MEDLINE; 92017079.
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
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CC -----
DR EMBL; X56125; CRA39590.1; -
DR HSP; P05067; IAML.
DR PROSITE; PS00319; A4 EXTRA; PARTIAL.
DR PROSITE; PS00320; A4 INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1
FT CHAIN 7 49 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 58 POTENTIAL.
FT NON_TER 58
FT SEQUENCE 58 AA; 6285 MW; 8469D488A2E12DFA CRC64;
SQ
Query Match 100.0%; Score 92; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAFFRHDGSEYVHHQK 16
DB 7 DAFFRHDGSEYVHHQK 22
| | | | | | | | | | | | | | | |

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DR EMBL; X56129; CAA39594.1; -  
 DR HSP; P05067; IAML  
 DR PROSITE; PS00319; A4\_EXTRA; PARTIAL.  
 DR PROSITE; PS00320; A4\_INTRA; PARTIAL.  
 KW Glycoprotein; Amyloid; Neurone; Transmembrane.  
 FT NON\_TER 1 1  
 FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).  
 FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 34 57  
 FT DOMAIN 58 >58 POTENTIAL.  
 FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).  
 FT NON\_TER 58 58  
 SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 100.0%; Score 92; DB 1; Length 58;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-08;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16  
 |||||  
 Db 6 DAEFRHDSGYEVHHQK 21

## RESULT 5

A4\_SHEEP  
 ID A4\_SHEEP STANDARD; PRT; 58 AA.  
 AC Q28757;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID  
 DE PROTEIN (BETA-APP)] (FRAGMENT).  
 GN APP.  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Ovis.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=HEART;  
 RX MEDLINE; 92017079.

RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;  
 RT "Conservation of the sequence of the Alzheimer's disease amyloid  
 RT peptide in dog, polar bear and five other mammals by cross-species  
 RT polymerase chain reaction analysis."  
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).  
 CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO  
 CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN

G(O) (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.

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DR EMBL; X56130; CAA39595.1; -  
 DR HSP; P05067; IAML  
 DR PROSITE; PS00319; A4\_EXTRA; PARTIAL.  
 DR PROSITE; PS00320; A4\_INTRA; PARTIAL.  
 KW Glycoprotein; Amyloid; Neurone; Transmembrane.

FT NON\_TER 1 1  
 FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).  
 FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 34 57  
 FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).  
 FT NON\_TER 58 58  
 SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 100.0%; Score 92; DB 1; Length 58;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-08;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16  
 |||||  
 Db 6 DAEFRHDSGYEVHHQK 21

## RESULT 6

A4\_BOVIN  
 ID A4\_BOVIN STANDARD; PRT; 59 AA.  
 AC Q28053;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID  
 DE PROTEIN (BETA-APP)] (FRAGMENT).  
 GN APP.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BRAIN;  
 RX MEDLINE; 92017079.

RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;  
 RT "Conservation of the sequence of the Alzheimer's disease amyloid  
 RT peptide in dog, polar bear and five other mammals by cross-species  
 RT polymerase chain reaction analysis."  
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).  
 CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO  
 CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN

G(O) (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.

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DR EMBL; X56124; CAA39589.1; -  
 DR EMBL; X56126; CAA39591.1; -  
 DR HSP; P05067; IAML  
 DR PROSITE; PS00319; A4\_EXTRA; PARTIAL.  
 DR PROSITE; PS00320; A4\_INTRA; PARTIAL.  
 KW Glycoprotein; Amyloid; Neurone; Transmembrane.  
 FT NON\_TER 1 1  
 FT CHAIN 7 49 BETA-AMYLOID PROTEIN (POTENTIAL).  
 FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 35 58  
 FT DOMAIN 59 >59 POTENTIAL.  
 FT NON\_TER 59 59  
 SQ SEQUENCE 59 AA; 6414 MW; F43469D488A2E12D CRC64;

Query Match 100.0%; Score 92; DB 1; Length 59;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-08;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Wed Sep 13 08:11:42 2000

us-09-155-076-2\_1.rsp

OY 1 DAEFRHDSGYEVHOK 16  
 DB 7 DAEFRHDSGYEVHOK 22

RESULT 7  
 AA\_SAISC STANDARD; PRT; 751 AA.  
 ID A4\_SAISC  
 AC Q95241;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-FEB-2000 (Rel. 39, Last annotation update)  
 DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN PRECURSOR [CONTAINS: BETA-AMYLLOID PROTEIN (BETA-APP)].  
 GN APP.  
 OS Saimiri sclerous (Common squirrel monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LIVER, AND KIDNEY;  
 RX MEDLINE; 96108492.  
 RA Levy E., Anorim A., Frangione B., Walker L.C.;  
 RT "Beta-amyloid precursor protein gene in squirrel monkeys with cerebral amyloid angiopathy";  
 RL Neurobiol. Aging 16:805-808(1995).  
 CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O).  
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; S81024; AAD14347.1;  
 DR FRAM; PF00014; Kunitz\_BPTI; 1.  
 DR PRINTS; PRO0203; AMYLOIDA4.  
 DR PRINTS; PRO0204; BETAAMYLOID.  
 DR PRINTS; PRO0759; BASICPTASE.  
 DR PROSITE; PS00280; BPTI\_KUNITZ; 1.  
 DR PROSITE; PS00319; A4\_EXTRA; 1.  
 DR PROSITE; PS00320; A4\_INTRA; 1.  
 DR Glycoprotein; Amyloid; Neurone; Transmembrane; Alternative splicing;  
 KW Signal; Serine protease inhibitor.  
 FT SIGNAL 1 17 BY SIMILARITY.  
 FT CHAIN 18 751 A4 PROTEIN.  
 FT CHAIN 653 695 BETA-AMYLOID PROTEIN (POTENTIAL);  
 FT DOMAIN 18 680 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 681 704 POTENTIAL.  
 FT DOMAIN 705 751 CYTOPLASMIC (POTENTIAL).  
 FT SITE 740 743 CLATHRIN-BINDING (BY SIMILARITY).  
 FT CARBOHYD 523 523 PROBABLE.  
 FT CARBOHYD 552 552 PROBABLE.  
 FT DOMAIN 287 345 BPTI/KUNITZ INHIBITOR.  
 FT ACT\_SITE 301 302 REACTIVE BOND.  
 FT DISULFID 291 341 BY SIMILARITY.  
 FT DISULFID 300 321 BY SIMILARITY.  
 FT DISULFID 316 337 BY SIMILARITY.  
 SQ SEQUENCE 751 AA; 84893 MW; 6C3E431089569049 CRC64;

Query Match 100.0%; Score 92; DB 1; Length 751;  
 Best Local Similarity 100.0%; Pred. NO; 2.7e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHOK 16

DB 653 DAEFRHDSGYEVHOK 668  
 RESULT 8  
 ID A4\_HUMAN STANDARD; PRT; 770 AA.  
 AC P05067; P09000; Q16011;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 01-NOV-1991 (Rel. 20, Last sequence update)  
 DT 15-FEB-2000 (Rel. 39, Last annotation update)  
 DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN PRECURSOR (PROTEASE NEXIN-II) (PN-II) (APPI) [CONTAINS: BETA-AMYLLOID PROTEIN (BETA-APP)].  
 GN APP OR A4 OR CVAP OR ADL.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BRAIN;  
 RX MEDLINE; 87144572.  
 RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L., Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;  
 RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface receptor";  
 RL Nature 325:733-736(1987).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 88122639.  
 RA Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D., Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F., Cordell B.;  
 RT "A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibitors";  
 RL Nature 331:525-527(1988).  
 [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 89128427.  
 RA Lemaire H.G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M., Unterbeck A., Beyreuther K., Mueller-Hill B.;  
 RT "The preA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded by 16 exons";  
 RL Nucleic Acids Res. 17:517-522(1989).  
 [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 97263807.  
 RA Hattori M., Tsukahara F., Furuhashi Y., Tanahashi H., Hirose M., Saito M., Tsukuni S., Sakaki Y.;  
 RT "A novel method for making nested deletions and its application for sequencing of a 300 kb region of human APP locus";  
 RL Nucleic Acids Res. 25:1802-1808(1997).  
 [5]  
 RP SEQUENCE OF 286-345 AND 365-366 FROM N.A.  
 RX MEDLINE; 88122640.  
 RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L., Gusella J.F., Neve R.L.;  
 RT "Protease inhibitor domain encoded by an amyloid protein precursor mRNA associated with Alzheimer's disease";  
 RL Nature 331:528-530(1988).  
 [6]  
 RP SEQUENCE OF 287-367 FROM N.A.  
 RX MEDLINE; 88122641.  
 RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;  
 RT "Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitory activity";  
 RL Nature 331:530-532(1988).  
 [7]  
 RP SEQUENCE OF 284-289 AND 365-770 FROM N.A.  
 RX MEDLINE; 87231971.  
 RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;  
 RT "Molecular cloning and characterization of a cDNA encoding the cerebrovascular and the neuritic plaque amyloid peptides";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).

RN [9] SEQUENCE OF 507-770 FROM N.A.  
 RX MEDLINE; 88124954.  
 RA Zain S.B., Salim M., Chou W.G., Saydel-Sulkowska E.M., Majocha R.E.,  
 RA Marotta C.A.;  
 RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer  
 RT disease brain: coding and noncoding regions of the fetal precursor  
 RT mRNA are expressed in the cortex.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).  
 RN [9]  
 RP SEQUENCE OF 672-681.  
 RX MEDLINE; 88035004.  
 RA Partridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,  
 RA Tourtellotte W.W., Huebner V., Shively J.E.;  
 RT "Amyloid angiopathy of Alzheimer's disease: amino acid composition  
 RT and partial sequence of a 4,200-dalton peptide isolated from cortical  
 RT microvessels.";  
 RL J. Neurochem. 49:1394-1401(1987).  
 RN [10]  
 RP SEQUENCE OF 739-770 FROM N.A.  
 RX MEDLINE; 90236318.  
 RA Yoshikai S.-I., Sasaki H., Doh-Ura K., Furiya H., Sakaki Y.;  
 RT "Genomic organization of the human amyloid beta-protein precursor  
 RT gene.";  
 RL Gene 87:257-263(1990).  
 RN [11]  
 RP SEQUENCE OF 1-10 FROM N.A.  
 RX MEDLINE; 89016647.  
 RA Schon E.A., Mita S., Sadlock J., Herbert J.;  
 RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)  
 RT encodes a 95-kDa polypeptide.";  
 RL Nucleic Acids Res. 16:9351-9351(1988).  
 RN [12]  
 RP SEQUENCE OF 18-50.  
 RX MEDLINE; 87250462.  
 RA van Nostrand W.E., Cunningham D.D.;  
 RT "Purification of protease nexin II from human fibroblasts.";  
 RL J. Biol. Chem. 262:8508-8514(1987).  
 RN [13]  
 RP IDENTITY OF APP WITH NEXIN-II.  
 RX MEDLINE; 89384866.  
 RA Oltersdorf T., Fritz L.C., Schenk D.B., Lieberburg I.,  
 RA Johnson-Wood K.L., Beattie E.C., Ward P.J., Blacher R.W., Dovey H.F.,  
 RA Sinha S.;  
 RT "The secreted form of the Alzheimer's amyloid precursor protein with  
 RT the Kunitz domain is protease nexin-II.";  
 RL Nature 341:144-147(1989).  
 RN [14]  
 RP PROTEASE-SPECIFICITY OF INHIBITOR DOMAIN.  
 RX MEDLINE; 90211252.  
 RA Kido H., Fukutomi A., Schilling J., Wang Y., Cordell B., Katunuma N.;  
 RT "Protease-specificity of Kunitz inhibitor domain of Alzheimer's  
 RT disease amyloid protein precursor.";  
 RL Biochem. Biophys. Res. Commun. 167:716-721(1990).  
 RN [15]  
 RP COMPLEX WITH G(O).  
 RX MEDLINE; 93188965.  
 RA Nishimoto I., Okamoto T., Matsuura Y., Takahashi S., Okamoto T.,  
 RA Murayama Y., Ogata E.;  
 RT "Alzheimer amyloid protein precursor complexes with brain GTP-binding  
 RT protein G(O).";  
 RL Nature 362:75-79(1993).  
 RN [16]  
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 28-133.  
 RX MEDLINE; 99215582.  
 RA Rossjohn J., Cappai R., Feil S.C., Henry A., McKinsty W.J.,  
 RA Galatis D., Hesse L., Multhaup G., Beyreuther K., Masters C.L.,  
 RA Parker M.W.;  
 RT "Crystal structure of the N-terminal, growth factor-like domain of  
 RT Alzheimer amyloid precursor protein.";  
 RL Nat. Struct. Biol. 6:327-331(1999).  
 RN [17]

RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 287-344.  
 RX MEDLINE; 91104913.  
 RA Hynes T.R., Randal M., Kennedy L.A., Eigenbrot C., Kossiakof A.A.;  
 RT "X-ray crystal structure of the protease inhibitor domain of  
 RT Alzheimer's amyloid beta-protein precursor.";  
 RL Biochemistry 29:10018-10022(1990).  
 RN [18]  
 RP STRUCTURE BY NMR OF 289-344.  
 RX MEDLINE; 92031488.  
 RA Heald S.L., Tilton R.F. Jr., Hammond L.S., Lee A., Bayney R.M.,  
 RA Kamark M.E., Ramabhadran T.V., Drayer R.N., Davis G., Unterbeck A.,  
 RA Tamburini P.P.;  
 RT "Sequential NMR resonance assignment and structure determination of  
 RT the Kunitz-type inhibitor domain of the Alzheimer's beta-amyloid  
 RT precursor protein.";  
 RL Biochemistry 30:10467-10478(1991).  
 RN [19]  
 RP STRUCTURE BY NMR OF 672-699.  
 RX MEDLINE; 94281210.  
 RA Talafous J., Marciniowski K.J., Klopman G., Zagorski M.G.;  
 RT "Solution structure of residues 1-28 of the amyloid beta-peptide.";  
 RL Biochemistry 33:7788-7796(1994).  
 RN [20]  
 RP STRUCTURE BY NMR OF 696-706.  
 RX MEDLINE; 97128622.  
 RA Kohno T., Kobayashi K., Maeda T., Sato K., Takashima A.;  
 RT "Three-dimensional structures of the amyloid beta peptide (25-35) in  
 RT membrane-mimicking environment.";  
 RL Biochemistry 35:16094-16104(1996).  
 RN [21]  
 RP STRUCTURE BY NMR OF 672-711.  
 RX MEDLINE; 98359783.  
 RA Coles M., Bicknell W., Watson A.A., Fairlie D.P., Craik D.J.;  
 RT "Solution structure of amyloid beta-peptide(1-40) in a water-miscible  
 RT environment. Is the membrane-spanning domain where we think it is?";  
 RL Biochemistry 37:11064-11077(1998).  
 RN [22]  
 RP STRUCTURE BY NMR OF 672-699.  
 RA Poulsen S.-A., Watson A.A., Craik D.J.;  
 RT Submitted (JUN-1998) to the PDB data bank.  
 RN [23]  
 RP SIGNAL SEQUENCE CLEAVAGE SITE, AND TOPOLOGY.  
 RX MEDLINE; 88296437.  
 RA Dykx T., Weidemann A., Multhaup G., Salbaum J.M., Lemaire H.-G.,  
 RA Kang J., Mueller-Hill B., Masters C.L., Beyreuther K.;  
 RT "Identification, transmembrane orientation and biogenesis of the  
 RT amyloid A4 precursor of Alzheimer's disease.";  
 RL EMBO J. 7:949-957(1988).  
 RN [24]  
 RP REVIEW.  
 RX MEDLINE; 92271194.  
 RA Kosik K.S.;  
 RT "Alzheimer's disease: a cell biological perspective.";  
 RL Science 256:780-783(1992).  
 RN [25]  
 RP REVIEW ON VARIANTS.  
 RX MEDLINE; 93250996.  
 RA Hardy J.;  
 RT "Framing beta-amyloid.";  
 RL Nat. Genet. 1:233-234(1992).  
 RN [26]

Query Match 100.0% Score 92; DB 1; Length 770;  
 Best Local Similarity 100.0% Pred. No. 2.7e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHOK 16  
 Db 672 DAEFRHDSGYEVHOK 687  
 |||||

RESULT 9  
 ID A4\_MOUSE STANDARD; PRT; 770 AA.

AC P12023;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 15-FEB-2000 (Rel. 39, Last annotation update)  
 DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG PRECURSOR  
 DE (AMYLOIDOGENIC GLYCOPROTEIN) (AG).  
 GN APP.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.  
 RC STRAIN-BALB/C; TISSUE-BRAIN;  
 RX MEDLINE; 92096458.  
 RA de Strooper B., van Leuven F., van den Berghe H.;  
 RT "The amyloid beta protein precursor or protease nexin II from mouse  
 RT is closer related to its human homolog than previously reported."  
 RL Biochem. Biophys. Acta 1129:141-143(1991).  
 RN [2]  
 RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.  
 RC TISSUE-BRAIN;  
 RX MEDLINE; 88106489.  
 RA Yamada T., Sakaki H., Furuya H., Miyata T., Goto I., Sakaki Y.;  
 RT "Complementary DNA for the mouse homolog of the human amyloid beta  
 RT protein precursor."  
 RL Biochem. Biophys. Res. Commun. 149:665-671(1987).  
 RN [3]  
 RP REVISIONS.  
 RA Yamada T.;  
 RL Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 289-364 FROM N.A.  
 RC STRAIN-CD-1; TISSUE-PLACENTA;  
 RX MEDLINE; 89345111.  
 RA Fukuchi K., Martin G.M., Deeb S.S.;  
 RT "Sequence of the protease inhibitor domain of the A4 amyloid protein  
 RT precursor of Mus domesticus."  
 RL Nucleic Acids Res. 17:5396-5396(1989).  
 RN [5]  
 RP SEQUENCE OF 1-19 FROM N.A.  
 RX MEDLINE; 92209998.  
 RA Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,  
 RA Sakai Y.;  
 RT "Positive and negative regulatory elements for the expression of the  
 RT Alzheimer's disease amyloid precursor-encoding gene in mouse."  
 RL Gene 112:189-195(1992).  
 RN [6]  
 RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.  
 RC TISSUE-BRAIN, AND KIDNEY;  
 RX MEDLINE; 89149813.  
 RA Yamada T., Sakaki H., Dohura K., Goto I., Sakaki Y.;  
 RT "Structure and expression of the alternatively-spliced forms of mRNA  
 RT for the mouse homolog of Alzheimer's disease amyloid beta protein  
 RT precursor."  
 RL Biochem. Biophys. Res. Commun. 158:906-912(1989).  
 CC -1- SURCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- ALTERNATIVE PRODUCTS: SIX FORMS OF APP ARE FOUND: APP(395),  
 CC APP(563), APP(695), APP(751) AND APP(770) (SHOWN HERE); WHICH ARE  
 CC PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: AAA(770) IS EXPRESSED IN KIDNEY. AAA(751) IS  
 CC WIDELY EXPRESSED. AAA(695) IS EXPRESSED IN BRAIN, KIDNEY AND  
 CC LIVER.  
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.  
 CC -1- SIMILARITY: APP(751) AND APP(770) CONTAIN A PROTEASE INHIBITOR  
 CC DOMAIN BELONGING TO THE BPTI/KUNITZ FAMILY OF INHIBITORS.  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL; X59379; -- NOT\_ANNOTATED\_CDS.  
 DR EMBL; M18373; AAA37139.1; --  
 DR EMBL; X15210; CAA3280.1; --  
 DR EMBL; D10603; BAA01456.1; --  
 DR EMBL; M24397; AAA39929.1; --  
 DR PIR; A27485; A27485.  
 DR PIR; S04855; S04855.  
 DR PIR; S19727; S19727.  
 DR MGD; MGI:88059; APP.  
 DR PFAM; PF00014; Kunitz\_BPTI; 1.  
 DR PRINTS; PRO0203; AMYLOIDA4.  
 DR PRINTS; PRO0204; BETAAMYLOID.  
 DR PRINTS; PRO0759; BASICPTASE.  
 DR PROSITE; PS00280; BPTI\_KUNITZ; 1.  
 DR PROSITE; PS00319; A4\_EXTRA; 1.  
 DR PROSITE; PS00320; A4\_INTRA; 1.  
 KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;  
 KW Alternative splicing; Serine protease inhibitor.  
 FT SIGNAL 1 17  
 FT CHAIN 18 770  
 FT DOMAIN 18 599  
 FT TRANSMEM 700 723  
 FT DOMAIN 724 770  
 FT DOMAIN 673 715  
 FT DOMAIN 287 345  
 FT SITE 759 762  
 FT DISULFID 291 341  
 FT DISULFID 300 324  
 FT DISULFID 316 337  
 FT CARBOHYD 542 542  
 FT CARBOHYD 571 571  
 FT VARSPLIC 289 289  
 FT VARSPLIC 290 364  
 FT VARSPLIC 346 380  
 FT SEQUENCE 770 AA; 86752 MW; 26C50DE0890CAF7A CRC64;  
 SQ  
 QY 1 DAEFRHDSGVEVHOK 16  
 DB 672 DAEFRHDSGVEVHOK 687  
 Query Match 79.3%; Score 73; DB 1; Length 770;  
 Best Local Similarity 81.2%; Pred. No. 0.0003;  
 Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 RESULT 10  
 ID A4\_RAT STANDARD; PRT; 770 AA.  
 AC P08592;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 15-FEB-2000 (Rel. 39, Last annotation update)  
 DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG PRECURSOR  
 DE (AMYLOIDOGENIC GLYCOPROTEIN) (AG).  
 GN APP.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN [1]  
 RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.  
 RC TISSUE-BRAIN;  
 RX MEDLINE; 88312583.  
 RA Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K.,  
 RA Seeburg P.H.;  
 RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern  
 RT in rat brain suggests a role in cell contact."  
 RL EMBO J. 7:1365-1370(1988).  
 RN [2]  
 RP SEQUENCE OF 289-364 FROM N.A.  
 RC TISSUE=LIVER;

XX MEDLINE; 89183625.  
RA Kang J., Mueller-Hill B.;  
RT "The sequence of the two extra exons in rat preA4";  
RL Nucleic Acids Res. 17:2130-2130(1989).  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -1- ALTERNATIVE PRODUCTS: SIX FORMS OF APP ARE FOUND; APP(395),  
CC APP(563), APP(695), APP(751) AND APP(770) (SHOWN HERE); WHICH ARE  
CC PRODUCED BY ALTERNATIVE SPLICING.  
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.  
CC -1- SIMILARITY: APP(751) AND APP(770) CONTAIN A PROTEASE INHIBITOR  
CC DOMAIN BELONGING TO THE BPTI/KUNITZ FAMILY OF INHIBITORS.  
CC  
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CC  
DR EMBL; X07648; CAA30488.1; -.  
DR EMBL; X14066; CAA32229.1; -.  
DR PIR; S00550; S00550.  
DR PIR; S03607; S03607.  
DR PFAM; PF00014; Kunitz\_BPTI; 1.  
DR PRINTS; PR00203; AMYLOID4.  
DR PRINTS; PR00204; BETAAMYLOID.  
DR PRINTS; PR00759; BASICPTASE.  
DR PROSITE; PS00280; BPTI\_KUNITZ; 1.  
DR PROSITE; PS00319; A4\_EXTRA; 1.  
DR PROSITE; PS00320; A4\_INTRA; 1.  
DR Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;  
KW Alternative splicing; Serine protease inhibitor.  
FT SIGNAL 1 17  
FT CHAIN 18 770  
FT DOMAIN 18 699  
FT TRANSMEM 700 723  
FT POTENTIAL.  
FT CYTOPLASMIC (POTENTIAL).  
FT EQUIVALENT OF BETA-AMYLOID PROTEIN.  
FT BPTI/KUNITZ INHIBITOR.  
FT CLATHRIN-BINDING (BY SIMILARITY).  
FT BY SIMILARITY.  
FT BY SIMILARITY.  
FT POTENTIAL.  
FT CARBOHYD 542 542  
FT CARBOHYD 571 571  
FT VARSPLIC 289 289  
FT VARSPLIC 290 364  
FT MISSING (IN ISOFORM APP(695)).  
FT MISSING (IN ISOFORM APP(695)).  
FT SEQUENCE 770 AA; 86704 MW; C26C9D6BB2929A7 CRC64;  
Query Match 79.3%; Score 73; DB 1; Length 770;  
Best Local Similarity 81.2%; Pred. No. 0.0003;  
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 DAEFRHDSGYEVHHQK 16  
Db 672 DAEEFGHDSGYEVHHQK 687  
RESULT 11  
POLG\_PVYVO STANDARD; PRT; 284 AA.  
ID POLG\_PVYVO  
AC P11897;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE GENOME POLYPROTEIN [CONTAINS: NUCLEAR INCLUSION PROTEIN B (NI-B) (NIB)  
DE (RNA-DIRECTED RNA POLYMERASE) (EC 2.7.7.48); COAT PROTEIN (CP)]  
DE (FRAGMENT).  
OS Potato virus Y (strain Yo) (PVY).  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;  
CC

OC Potyvirus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE; 89296509.  
RA Bravo-Almonacid F.F., Mentaberry A.N.;  
RT "Nucleotide cDNA sequence coding for the PVY coat protein.";  
RL Nucleic Acids Res. 17:4401-4401(1989).  
CC -1- PFM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE  
CC POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC  
CC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT  
CC INDIVIDUAL PROTEINS.  
CC -1- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.  
CC  
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CC  
DR EMBL; X14136; CAA32356.1; -.  
DR PIR; S04723; S04723.  
DR PFAM; PF00767; Poty\_coat; 1.  
KW Transferase; RNA-directed RNA polymerase; Coat protein; Polyprotein.  
FT NON\_TER 1 1  
FT CHAIN <1 17 NUCLEAR INCLUSION PROTEIN B.  
FT CHAIN 18 284 COAT PROTEIN.  
FT SEQUENCE 284 AA; 31971 MW; E98535C4607898E2 CRC64;  
Query Match 54.9%; Score 50.5; DB 1; Length 284;  
Best Local Similarity 73.3%; Pred. No. 0.4;  
Matches 11; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
QY 1 DAEFRHDSGYEVHHQ 15  
Db 4 DDEFEFDS-YEVHHQ 17  
RESULT 12  
POLG\_PVYCH STANDARD; PRT; 327 AA.  
ID POLG\_PVYCH  
AC P21294;  
DT 01-MAY-1991 (Rel. 18, Created)  
DT 01-MAY-1991 (Rel. 18, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE GENOME POLYPROTEIN [CONTAINS: NUCLEAR INCLUSION PROTEIN B (NI-B) (NIB)  
DE (RNA-DIRECTED RNA POLYMERASE) (EC 2.7.7.48); COAT PROTEIN (CP)]  
DE (FRAGMENT).  
OS Potato virus Y (strain Chinese isolate) (PVY).  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;  
OC Potyvirus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE; 91016851.  
RA Zhou X.R., Fang R.X., Wang C.Q., Mang K.Q.;  
RT "cDNA sequence of the 3'-coding region of PVY genome (the Chinese  
RT isolate).";  
RL Nucleic Acids Res. 18:5554-5554(1990).  
CC -1- PFM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE  
CC POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC  
CC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT  
CC INDIVIDUAL PROTEINS.  
CC -1- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.  
CC  
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CC

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CC -----
DR EMBL; X54058; CAA37993.1; -.
DR PIR; S11549; S11549.
DR HSP; P05067; IAMB.
DR FRAM; PF00767; Poty-coat; 1.
KW Transferase; RNA-directed RNA polymerase; Coat protein; Polyprotein.
FT NON_TER 1 1
FT CHAIN <1 60 NUCLEAR INCLUSION PROTEIN B.
FT CHAIN 61 327 COAT PROTEIN.
SQ SEQUENCE 327 AA; 36868 MW; 8f8355E2DE6F2F18 CRC64;

Query Match 54.9%; Score 50.5; DB 1; Length 327;
Best Local Similarity 73.3%; Pred. No. 0.47;
Matches 11; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 DAEFRHDSGYEVHHQ 15
DB 47 DDEFEFDS-YEVHHQ 60

RESULT 13
V228_BORBU
ID Y228_BORBU STANDARD; PRT; 971 AA.
AC OS1246;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE HYPOTHETICAL PROTEIN BB0228.
GN BB0228
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35210 / B31;
RX MEDLINE: 98065943.
RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
RA Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
RA Utterback T., Wathley L., McDonald L., Artiach P., Bowman C.,
RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
RA Smith H.O., Venter J.C.;
RT "Genomic sequence of a Lyme disease spirochete, Borrelia
RT burgdorferi.";
RL Nature 390:580-586(1997).

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CC -----
DR EMBL; AE001133; AAC66621.1; -.
DR TIGR; BB0228; -.
KW Hypothetical protein.
SQ SEQUENCE 971 AA; 112959 MW; 088A688D7B8C591A CRC64;

Query Match 53.8%; Score 49.5; DB 1; Length 971;
Best Local Similarity 57.9%; Pred. No. 2.1;
Matches 11; Conservative 2; Mismatches 3; Indels 3; Gaps 1;

QY 1 DAE---FRHDSGYEVHHQ 16
DB 19 DAEGYFKHESGLVEVHLK 37

RESULT 14
COAT_PEMV

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ID COAT_PEMV STANDARD; PRT; 330 AA.
AC P07993;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE COAT PROTEIN.
OS Pepper mottle virus (PEMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
RN [1]
RP SEQUENCE FROM N.A.
RA Dougherty W.G., Allison R.F., Parks T.D., Johnston R.E., Feild M.J.,
RA Armstrong F.B.;
RT "Nucleotide sequence at the 3' terminus of pepper mottle virus
RT genomic RNA: evidence for an alternative mode of potyvirus capsid
RT protein gene organization.";
RL Virology 146:282-291(1985).
CC -----
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CC -----
DR EMBL; M11598; AAA46902.1; -.
DR PIR; A26205; A26205.
DR PFAM; PF00767; Poty-coat; 1.
KW Coat protein.
SQ SEQUENCE 330 AA; 37028 MW; C63A2F810D95820E CRC64;

Query Match 52.7%; Score 48.5; DB 1; Length 330;
Best Local Similarity 73.3%; Pred. No. 0.99;
Matches 11; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 DAEFRHDSGYEVHHQ 15
DB 50 DDEFEFDS-YEVHHQ 63

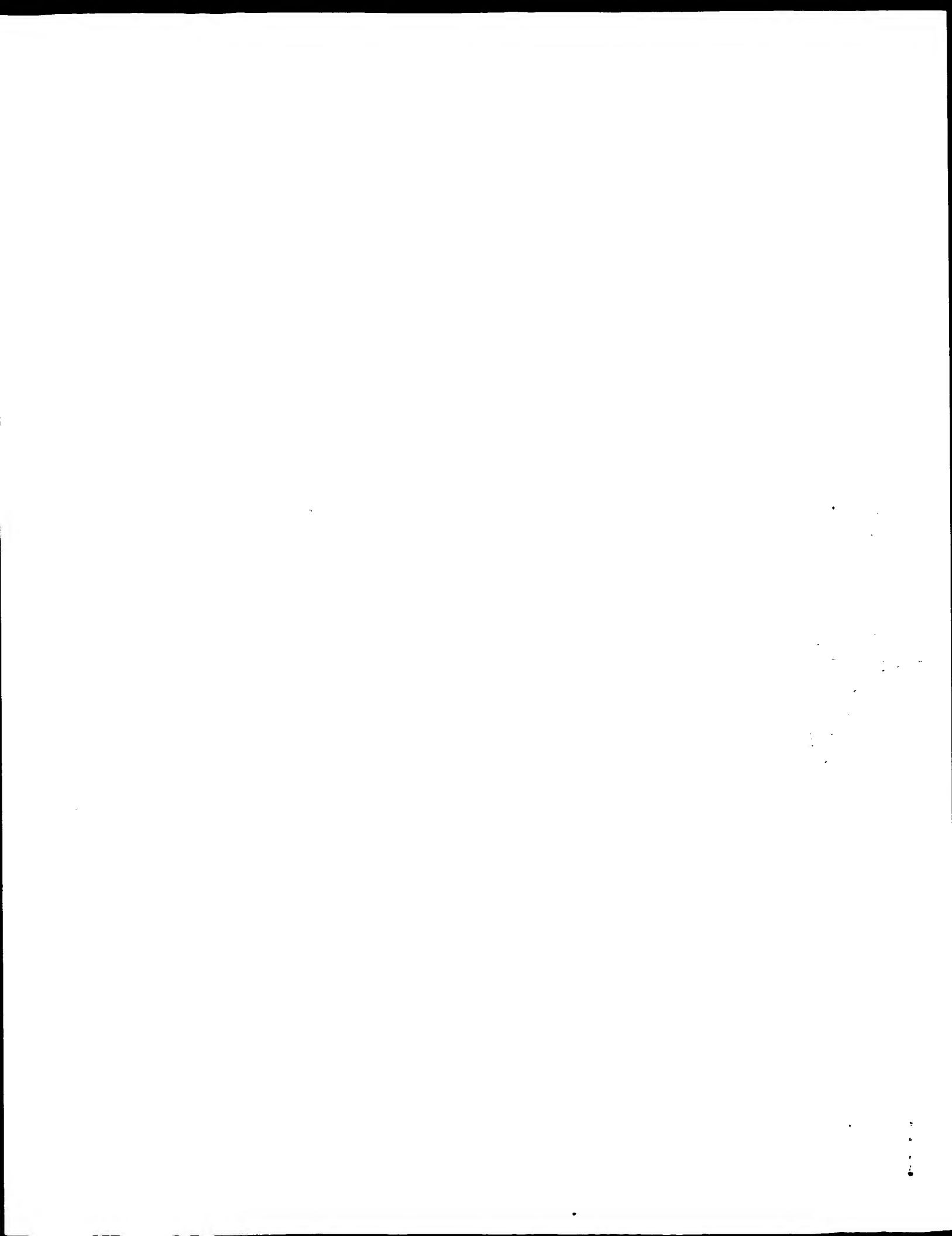
RESULT 15
POLG_PVYN
ID POLG_PVYN STANDARD; PRT; 3063 AA.
AC P18247; Q85266; Q85267; Q85268; Q85269; Q85270; Q85271; Q85272;
AC Q85273;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER
DE COMPONENT PROTEINASE (EC 3.4.22.-) (HC-PRO); 6 KDA PROTEIN 2 (6K2);
DE 1 (6K1); CYTOPLASMIC INCLUSION PROTEIN (CI); 6 KDA PROTEIN A (NI-A) (NIA)
DE GENOME-LINKED PROTEIN (VPG); NUCLEAR INCLUSION PROTEIN A (NI-A) (NIA)
DE (EC 3.4.22.-) (49 KDA PROTEINASE) (49 KDA-PRO); NUCLEAR INCLUSION
DE PROTEIN B (NI-B) (NIB) (RNA-DIRECTED RNA POLYMERASE) (EC 2.7.7.48);
DE COAT PROTEIN (CP)].
OS Potato virus Y (strain N) (PVY).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 89279275.
RA Robaglia C., Durand-Tardif M., Tronchet M., Boudazin G.,
RA Astier-Manificier S., Casse-Delbart F.;
RT "Nucleotide sequence of potato virus Y (N Strain) genomic RNA.";
RL J. Gen. Virol. 70:935-947(1989).
RN [2]
RP REVISIONS.
RA Durand-Tardif M.;
RA Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: HELPER COMPONENT-PROTEINASE IS REQUIRED FOR APHID
CC TRANSMISSION AND ALSO HAS PROTEOLYTIC ACTIVITY.
CC

```

CC -!- FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICASE ACTIVITY. IT  
 CC MAY BE INVOLVED IN REPLICATION.  
 CC -!- FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.  
 CC -!- FPM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.  
 CC -!- FPM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE  
 CC POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC  
 CC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT  
 CC INDIVIDUAL PROTEINS.  
 CC -!- SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.  
 CC -!- SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4.  
 CC -!- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.  
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 CC -----  
 CC EMBL: X12456; CAA30988.1; -;  
 CC EMBL: D00441; BAA0342.1; -;  
 CC PIR: JS0166; JS0166.  
 CC PFAM: PF00270; DEAD; 1.  
 CC PFAM: PF00863; Peptidase\_C4; 1.  
 CC PFAM: PF00851; Peptidase\_C6; 1.  
 CC PFAM: PF01577; Poty\_P1; 1.  
 CC PFAM: PF00767; Poty\_coat; 1.  
 CC PFAM: PF00680; RNA\_dep\_RNA\_pol; 1.  
 CC PFAM: PF00271; helicase\_C; 1.  
 CC PRINTS: PR00966; NIAPOTYPTASE.  
 CC Hydrolase; Transferase; Thiol protease; RNA-directed RNA polymerase;  
 CC Coat protein; Polyprotein; Covalent protein-RNA linkage; Helicase;  
 CC ATP-binding.  
 CC CHAIN 1 275 N-TERMINAL PROTEIN.  
 CC CHAIN 276 824 HELPER COMPONENT PROTEINASE.  
 CC CHAIN 825 ? PROTEIN P3.  
 CC CHAIN ? 1157 6 kDa PROTEIN 1.  
 CC CHAIN 1158 1791 CYTOPLASMIC INCLUSION PROTEIN.  
 CC CHAIN 1792 1843 6 kDa PROTEIN 2.  
 CC CHAIN 1844 ? GENOME-LINKED PROTEIN.  
 CC CHAIN ? 2275 NUCLEAR INCLUSION PROTEIN A.  
 CC CHAIN 2276 2796 NUCLEAR INCLUSION PROTEIN B.  
 CC CHAIN 2797 3063 COAT PROTEIN.  
 CC BINDING 1907 1907 COVALENT LINKAGE OF VIRAL RNA (BY  
 CC SIMILARITY).  
 CC FT NP\_BIND 1242 1249 ATP (POTENTIAL).  
 CC SQ SEQUENCE 3063 AA; 347535 MW; 3EC79125DE33F1BB CRC64;

Query Match 52.7%; Score 48.5; DB 1; Length 3063;  
 Best Local Similarity 73.3%; Pred. No. 10;  
 Matches 11; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
 QY 1 DAEFRHDSGYEVHHQ 15  
 ||| |||||  
 Db 2783 DDEEELDS-YEVHHQ 2796

Search completed: September 13, 2000, 02:24:32  
 Job time: 170 sec





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 13, 2000, 02:24:09 : Search time 22.49 seconds  
(without alignments)  
49.326 Million cell updates/sec

Title: US-09-155-076-2  
Perfect score: 92  
Sequence: 1 DAEFRHDSGYEVHHQK 16

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 225878 seqs, 69334122 residues  
Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0  
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_12:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rudent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	92	100.0	82	4	Q16020	Q16020 homo sapien
2	92	100.0	82	4	Q16019	Q16019 homo sapien
3	92	100.0	82	4	Q16014	Q16014 homo sapien
4	92	100.0	82	4	P78438	P78438 homo sapien
5	92	100.0	534	13	Q93296	Q93296 gallus gall
6	92	100.0	695	11	Q60496	Q60496 cavia porce
7	82	89.1	97	4	Q13778	Q13778 homo sapien
8	77	83.7	747	13	Q91963	Q91963 xenopus lae
9	73	79.3	79	11	O35463	O35463 cricetus lae
10	73	79.3	695	11	P97487	P97487 mus musculu
11	72	78.3	699	13	O57394	O57394 narke japon
12	50.5	54.9	292	12	Q85276	Q85276 potato viru
13	50.5	54.9	365	12	Q9WG05	Q9WG05 potato viru
14	50.5	54.9	1555	12	Q85274	Q85274 potato viru
15	50	54.3	780	13	O73683	O73683 tetraodon f
16	49	53.3	737	13	O93279	O93279 fugu rubrip
17	47	51.1	206	2	O44945	O44945 borrelia bu
18	46	50.0	372	2	O85339	O85339 escherichia
19	45.5	49.5	313	12	Q85259	Q85259 potato viru

20	45.5	49.5	976	12	Q85104	Q85104 potato viru
21	45.5	49.5	3061	12	Q85265	Q85265 potato viru
22	44.5	48.4	519	12	O72606	O72606 potato viru
23	44.5	48.4	3081	12	Q85105	Q85105 potato viru
24	44	47.8	297	2	O92NC1	O92NC1 nitrosomona
25	42.5	46.2	539	3	O14283	O14283 schizosacch
26	42	45.7	339	4	O75357	O75357 homo sapien
27	42	45.7	372	4	O60547	O60547 homo sapien
28	42	45.7	373	2	O60952	O60952 vibrio chol
29	42	45.7	667	3	Q12101	Q12101 saccharomyc
30	41	44.6	213	6	Q29520	Q29520 oryctolagus
31	41	44.6	213	6	Q29522	Q29522 oryctolagus
32	41	44.6	213	6	Q29521	Q29521 oryctolagus
33	41	44.6	356	10	O22331	O22331 hevea brasili
34	41	44.6	367	3	O43120	O43120 schizosacch
35	41	44.6	494	2	O53677	O53677 mycobacteri
36	41	44.6	551	2	Q52519	Q52519 pseudomonas
37	41	44.6	672	3	Q04562	Q04562 saccharomyc
38	41	44.6	944	4	O14697	O14697 homo sapien
39	41	44.6	966	11	O08794	O08794 mus musculu
40	41	44.6	1919	6	Q29518	Q29518 oryctolagus
41	41	44.6	1920	6	Q29519	Q29519 oryctolagus
42	40.5	44.0	559	10	O23409	O23409 arabidopsis
43	40	43.5	104	2	Q925P5	Q925P5 enterococcu
44	40	43.5	155	5	O19475	O19475 caenorhabdi
45	40	43.5	311	10	Q39500	Q39500 cylindroche

## ALIGNMENTS

RESULT 1

Q16020 PRELIMINARY; PRT; 82 AA.

AC Q16020; 01-NOV-1996 (TREMREL. 01, Created)

DT 01-NOV-1996 (TREMREL. 01, Last sequence update)

RT mutations on the processing of the beta-amyloid peptide precursor.

DE BETA-AMYLOID PEPTIDE (FRAGMENT).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 93236601.

RA DENMAN R.B., ROSENZWAIG R., MILLER D.L.;

RT "A system for studying the effect(s) of familial Alzheimer disease

RL Biochem. Biophys. Res. Commun. 192:96-103(1993).

DR EMBL; S61383; CAB32008.1; -

DR HSSP; P05067; IAML.

FT NON\_TER 1

FT NON\_TER 82

SQ SEQUENCE 82 AA; 8882 MW; 55734509 CRC32;

Query Match 100.0%; Score 92; DB 4; Length 82;  
Best Local Similarity 100.0%; Pred. No. 4.9e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16  
|||||

Db 18 DAEFRHDSGYEVHHQK 33  
|||||

RESULT 2

Q16019 PRELIMINARY; PRT; 82 AA.

ID Q16019; 01-NOV-1996 (TREMREL. 01, Created)

AC Q16019; 01-NOV-1996 (TREMREL. 01, Last sequence update)

DT 01-NOV-1996 (TREMREL. 01, Last sequence update)

DE BETA-AMYLOID PEPTIDE (FRAGMENT).

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us-09-155-076-2\_1.rspt

OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 93236601.

RA DENMAN R.B., ROSENZWAIG R., MILLER D.L.;

RT "A system for studying the effect(s) of familial Alzheimer disease mutations on the processing of the beta-amyloid peptide precursor.";

RL Biochem. Biophys. Res. Commun. 192:96-103(1993).

DR EMBL; S61380; CAB32007.1; -.

DR HSSP; P05067; IAML.

FT NON\_TER 1

FT NON\_TER 82

SQ SEQUENCE 82 AA; 8938 MW; 4C8B0E6E CRC32;

Query Match 100.0%; Score 92; DB 4; Length 82;

Best Local Similarity 100.0%; Pred. No. 4.9e-08;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16

DB 18 DAEFRHDSGYEVHHQK 33

RESULT 3

Q16014

TID Q16014 PRELIMINARY; PRT; 82 AA.

AC Q16014;

DT 01-NOV-1996 (TRENBLrel. 01, Created)

DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)

DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)

DE BETA-AMYLLOID PEPTIDE (FRAGMENT).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 93236601.

RA DENMAN R.B., ROSENZWAIG R., MILLER D.L.;

RT "A system for studying the effect(s) of familial Alzheimer disease mutations on the processing of the beta-amyloid peptide precursor.";

RL Biochem. Biophys. Res. Commun. 192:96-103(1993).

DR EMBL; S60721; CAB31888.1; -.

DR HSSP; P05067; IAML.

FT NON\_TER 1

FT NON\_TER 82

SQ SEQUENCE 82 AA; 8972 MW; 30147E4F CRC32;

Query Match 100.0%; Score 92; DB 4; Length 82;

Best Local Similarity 100.0%; Pred. No. 4.9e-08;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16

DB 18 DAEFRHDSGYEVHHQK 33

RESULT 4

P78438

ID P78438 PRELIMINARY; PRT; 82 AA.

AC P78438;

DT 01-MAY-1997 (TRENBLrel. 03, Created)

DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)

DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)

DE AMYLLOID PROTEIN (BETA-AMYLLOID PROTEIN) (FRAGMENT).

GN APP.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

RN [1]

SEQUENCE FROM N.A.

RX MEDLINE; 8932030.

RA JOHNSTONE E.M., CHANEY M.O., MOORE R.E., WARD K.E., NORRIS F.H.,

RA LITTLE S.P.;

RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows similarity to soybean trypsin inhibitor.";

RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).

[2]

RN SEQUENCE OF 19-48 FROM N.A.

RP MEDLINE; 87120329.

RA TANZI R.E., GUSELLA J.F., WATKINS P.C., BRUNS G.A., GEORGE-HYSLOP P.,

RA VAN KEUREN M.L., PATTERSON D., PAGAN S., KURNIT D.M., NEVE R.L.;

RT "Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near the Alzheimer locus.";

RL Science 235:880-884(1987).

[3]

RN SEQUENCE OF 32-63 FROM N.A.

RP MEDLINE; 93035397.

RA KAMINO K., ORR H.T., PAYAMI H., WIJSMAN E.M., ALONSO M.E., PULST S.M.,

RA ANDERSON L., O'DAHL S., NEMENS E., WHITE J.A.;

RT "Linkage and mutational analysis of familial Alzheimer disease

kindreds for the APP gene region.";

RL Am. J. Hum. Genet. 51:998-1014(1992).

DR EMBL; M29270; AAA51768.1; -.

DR EMBL; M29269; AAA51768.1; JOINED.

DR EMBL; M15532; AAA51564.1; -.

DR EMBL; S45136; AAB23646.1; -.

DR HSSP; P05067; IAML.

FT NON\_TER 1

FT NON\_TER 82

SQ SEQUENCE 82 AA; 8994 MW; 5399FFA4 CRC32;

Query Match

Best Local Similarity 100.0%; Score 92; DB 4; Length 82;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16

DB 17 DAEFRHDSGYEVHHQK 32

RESULT 5

O93296

ID O93296 PRELIMINARY; PRT; 534 AA.

AC O93296;

DT 01-NOV-1998 (TRENBLrel. 08, Created)

DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)

DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)

DE AMYLLOID PRECURSOR PROTEIN (FRAGMENT).

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;

OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

RN [1]

RP SEQUENCE FROM N.A.

RA BARNES N.Y., LING L., YOSHIKAWA K., SCHWARTZ L.M., OPPENHEIM R.W.,

RA MILLIGAN C.E.;

RT "Increased production of amyloid precursor protein provides a

substrate for Caspase 3 in dying motoneurons.";

RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF042098; AAC25052.1; -.

DR HSSP; P05067; IAML.

DR PROSITE; PS00319; A4\_EXTRA; 1.

DR PROSITE; PS00320; A4\_INTRA; 1.

FT NON\_TER 1

FT NON\_TER 534

SQ SEQUENCE 534 AA; 60597 MW; 6F117D2F CRC32;

Query Match

Best Local Similarity 100.0%; Score 92; DB 13; Length 534;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16

|||||

Db 436 DAEFRHDSGYEVHHQK 451

RESULT 6  
Q60496 PRELIMINARY; PRT; 695 AA.  
AC Q60496;  
DT 01-NOV-1996 (TREMELrel. 01, Created)  
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)  
DT 01-NOV-1999 (TREMELrel. 12, Last annotation update)  
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN.  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-BRAIN;  
RA BECK M., MUELLER D., BIGL V.;  
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO  
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN  
CC G(O).  
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -!- SIMILARITY: TO OTHER SPECIES APP ANALOGUES.  
DR EMBL; X97631; CAA66230.1; -.  
DR HSSP; P05067; 1AML.  
DR PRINTS; PR00203; AMYLOIDA4.  
DR PRINTS; PR00204; BETAMAMYLID.  
DR PRINTS; PR00204; BETAMAMYLID.  
SQ SEQUENCE 695 AA; 78701 MW; CE05C651 CRC32;

Query Match 100.0%; Score 92; DB 11; Length 695;  
Best Local Similarity 100.0%; Pred. No. 4.6e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DAEFRHDSGYEVHHQK 16  
| | | | | | | | | | | | | | | | | |  
Db 597 DAEFRHDSGYEVHHQK 612

RESULT 7  
Q13778 PRELIMINARY; PRT; 97 AA.  
AC Q13778;  
DT 01-NOV-1996 (TREMELrel. 01, Created)  
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)  
DT 01-NOV-1999 (TREMELrel. 12, Last annotation update)  
DE AMYLOID PROTEIN (AD-AP) (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.  
RN [1]  
RP SEQUENCE FROM N.A.  
EX MEDLINE; 87120328.  
RA GOLDGABER D., LERMAN M.I., MCBRIDE O.W., SAFFIOTTI U., GAJDUSEK D.C.;  
RT "Characterization and chromosomal localization of a cDNA encoding  
RT brain amyloid of Alzheimer's disease."  
RL Science 235:877-880(1987).  
DR EMBL; M15533; AAA35540.1; -.  
DR HSSP; P05067; 1AML.  
DR NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 97 AA; 10884 MW; C4D32AA2 CRC32;

Query Match 89.1%; Score 82; DB 4; Length 97;  
Best Local Similarity 100.0%; Pred. No. 2.4e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 EFRHDSGYEVHHQK 16  
| | | | | | | | | | | | | | | | | |  
Db 1 EFRHDSGYEVHHQK 14

RESULT 8

Q91963 PRELIMINARY; PRT; 747 AA.  
AC Q91963;  
DT 01-NOV-1996 (TREMELrel. 01, Created)  
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)  
DT 01-NOV-1999 (TREMELrel. 12, Last annotation update)  
DE APP747.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;  
OC Batrachia; Anura; Mesobatrachia; Pipidae; Xenopodinae;  
OC Xenopus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 93129227.  
RA OKADO H., OKAMOTO H.;  
RT "A Xenopus homologue of the human beta-amyloid precursor protein:  
RT developmental regulation of its gene expression."  
RL Biochem. Biophys. Res. Commun. 189:1561-1568(1992).  
DR EMBL; S52417; AAB24853.1; -.  
DR PROSITE; PS00320; A4\_INTRA; 1.  
DR PROSITE; PS00280; BPTI\_KUNITZ; 1.  
DR PROSITE; PS00319; A4\_EXTRA; 1.  
DR PFAM; PF00014; Kunitz\_BPTI; 1.  
DR PRINTS; PR00203; AMYLOIDA4.  
DR PRINTS; PR00204; BETAMAMYLID.  
DR PRINTS; PR00759; BASICPTASE.  
KW Serine protease inhibitor.  
SQ SEQUENCE 747 AA; 84892 MW; A7580143 CRC32;

Query Match 83.7%; Score 77; DB 13; Length 747;  
Best Local Similarity 75.0%; Pred. No. 0.00013;  
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
QY 1 DAEFRHDSGYEVHHQK 16  
| | | | | | | | | | | | | | | | | |  
Db 649 DSEYRHDATAYEVHHQK 664

RESULT 9  
O35463 PRELIMINARY; PRT; 79 AA.  
AC O35463;  
DT 01-JAN-1998 (TREMELrel. 05, Created)  
DT 01-JAN-1998 (TREMELrel. 05, Last sequence update)  
DT 01-NOV-1999 (TREMELrel. 12, Last annotation update)  
DE ALZHEIMER'S AMYLOID BETA PROTEIN PRECURSOR (FRAGMENT).  
GN BETA APP.  
OS Cricetulus griseus (Chinese hamster).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Rodentia; Sclurognathi; Muridae; Cricetinae; Cricetulus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA SAMBAMURTI K., PINNIX I., GANDHI S.;  
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF030413; AAB86608.1; -.  
DR HSSP; P05067; 1QCM.  
DR NON\_TER 1  
FT NON\_TER 79  
SQ SEQUENCE 79 AA; 8538 MW; EB3BB61F CRC32;

Query Match 79.3%; Score 73; DB 11; Length 79;  
Best Local Similarity 81.2%; Pred. No. 5.5e-05;  
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 DAEFRHDSGYEVHHQK 16  
| | | | | | | | | | | | | | | | | |  
Db 21 DAEFRHDSGYEVHHQK 36  
RESULT 10

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P97487
ID P97487 PRELIMINARY; PRT; 695 AA.
AC P97487; P97942;
DT 01-MAY-1997 (TREMREL. 03, Created)
DT 01-MAY-1997 (TREMREL. 03, Last sequence update)
DT 01-NOV-1999 (TREMREL. 12, Last annotation update)
DE HIPPOCAMPAL AMYLOID PROTEIN.
GN APP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SAMP8; TISSUE-HIPPOCAMPUS;
RA FLOOD J.F., KUMAR V.B., SASSER T., WORD I., MORLEY J.E.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 581-662 FROM N.A.
RC STRAIN-129SV;
RA WRAGG M.A., BUSFIELD F., DUFF K., KORENBLAT K., CAPECCHI M.,
RA LORING J.F., GOATE A.M.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U84012; AAB41502.1; -
DR EMBL; U83624; ABA40919.1; -
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00204; BETAAMYLOID.
SQ SEQUENCE 695 AA; 78414 MW; B709D560 CRC32;

Query Match 79.3%; Score 73; DB 11; Length 695;
Best Local Similarity 81.2%; Pred. No. 0.00054;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQ 16
| | | | | | | | | | | | | | | |
DB 597 DAEFGHDSGFVHHQ 612

RESULT 11
Q57394 PRELIMINARY; PRT; 699 AA.
AC Q57394;
DT 01-JUN-1998 (TREMREL. 06, Created)
DT 01-JUN-1998 (TREMREL. 06, Last sequence update)
DT 01-NOV-1999 (TREMREL. 12, Last annotation update)
DE EL AMYLOID PRECURSOR PROTEIN 699.
GN EL APP699.
OS Narke japonica (Electric ray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Rajiformes; Narke.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-ELECTRIC LOBE;
RA IJIMA K., LEE D., OKUTSU J., TOMITA S., HIRASHIMA N., KIRINO Y.,
RA SUZUKI T.;
RL Biochem. J. 0:0-0(1998).
DR EMBL; AB005544; BAA24230.1; -
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00204; BETAAMYLOID.
SQ SEQUENCE 699 AA; 78879 MW; 11604C05 CRC32;

Query Match 78.3%; Score 72; DB 13; Length 699;
Best Local Similarity 75.0%; Pred. No. 0.00079;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps -0;

QY 1 DAEFRHDSGYEVHHQ 16
: | | | | | | | | | | | | | | | |
DB 601 ETEFGHDSGFVHHQ 616

P97487
ID P97487 PRELIMINARY; PRT; 292 AA.
AC Q85276;
DT 01-NOV-1996 (TREMREL. 01, Created)
DT 01-NOV-1996 (TREMREL. 01, Last sequence update)
DT 01-NOV-1998 (TREMREL. 08, Last annotation update)
DE POLYPROTEIN (FRAGMENT).
OS Potato virus Y.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
RN [1]
RP SEQUENCE FROM N.A.
RA GRIFFIN J.D., SHIEL P.S., BERGER P.H., THORNBURY D.W.;
RL Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.
DR EMBL; M81435; AAA47185.1; -
DR PFAM; PF00767; Poty_coat; 1.
KW Polyprotein.
FT NON_TER 1 1 NIB.
FT CHAIN 26 292 COAT PROTEIN.
SQ SEQUENCE 292 AA; 32945 MW; 8CB34E72 CRC32;

Query Match 54.9%; Score 50.5; DB 12; Length 292;
Best Local Similarity 73.3%; Pred. No. 0.94;
Matches 11; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 DAEFRHDSGYEVHHQ 15
| | | | | | | | | | | | | | | |
DB 12 DDEFEFDS-YEVHHQ 25

RESULT 13
Q9WG05 PRELIMINARY; PRT; 365 AA.
AC Q9WG05;
DT 01-NOV-1999 (TREMREL. 12, Created)
DT 01-NOV-1999 (TREMREL. 12, Last sequence update)
DT 01-NOV-1999 (TREMREL. 12, Last annotation update)
DE POLYPROTEIN (FRAGMENT).
OS Potato virus Y.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ORDINARY; O;
RA BHAT A.I., VARMA A., PAPPU H.R., RAJAMANNAR M., JAIN R.K., PRAVEEN S.;
RT "N-terminal serology and sequence relationships indicate that a
RT potyvirus from eggplant, Solanum melongena L., is a strain of potato
RT virus Y."
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF118153; AAD24563.1; -
KW NON_TER 1 1
FT CHAIN 1 1
SQ SEQUENCE 365 AA; 41418 MW; F3CF9EBD CRC32;

Query Match 54.9%; Score 50.5; DB 12; Length 365;
Best Local Similarity 73.3%; Pred. No. 1.2;
Matches 11; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 DAEFRHDSGYEVHHQ 15
| | | | | | | | | | | | | | | |
DB 85 DDEFEFDS-YEVHHQ 98

RESULT 14
Q85274 PRELIMINARY; PRT; 1555 AA.
ID Q85274
AC Q85274;

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DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)  
 DE POLYPROTEIN (FRAGMENT).  
 OS Potato virus Y.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;  
 OC Potyvirus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=O;  
 RX MEDLINE; 92335011.  
 RA HIDAKA M., YOSHIDA Y., MASAKI H., NAMBA S., YAMASHITA S.,  
 RA TSUCHIZAKI T., UOZUMI T.;  
 RT "Cloning and sequencing of the 3' half of a potato virus Y (O strain)  
 RT genome encoding the 5k protein, protease, polymerase and coat  
 RT protein.";  
 RL Nucleic Acids Res. 20:3515-3515(1992).  
 DR EMBL; D12539; BAA02107.1; .  
 DR PFAM; PF00863; Peptidase\_C4; 1.  
 DR PFAM; PF00767; Poty\_coat; 1.  
 DR PFAM; PF00680; RNA\_dep\_RNA\_pol; 1.  
 KW Polyprotein; Coat protein; Protease.  
 FT NON\_TER 1  
 FT CHAIN 1 285 CYTOPLASMIC INCLUSION BODY.  
 FT CHAIN 286 337 5-KD PROTEIN.  
 FT CHAIN 338 769 PROTEASE.  
 FT CHAIN 770 1288 RNA POLYMERASE.  
 FT CHAIN 1289 1555 COAT PROTEIN.  
 SQ SEQUENCE 1555 AA; 176933 MW; 4403DDF0 CRC32;

Query Match 54.9%; Score 50.5; DB 12; Length 1555;  
 Best Local Similarity 73.3%; Pred. No. 5.4;  
 Matches 11; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 DAEFRHDSGYEVHHQ 15  
 DB 1275 DDEFEFDS-YEVHHQ 1288  
 | | | | | | | | | |

RESULT 15  
 073683  
 ID 073683 PRELIMINARY; PRT; 780 AA.  
 AC 073683;  
 DT 01-AUG-1998 (TREMBlrel. 07, Created)  
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)  
 DE AMYLOID PRECURSOR PROTEIN.  
 OS Tetraodon fluviatilis (Puffer fish).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;  
 OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;  
 OC Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 98252138.  
 RA VILLARD L., TASSONE F., CRNOGORAC-JURCEVIC T., CLANCY K., GARDINER K.;  
 RT "Analysis of pufferfish homologues of the AT-rich human APP gene.";  
 RL Gene 210:17-24(1998).  
 DR EMBL; AF018165; AAC41275.1; .  
 DR PROSITE; PS00319; A4\_EXTRA; 1.  
 DR PROSITE; PS00320; A4\_INTRA; 1.  
 DR PFAM; PF00014; Kunitz\_BPTI; 1.  
 DR PRINTS; PR00203; AMYLOIDA4.  
 DR PRINTS; PR00204; BETAAMYLOID.  
 DR PRINTS; PR00759; BASICPTASE.  
 SQ SEQUENCE 780 AA; 88238 MW; 99DD89A8 CRC32;

Query Match 54.3%; Score 50; DB 13; Length 780;  
 Best Local Similarity 56.2%; Pred. No. 3.2;  
 Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQ 16

Db 682 ETEDEQSTEEYEVHHQK 697  
 : | | : | | | | |

Search completed: September 13, 2000, 02:24:10  
 Job time: 178 sec

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Wed Sep 13 08:11:43 2000

OM of: US-09-155-076-2 to: EST:\* out\_format : pfs

Date: Sep 13, 2000 2:42 AM

About: Results were produced by the GenCore software, version 4.5,  
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Command line parameters:

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-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -QGAPOP=4.500
-GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FCAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blossum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
-MAXLEN=1000000 -USER=US09155076 @CGN1_1_1327 -NCPU=6
-LONGLOG -NO_XLPXY -WAIT -THREADS=1
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Search information block:

Query: US-09-155-076-2

Query length: 16

Database: EST:\*

Database sequences: 5247842

Database length: -2090053206

Search time (sec): 875.890000

score\_list:

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gb_est4:AA385402	-	92.00	280.72	8.3e-07	277
gb_est27:AA1909276	-	92.00	280.68	8.3e-07	278
gb_est5:AA303751	+	92.00	279.17	9.0e-07	297
gb_est47:FA06018	+	92.00	280.87	9.3e-07	305
gb_est46:AA1902528	-	92.00	279.85	9.3e-07	306
gb_est26:AA1902528	-	92.00	279.05	9.1e-06	335
gb_est5:AA322074	+	92.00	278.98	1.0e-06	338
gb_est26:AA1902529	+	92.00	278.98	1.0e-06	338
gb_est5:AA304003	+	92.00	278.57	1.1e-06	334
gb_est52:TA99906	+	92.00	277.88	1.2e-06	333
gb_est51:RI19709	+	92.00	277.53	1.3e-06	339
gb_est16:AA134479	+	92.00	277.14	1.3e-06	417
gb_est16:AA1124771	+	92.00	276.26	1.5e-06	461
gb_est44:AA601576	+	92.00	276.11	1.5e-06	489
gb_est51:R25913	+	92.00	275.82	1.6e-06	485
gb_est3:AA218652	+	92.00	275.36	1.6e-06	511
gb_est44:AA602193	+	92.00	274.85	1.8e-06	542
gb_est45:AA6073480	+	92.00	273.87	2.0e-06	606
gb_est2:AA082598	+	92.00	273.80	2.0e-06	611
gb_est2:AA081869	+	92.00	273.66	2.1e-06	621
gb_est28:AA1980795	+	92.00	273.23	2.2e-06	632
gb_est41:AA362085	+	88.00	271.82	2.6e-06	284
gb_est44:AA581403	+	88.00	260.89	1.1e-05	647
gb_est44:AA607890	+	86.00	261.81	9.4e-06	286
gb_est44:AA608448	+	86.00	254.14	2.5e-05	688
gb_est5:AA299326	+	84.00	256.20	1.9e-05	381
gb_est41:AA364975	+	84.00	252.72	3.0e-05	398
gb_est28:AA046001	+	84.00	250.21	4.2e-05	530
gb_est1:AA0342972	+	82.00	249.31	4.7e-05	289
gb_est4:AA608486	+	82.00	245.63	7.5e-05	440
gb_est44:AA577954	+	81.00	242.37	0.0001	639
gb_est54:AA577954	+	81.00	255.05	2.2e-05	105
gb_est54:AA577954	+	76.00	222.66	0.0014	724
gb_est13:AA669182	+	73.00	220.96	0.0018	241
gb_est13:AA669182	+	73.00	220.93	0.0018	304
gb_est53:AA13829	+	73.00	218.71	0.0023	389
gb_est2:AA074807	+	73.00	218.31	0.0025	410
gb_est13:AA914658	+	73.00	218.00	0.0026	425
gb_est24:AA1717076	+	73.00	218.00	0.0026	425
gb_est7:AA462949	+	73.00	217.62	0.0027	444

gb\_est15:AI045218 - 73.00 217.33 0.0028 459 ! AI045218 UI-R-Cl-ju-g-11-0-0  
gb\_est2:AA137593 + 73.00 217.16 0.0029 468 ! AA137593 mq28a02.r1 Barstead  
gb\_est41:AA321190 + 73.00 216.97 0.0029 478 ! AW321190 uc27a05.y1 NCI CGAP  
gb\_est3:AA174337 + 73.00 216.51 0.0031 504 ! AA174337 mo96g11.r1 Stratage

seq\_name: gb\_est6:AA385402

seq\_documentation\_block:

LOCUS AA385402 246 bp mRNA EST 21-APR-1997  
DEFINITION EST99048 Thyroid Homo sapiens cDNA 5' end similar to amyloid, A4  
beta subunit, mRNA sequence.  
ACCESSION AA385402  
VERSION AA385402.1 GI:2037720  
KEYWORDS EST.  
SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 246)

AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,

Buit,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,  
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,  
Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,  
Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,  
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,  
Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,  
Moreno-Palanco,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,  
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,  
Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,  
Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,  
Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,  
He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,  
Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,  
Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,  
Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,  
Fraser,C.M. and Venter,J.C.

TITLE Initial assessment of human gene diversity and expression patterns  
based upon 83 million nucleotides of cDNA sequence

NATURE 377 (6547 Suppl), 3-174 (1995)

12140200

COMMENT

Other\_ESTs: THC172078

Contact: Kerlavage, AR

Bioinformatics

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850 USA

Tel: 3018699056

Fax: 3018699423

Email: arkerlavet@tigr.org

For clone availability, additional sequence and expression

information related to this EST, please check the TIGR Human Gene

Index (<http://www.tigr.org/tdb/hgi/hgi.html>)

Seq primer: M13 Reverse.

Location/Qualifiers

1. 246

/organism="Homo sapiens"

/db\_xref="ATCC (inhst):189572"

/db\_xref="taxon:9606"

/clone\_lib="Thyroid"

/dev\_stage="adult"

/note="Organ: thyroid gland; Vector: pBluescript SK-;

Site\_1: EcoRI; Site\_2: XhoI"

BASE COUNT 70 a 48 c 68 g 58 t

ORIGIN

alignment\_scores:

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Ratio: 5.750 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-155-076-2 x AA385402 ..

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Align seg 1/1 to: AA385402 from: 1 to: 246

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seq_name: gb_est41:AW379017

seq_documentation_block: 277 bp mRNA EST 04-FEB-2000
LOCUS AW379017
DEFINITION RC3-HT0230-241099-012-c12 HT0230 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW379017
VERSION AW379017.1 GI:6883676
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 277)
AUTHORS HCGP http://www.ludwig.org.br/ORESTES.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT On Apr 7, 1998 this sequence version replaced gi:3036339.
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC3&t2=RC3-HT0230-
241099-012-c12&t3=1999-10-24&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 277.
Location/Qualifiers
1..277
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/db_xref="taxon:9606"
/clone_lib="HT0230"
/dev_stage="Adult"
/note="Organ: head neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 70 a 79 c 51 g 77 t
ORIGIN

alignment_scores:
Quality: 92.00 Length: 16
Ratio: 5.750 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-2 x AW379017/rev ..
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|||||
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seq_name: gb_est27:AI909276

seq_documentation_block: 278 bp mRNA EST 30-MAR-2000
LOCUS AI909276
DEFINITION QV-BT202-070599-188 BT202 Homo sapiens cDNA, mRNA sequence.
ACCESSION AI909276
VERSION QV-BT202-070599-188 BT202 Homo sapiens cDNA, mRNA sequence.
KEYWORDS EST.
SOURCE human.

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ACCESSION AI909276
VERSION AI909276.1 GI:6499956
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 278)
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Negai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7): 3491-3496 (2000)
COMMENT On Jan 19, 1998 this sequence version replaced gi:2284565.
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/seg/gethtml.pl?tl=QV&t2=QV-BT202-188.html
&t3=070599&t4=1)
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Location/Qualifiers
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/db_xref="taxon:9606"
/clone_lib="BT202"
/sex="female"
/dev_stage="Adult"
/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT 71 a 79 c 54 g 74 t
ORIGIN

alignment_scores:
Quality: 92.00 Length: 16
Ratio: 5.750 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-2 x AI909276/rev ..
Align seg 1/1 to reverse of: AI909276 from: 1 to: 278

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207 GATGAGAAATCCGACATGACTCAGGATATGAGTTCATCATCAAAA 160

seq_name: gb_est5:AA303751

seq_documentation_block: 297 bp mRNA EST 18-APR-1997
LOCUS AA303751
DEFINITION EST16434 Aorta endothelial cells, TNF alpha-treated Homo sapiens
cDNA 5' end similar to amyloid, A4 beta subunit, mRNA sequence.
ACCESSION AA303751
VERSION AA303751.1 GI:1956103
KEYWORDS EST.
SOURCE human.

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**ORGANISM** Homo sapiens  
**REFERENCE** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
**AUTHORS** 1 (bases 1 to 297)  
 Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Feldner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Van-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodak,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarek,D.P., Caol., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,J., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.  
**TITLE** Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence  
**JOURNAL** Nature 377 (6547 Suppl), 3-174 (1995)  
**MEDLINE** 12140200  
**COMMENT** On Sep 29, 1997 this sequence version replaced qi:1520591.

VERSION	F06018.1	GI:669834
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.	
AUTHORS	1 (bases 1 to 305) Auffray, C., Behar, G., Bois, F., Bouchier, C., da Silva, C., Denzovo, M.D., Duprat, S., Houligatte, R., Jumeau, M.N., Lamy, B., Lorenzo, F., Mitchell, H., Mariage-Samson, R., Pietu, G., Pouliot, Y., Sebastiani-Kabatchis, C. and Tessier, A.	
TITLE	IMAGE: molecular integration of the analysis of the human genome and its expression	
JOURNAL	C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)	
MEDLINE	95277534	
COMMENT	On May 20, 1999 this sequence version replaced gi:4878117. Contact: Genethon Genexpress-Genethon Genethon Centre de recherche sur le Genome Humain 1 rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE Tel: 33169472800 Fax: 33160778698 Email: genexpress@genethon.fr Single read. Genexpress.library_id: C; Genexpress_sequence_id: ylc-0ua10 Seq primer: (-21)M31 universal	

REFERENCE 1 (bases 1 to 306)  
 AUTHORS HCGP http://www.ludwig.org.br/ORESTES.  
 TITLE The FAPESP/LICR Human Cancer Genome Project  
 JOURNAL Unpublished (1999)  
 COMMENT On Jan 6, 2000 this sequence version replaced gi:6676947.  
 CONTACT: Simpson A.J.G.  
 LABORATORY OF Cancer Genetics  
 RUA Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 TEL: +55-11-2704922  
 FAX: +55-11-2707001  
 EMAIL: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC4&t2=RC4-LT0011-  
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 Seq primer: puc 18 forward  
 High quality sequence start: 6  
 High quality sequence stop: 306.

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 /note="Organ: leiomyos; Vector: puc18; Site1: SmaI;  
 Site2: SmaI; A mini-library was made by cloning products  
 derived from ORESTES PCR (U.S. Letters Patent application  
 No. 196,716 - Ludwig Institute for Cancer Research)  
 profiles into the puc 18 vector. Reverse transcription of  
 tissue mRNA and cDNA amplification were performed under  
 low stringency conditions."  
 72 a 80 c 65 g 89 t

BASE COUNT  
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 Ratio: 5.750 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
 US-09-155-076-2 x AW580695/rev ..  
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seq\_name: gb\_est26:AI902528

seq\_documentation\_block:  
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 DEFINITION QV-BT009-101198-075 BT009 Homo sapiens cDNA, mRNA sequence.  
 ACCESSION AI902528  
 VERSION AI902528.1 GI:6492915  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 335)  
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
 Nagai,M.A., da Silva,W. Jr., Zagó,M.A., Bordin,S., Costa,F.F.,  
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,  
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,  
 O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
 Simpson,A.J.  
 Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags  
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

## COMMENT

On May 18, 1998 this sequence version replaced gi:3138510.  
 CONTACT: Simpson A.J.G.  
 LABORATORY OF Cancer Genetics  
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 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
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 FAX: +55-11-2707001  
 EMAIL: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/seq/gethtml.pl?tl=QV&t2=QV-BT009-075.html  
 &t3=101198&t4=1)

Seq primer: puc 18 forward.

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 /clone\_lib="BT009"  
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 /dev\_stage="Adult"  
 /note="Organ: breast; Vector: puc18; Site1: SmaI; Site2:  
 SmaI; A mini-library was made by cloning products derived  
 from ORESTES PCR (U.S. Letters Patent application No.  
 196,716 - Ludwig Institute for Cancer Research) profiles  
 into the puc 18 vector. Reverse transcription of tissue  
 mRNA and cDNA amplification were performed under low  
 stringency conditions."  
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BASE COUNT  
ORIGIN

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 Ratio: 5.750 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

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US-09-155-076-2 x AI902528/rev ..  
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 312 GATGCGAATTCGACATGACTGACGATATGAGTTCATCATCAAAAA 265

seq\_name: gb\_est5:AA322074

seq\_documentation\_block:  
 LOCUS AA322074 338 bp mRNA EST 19-APR-1997  
 DEFINITION EST24653 Cerebellum II Homo sapiens cDNA 5' end similar to amyloid,  
 A4 beta subunit, mRNA sequence.

ACCESSION AA322074  
 VERSION AA322074.1 GI:1974399  
 KEYWORDS EST.  
 SOURCE human.

## ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

## AUTHORS

1 (bases 1 to 338)  
 Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,  
 Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gockayne,J.D.,  
 White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,  
 Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,  
 Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,  
 Glodok,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,  
 Kelley,J.M., Kelley,J.C., Liu,J.-I., Marmaros,S.M., Merrick,J.M.,  
 Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,  
 Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,  
 Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,  
 Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,  
 Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,  
 He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,

Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Weissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

Nature 377 (6547 Suppl), 3-174 (1995)

12140200

Other\_ESTs: THC172078

Contact: Kerlavage, AR

Bioinformatics

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850 USA

Tel: 3018699056

Fax: 3018699423

Email: arkerlav@tigr.org

For clone availability, additional sequence and expression

information related to this EST, please check the TIGR Human Gene

Index (<http://www.tigr.org/tdb/hgi/hgi.html>)

Seq primer: M13 Reverse:

Location/Qualifiers

1. .338

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/db\_xref="ATCC (inhost):122569"

/db\_xref="taxon:9606"

/clone\_lib="Cerebellum II"

/tissue\_type="cerebellum"

/dev\_stage="adult"

/note="Organ: brain; Vector: pBluescript SK-; Site\_1:

EcoRI; Site\_2: XhoI"

BASE COUNT 86 a 78 c 95 g 79 t

ORIGIN

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Quality: 92.00 Length: 16  
Ratio: 5.750 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

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US-09-155-076-2 x AA322074 ..

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LOCUS AI902529 338 bp mRNA EST 30-MAR-2000

DEFINITION QV-BT009-101198-074 BT009 Homo sapiens cDNA, mRNA sequence.

ACCESSION AI902529

VERSION AI902529.1 GI:6492916

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 338)

DIAS Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,

O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and

Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

On Oct 30, 1998 this sequence version replaced gi:3814489.

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL

(<http://www.ludwig.org.br/seq/gethtml.pl?cl=QV&t2=QV-BT009-074.html>)

Seq primer: puc 18 forward.

Location/Qualifiers

1. .338

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_lib="BT009"

/sex="female"

/dev\_stage="Adult"

/note="Organ: breast; Vector: puc18; Site\_1: SmaI; Site\_2:

SmaI; A mini-library was made by cloning products derived

from ORESTES PCR (U.S. Letters Patent application No.

196,716 - Ludwig Institute for Cancer Research) profiles

into the puc 18 vector. Reverse transcription of tissue

mRNA and cDNA amplification were performed under low

stringency conditions."

BASE COUNT 78 a 89 c 76 g 95 t

ORIGIN

#### alignment\_scores:

Quality: 92.00 Length: 16  
Ratio: 5.750 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

#### alignment\_block:

US-09-155-076-2 x AI902529/rev ..

Align seg 1/1 to reverse of: AI902529 from: 1 to: 338

1 AsplagluPheArgHisAspSerGlyTyrGluValHisHisGlnLys 16

|||||GATGAGAAATTCGACATGACTCAGGATATGAGTTCATCAAAAA 268

315 GATGAGAAATTCGACATGACTCAGGATATGAGTTCATCAAAAA 268

seq\_name: gb\_est5:AA304003

#### seq\_documentation\_block:

LOCUS AA304003 354 bp mRNA EST 18-APR-1997

DEFINITION EST16883 Aorta endothelial cells, TNF alpha-treated Homo sapiens

cDNA 5' end similar to amyloid, A4 beta subunit, mRNA sequence.

ACCESSION AA304003

VERSION AA304003.1 GI:1956491

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 354)

AUTHORS

ADAMS, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,

Bull, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,

White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,

Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,

Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,

Glocke, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,

Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,

Moreno-Palancas, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,

Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,

Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,

Bednarek, D.P., Cao, L., Cepeda, W.A., Coleman, T.A., Collins, E.J.,

Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,

He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,

Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Weissner, P.S., Olsen, H.,

Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,

Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,

Fraser, C.M. and Venter, J.C.  
Initial assessment of human gene diversity and expression patterns  
based upon 83 million nucleotides of cDNA sequence  
JOURNAL Nature 377 (6547 Suppl.), 3-174 (1995)  
MEDLINE 12140200  
COMMENT On Jan 17, 1998 this sequence version replaced gi:1900069.  
Other\_ESTs: THC172078  
Contact: Kerlavage, AR  
Bioinformatics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850 USA  
Tel: 3018699056  
Fax: 3018699423  
Email: arkerlav@etigr.org  
For clone availability, additional sequence and expression  
information related to this EST, please check the TIGR Human Gene  
Index (<http://www.tigr.org/tdb/hgi/hgi.html>)  
Seq primer: M13 Reverse.

FEATURES  
source  
1. .354  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="AFCC (inhost):115766"  
/db\_xref="taxon:9606"  
/clone\_lib="Aorta endothelial cells, TNF alpha-treated"  
/cell\_type="endothelial cell"  
/dev\_stage="adult"  
/note="Organ: aorta; Vector: pBluescript SK-; Site\_1:  
ECORI; Site\_2: XhoI"  
BASE COUNT 102 a 80 c 92 g 78 t 2 others  
ORIGIN

alignment\_scores:  
Quality: 92.00 Length: 16  
Ratio: 5.750 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
US-09-155-076-2 x AA304003 ..  
Align seg 1/1 to: AA304003 from: 1 to: 354

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisHisGlnLys 16  
|||||  
10 GATGCAGATTCGACATCGACTCAGATATGAGTTCATCATCAAAAA 57

seq\_name: gb\_est52:T49906

seq\_documentation\_block:  
LOCUS T49906 383 bp mRNA EST 06-FEB-1995  
DEFINITION Y99906 r1 Stratagene placenta (#937225) Homo sapiens cDNA clone  
IMAGE:69779 5' similar to gb:X06989\_rnal ALZHEIMER'S  
DISEASE AMYLOID A4 PROTEIN PRECURSOR (HUMAN), mRNA sequence.

ACCESSION T49906  
VERSION T49906.1 GI:651766  
KEYWORDS EST.  
SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 383)  
AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,  
Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W.,  
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,  
Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,  
Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierri-Meg, J.,  
Trevasakis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R.  
and Marra, M.

TITLE Generation and analysis of 280,000 human expressed sequence tags  
JOURNAL Genome Res. 6 (9), 807-828 (1996)  
MEDLINE 9704478  
COMMENT On Nov 2, 1998 this sequence version replaced gi:3828645.  
Contact: Wilson RK

Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
Source: IMAGE Consortium, LLNL  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
Seq primer: M13RPI  
High quality sequence stop: 384.

FEATURES  
source  
1. .383  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="GDB:490676"  
/db\_xref="taxon:9606"  
/clone\_lib="IMAG:69779"  
/clone\_lib="Stratagene placenta (#937225)"  
/sex="male"  
/lab\_host="SOLR cells (kanamycin resistant)"  
/note="Organ: placenta; Vector: pBluescript SK-; Site\_1:  
ECORI; Site\_2: XhoI; Cloned unidirectionally. Primer:  
Oligo dT. Caucasian. Average insert size: 1.2 kb; Uni-ZAP  
XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGAG 3' -3'  
adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"

BASE COUNT 113 a 81 c 103 g 86 t  
ORIGIN

alignment\_scores:  
Quality: 92.00 Length: 16  
Ratio: 5.750 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
US-09-155-076-2 x T49906 ..

Align seg 1/1 to: T49906 from: 1 to: 383

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisHisGlnLys 16  
|||||  
61 GATGCAGATTCGACATCGACTCAGATATGAGTTCATCATCAAAAA 108

seq\_name: gb\_est51:R19709

seq\_documentation\_block:  
LOCUS R19709 399 bp mRNA EST 17-APR-1995  
DEFINITION Y935f04.r1 Soares infant brain INIB Homo sapiens cDNA clone  
IMAGE:34389 5' similar to gb:X06989\_rnal ALZHEIMER'S DISEASE  
AMYLOID A4 PROTEIN PRECURSOR (HUMAN);, mRNA sequence.

ACCESSION R19709  
VERSION R19709.1 GI:774343  
KEYWORDS EST.  
SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 399)  
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
Wilson, R.

TITLE The WashU-Merck EST Project  
JOURNAL Unpublished (1995)  
COMMENT On Jan 19, 1998 this sequence version replaced gi:2284625.  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
Insert Size: 1369  
High quality sequence stops: 214 Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
 Insert length: 1369 Std Error: 0.00  
 Seq primer: M13RPI  
 High quality sequence stop: 214.

## FEATURES

## source

```

1. .399
/organism="Homo sapiens"
/db_xref="GBE:406736"
/cd_xref="taxon:9606"
/clone="IMAGE:34389"
/clone_lib="Soares infant brain INIB"
/sex="female"
/dev_stage="73 days post natal"
/lab_host="DH10B (ampicillin resistant)"
/notes="organ: whole brain; Vector: Larmid BA; Site_1: Not I; Site_2: Hind III; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' AACTGGAGAATTCGCGCGCAGGAATTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the Larmid BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT 104 a 85 c 106 g 94 t 10 others
ORIGIN

```

## alignment\_scores:

```

Quality: 92.00 Length: 16
Ratio: 5.750 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

```

## alignment\_block:

```
US-09-155-076-2 x R19709 ..
```

```
Align seg 1/1 to: R19709 from: 1 to: 399
```

```

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
|||||
219 GATGCAGAAATTCGACATGACTCAGGATATGAAATTCATCATCAAAAA 266

```

```
seq_name: gb_est2:AA134479
```

## seq\_documentation\_block:

```

LOCUS AA134479 417 bp mRNA EST 23-DEC-1997
DEFINITION ZO10904.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens
cDNA clone IMAGE:567318 5' similar to gb:X06989_rnal ALZHEIMER'S
DISEASE AMYLOID A4 PROTEIN PRECURSOR (HUMAN);, mRNA sequence.
AA134479
ACCESSION AA134479.1 GI:1692245
VERSION AA134479.1
KEYWORDS EST.
SOURCE human.

```

## ORGANISM

```

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

## REFERENCE

```

1 (bases 1 to 417)
Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissos,M., Dietrich,N., Dubuque,T., Favell,A., Gish,W.,
Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J.,
Trevaaskis,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R.
and Maria,M.

```

```
Generation and analysis of 280,000 human expressed sequence tags
```

```
Genome Res. 6 (9), 807-828 (1996)
```

```
97044478
```

```
Contact: Wilton RK
```

```
Washington University School of Medicine
```

```
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
```

```
Tel: 314 286 1800
```

```
Fax: 314 286 1810
```

```
Email: est@watson.wustl.edu
```

## TITLE

## JOURNAL

## COMMENT

```
Washington University School of Medicine
```

```
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
```

```
Tel: 314 286 1800
```

```
Fax: 314 286 1810
```

```
Email: est@watson.wustl.edu
```

```
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
```

WARNING: There is evidence that suggests that the 384-well parent plate of this clone contains both human and mouse derived clones. Thus, the origin of this clone is uncertain. This caution should be kept in mind should you use this clone.

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
 Insert length: 1384 Std Error: 0.00  
 Seq primer: -28M13 rev2 from Amersham  
 High quality sequence stop: 394.

## FEATURES

## source

```

1. .417
/organism="Homo sapiens"
/db_xref="GBE:459117"
/cd_xref="taxon:9606"
/clone="IMAGE:567318"
/dev_stage="Ntera-2/RA-MI neuroepithelial cells"
/lab_host="SOLR (kanamycin resistant)"
/notes="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT. NT2 (Ntera-2/cl.D1) precursor cells induced with Retinoic Acid for 1 week, followed by 3 weeks in mitotic inhibitors (Replate #2). Average insert size: 1.1 kb; Uni-ZAP XR Vector: -5' adaptor sequence: 5' GAATTCGGCAGAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'."
BASE COUNT 110 a 93 c 117 g 95 t 2 others
ORIGIN

```

## alignment\_scores:

```

Quality: 92.00 Length: 16
Ratio: 5.750 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

```

## alignment\_block:

```
US-09-155-076-2 x AA134479 ..
```

```
Align seg 1/1 to: AA134479 from: 1 to: 417
```

```

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
|||||
159 GATGCAGAAATTCGACATGACTCAGGATATGAAATTCATCATCAAAAA 206

```

```
seq_name: gb_est16:AA124771
```

## seq\_documentation\_block:

```

LOCUS AA124771 461 bp mRNA EST 11-SEP-1998
DEFINITION am61h12.x1 Johnston frontal cortex Homo sapiens cDNA clone
IMAGE:1540103 3' similar to gb:X06989_rnal ALZHEIMER'S DISEASE
AMYLOID A4 PROTEIN PRECURSOR (HUMAN);, mRNA sequence.
AA124771
ACCESSION AA124771
VERSION AA124771.1 GI:3593285
KEYWORDS EST.
SOURCE human.

```

## ORGANISM

```

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

## REFERENCE

```

1 (bases 1 to 461)
Hillier,L., Lennon,G., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krieman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Maria,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theising,B., White,V., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilton RK

```

## JOURNAL

## COMMENT

```
Washington University School of Medicine
```

```
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
```

```
Tel: 314 286 1800
```

```
Fax: 314 286 1810
```

```
Email: est@watson.wustl.edu
```

```
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
```

Seq primer: -40m13 fwd. ET from Amersham  
High quality sequence stop: 423.

# FEATURES source

1. .461  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1540103"  
/clone\_lib="Johnston frontal cortex"  
/sex="male"  
/tissue\_type="pooled frontal lobe"  
/dev\_stage="adult"  
/lab\_host="SOLR (kanamycin resistant)"  
/note="Organ: brain; Vector: Bluescript SK-; Site\_1:  
ECORI; Stanley NeuroPathology Consortium  
(www.stanleylab.org) brains S-58, S-65, S-67, S-78.  
Random + oligo-qt primed into EcoRI site of ZAP II Vector.  
Mass excised. Avg insert length 1.9kb. Custom library  
provided by Dr. Nancy Johnston [(410) 514-3918,  
nlj@welchlink.welch.jhu.edu].  
1 others  
BASE COUNT 101 a 123 c 110 g 126 t  
ORIGIN

alignment\_scores:  
Quality: 92.00 Length: 16  
Ratio: 5.750 Gaps: 0  
Percent Similarity: 100.000 Percent identity: 100.000

alignment\_block:  
US-09-155-076-2 x A1124771/rev ..  
Align seg 1/1 to reverse of: A1124771 from: 1 to: 461  
1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16  
|||||  
314 GATGCAGAAATTCGACATGACTCAGGATATGAAGTTCATCAAAAA 267

seq\_name: gb\_est44:AW601576

seq\_documentation\_block:  
LOCUS AW601576 469 bp mRNA EST 23-MAR-2000  
DEFINITION QV3-BT0381-270100-073-f06 BT0381 Homo sapiens cDNA, mRNA sequence.

ACCESSION AW601576  
VERSION AW601576.1 GI:7306315  
KEYWORDS EST.  
SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 469)  
HGCP <http://www.ludwig.org.br/ORESTES>.  
The FAPESP/LICR Human Cancer Genome Project  
Unpublished (1999)  
On Jan 6, 2000 this sequence version replaced gi:5677550.  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)

This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl-QV3st2-QV3-BT0381-270100-073-f06st3-2000-01-27st4-1>)  
Seq primer: puc 18 forward  
High quality sequence start: 111  
High quality sequence stop: 469.  
High quality sequence stop: 469.

# FEATURES source

1. .469  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"

/clone\_lib="BT0381"  
/dev\_stage="Adult"  
/note="Organ: breast; Vector: puc18; Site\_1: SmaI; Site\_2:  
SmaI; A mini-library was made by cloning products derived  
from ORESTES PCR (U.S. Letters Patent application No.  
196,716 - Ludwig Institute for Cancer Research) profiles  
into the pUC 18 vector. Reverse transcription of tissue  
mRNA and cDNA amplification were performed under low  
stringency conditions."  
BASE COUNT 128 a 120 c 117 g 104 t  
ORIGIN

alignment\_scores:  
Quality: 92.00 Length: 16  
Ratio: 5.750 Gaps: 0  
Percent Similarity: 100.000 Percent identity: 100.000

alignment\_block:  
US-09-155-076-2 x AW601576 ..  
Align seg 1/1 to: AW601576 from: 1 to: 469

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16  
|||||  
422 GATGCAGAAATTCGACATGACTCAGGATATGAAGTTCATCAAAAA 469

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 13, 2000, 02:25:00 ; Search time 17.65 seconds  
(without alignments)  
21.472 Million cell updates/sec

Title: US-09-155-076-2  
Perfect score: 16  
Sequence: 1 DAEFRHDSGYEVHHQK 16

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0  
Searched: 188963 seqs, 23686106 residues  
Word size : 0

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0  
Maximum DB seq length: 1000000

Post-processing: Listing first 45 summaries

Database : A\_Geneseq\_36:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	16	100.0	16	Beta-amyloid (1-16)
2	16	100.0	16	Human beta-amyloid
3	16	100.0	21	Beta-secretase sub
4	16	100.0	22	Beta-amyloid protri
5	16	100.0	28	Synthetic A4 amylo
6	16	100.0	28	Beta-amyloid fragm
7	16	100.0	28	Beta-amyloid (1-28
8	16	100.0	28	Beta/A4-amyloid pe
9	16	100.0	28	Beta/A4-amyloid pe
10	16	100.0	28	A4-O(1-28) a parti
11	16	100.0	28	Synthetic amyloid
12	16	100.0	30	Synthetic amyloid
13	16	100.0	33	Beta-secretase sub
14	16	100.0	33	Synthetic amyloid
15	16	100.0	33	Amyloid precursor
16	16	100.0	35	Beta-amyloid pepti
17	16	100.0	35	Beta-amyloid pepti
18	16	100.0	35	Beta-amyloid pepti
19	16	100.0	35	Beta-amyloid pepti
20	16	100.0	35	Beta-amyloid pepti
21	16	100.0	36	Synthetic amyloid
22	16	100.0	38	Beta-amyloid (1-38
23	16	100.0	38	Human tachykinin a
24	16	100.0	39	Beta-amyloid (1-39
25	16	100.0	39	Synthetic amyloid
26	16	100.0	40	Beta-amyloid pepti
27	16	100.0	40	Beta-amyloid pepti
28	16	100.0	40	Amyloid beta pepti
29	16	100.0	40	Amyloid beta pepti
30	16	100.0	40	Amyloid beta prote
31	16	100.0	40	Beta-amyloid pepti
32	16	100.0	40	Beta-amyloid pepti
33	16	100.0	40	Synthetic amyloid
				Human tachykinin a

34 16 100.0 40 1 W9584 Wild type aggregat  
35 16 100.0 41 1 R2206 Alzheimer's amyloi  
36 16 100.0 41 1 R60365 Beta-amyloid (1-41  
37 16 100.0 41 1 R65283 Beta-amyloid pepti  
38 16 100.0 42 1 R20330 Sequence of A99 (b  
39 16 100.0 42 1 R33192 Beta-amyloid pepti  
40 16 100.0 42 1 R60366 Beta-amyloid (1-42  
41 16 100.0 42 1 R65285 Beta amyloid pepti  
42 16 100.0 42 1 R65286 Beta amyloid pepti  
43 16 100.0 42 1 R65287 Beta amyloid pepti  
44 16 100.0 42 1 R65288 Beta amyloid pepti  
45 16 100.0 42 1 R94591 Alzheimer amyloid

ALIGNMENTS

RESULT 1  
R60371  
ID R60371 standard; peptide; 16 AA.  
AC R60371, 1995 (first entry)  
DE Beta-amyloid (1-16).  
KW Amyloid precursor protein; APP; Alzheimer's disease; beta-amyloid;  
KW anti-beta-amyloid antibody; diagnosis; immunogen; antigen; epitope.  
OS Homo sapiens.  
PN W09417197-A.  
PD 04-AUG-1994.  
PF 24-JAN-1994; J00089.  
PR 25-JAN-1993; JP-010132.  
PR 05-FEB-1993; JP-019035.  
PR 16-NOV-1993; JP-286985.  
PR 28-DEC-1993; JP-334773.  
PA (TAKE ) TAKEDA CHEM IND LTD.  
PI Kitada C, Odaoka A, Suzuki N;  
DR WPI; 94-264110/32.  
PT Antibodies recognising specific parts of beta-amyloid - can be  
PT used for diagnosis of diseases implicating beta-amyloid, such as  
PT Alzheimer's disease  
PS Claim 7; Page 85; 116pp; Japanese.  
CC Antibodies which recognise specific subfragments of the beta-amyloid  
CC protein are claimed. Specifically, the antibodies (which are pref.  
CC monoclonal) recognise residues 1-16 and/or 1-28 from the N-terminal  
CC portion of beta-amyloid or they recognise residues 25-35 or 35-43  
CC from the C-terminal portion. The antibodies are useful for assaying  
CC beta-amyloid and its derivatives for diagnosis of Alzheimer's  
CC disease.  
SQ Sequence 16 AA;

Query Match 100.0%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 5.6e-12; Mismatches 0; Gaps 0;  
Matches 16; Conservative 0; Indels 0;

QY 1 DAEFRHDSGYEVHHQK 16  
Db 1 DAEFRHDSGYEVHHQK 16  
|||||

RESULT 2  
W35344  
ID W35344 standard; peptide; 16 AA.  
AC W35344;  
DT 17-APR-1998 (first entry)  
DE Human beta-amyloid precursor 16-mer peptide.  
KW Beta-amyloid precursor polypeptide; acetylcholinesterase; AChE;  
KW neuronal degeneration; Parkinson's disease; Alzheimer's disease;  
OS Homo sapiens.  
PN W09735962-A1.  
PD 02-OCT-1997.  
PF 21-MAR-1997; G00796.  
PR 22-MAR-1996; GB-006040.

PA (ISIS-) ISIS INNOVATION LTD.  
 PI Greenfield SA, Vaux DJ;  
 DR WPI: 97-489626/45.  
 PT peptide(s) from acetylcholine esterase which open calcium channels -  
 PT used for treating disorders of the central nervous system, cancer  
 PT and stroke  
 PS Claim 3; Page 20; 27pp; English.  
 CC This 16-mer peptide is present in a region of the beta-amyloid precursor  
 CC polyptide. This region lies at the amino acid terminus of the 42  
 CC residue peptide which accumulates in Alzheimer's disease. The 16-mer  
 CC has at least 70% homology with the beta-amyloid precursor. This peptide  
 CC is known to act alone or in synergism with a fragment of  
 CC acetylcholinesterase (W5340-W5343) to contribute to neuronal  
 CC degeneration. Compounds that inhibit the biological activity of the  
 CC novel peptides, and antibodies, can be used to control cytoplasmic  
 CC calcium ion currents in vivo, and are useful for treating disorders of  
 CC the central nervous system (e.g. Parkinson's and Alzheimer's diseases),  
 CC stroke and cancer.  
 SQ Sequence 16 AA;

Query Match 100.0%; Score 16; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 5.6e-12;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16  
 DB 1 DAEFRHDSGYEVHHQK 16

RESULT 3

ID W08361 standard; peptide; 21 AA.  
 AC W08361;  
 DT 05-SEP-1997 (first entry)  
 DE Beta-secretase substrate #3.  
 KW Beta-cleavage site; beta amyloid precursor protein; APP; beta-secretase;  
 KW alpha-secretase; proteolytic cleavage; inhibitor; Alzheimer's disease.  
 OS Synthetic.  
 PN W09640885-A2.  
 PD 19-DEC-1996.  
 PF 07-JUN-1996; U09985.  
 PR 07-JUN-1995; US-487152.  
 PR 07-JUN-1995; US-460498.  
 PA (ATHE-) ATHENA NEUROSCIENCES INC.  
 PI Anderson JP, Chrysler SMS, Jacobson-croak KL, Keim PS;  
 PI McConlogue LC, Sinha S, Tan H;  
 DR WPI: 97-052304/05.  
 PT Beta-secretase which specifically cleaves beta-amyloid precursor  
 PT protein - useful to screen for inhibitors useful in treatment of  
 PT Alzheimer's disease  
 PS Disclosure; Page 45; 92pp; English.  
 CC W08359-W08362 represent substrates for the enzyme of the invention. The  
 CC enzyme of the invention is beta-secretase, and specifically cleaves  
 CC beta-amyloid precursor protein (beta-APP). Normal processing of beta-APP  
 CC is thought to occur via cleavage between residues 16 and 17 of the  
 CC beta-amyloid peptide region by an alpha-secretase. Pathogenic processing  
 CC is thought to occur by beta-secretase cleavage of beta-APP.  
 CC Beta-secretase activity can be detected and measured using a method of  
 CC the invention, which detects at least one of the beta-secretase cleavage  
 CC products formed on cleavage. The method can be used to determine whether  
 CC a test substance inhibits proteolytic cleavage, by beta-secretase, of  
 CC beta-APP. Compounds effective to at least partially inhibit  
 CC beta-secretase activity can be used to inhibit cleavage of beta-APP in  
 CC cells or mammalian hosts. Isolation and purification of beta-secretase  
 CC will permit chemical modelling of a critical event in the pathology of  
 CC Alzheimer's disease.  
 SQ Sequence 21 AA;

Query Match 100.0%; Score 16; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 7.1e-12;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16  
 DB 6 DAEFRHDSGYEVHHQK 21

RESULT 4

ID R07753 standard; protein; 22 AA.  
 AC R07753;  
 DT 22-FEB-1991 (first entry)  
 DE Beta-amyloid protein, SCVAP2.  
 KW Monoclonal antibody SV17-6E10; Down's syndrome; Alzheimer's disease;  
 KW beta-amyloid precursor; amyloid plaques.  
 OS Synthetic.  
 PN W09012871-A.  
 PD 01-NOV-1990.  
 PF 13-APR-1990; US-338983.  
 PR 14-APR-1989; US-338983.  
 PA (REME-) RES FOUND MENTAL HY.  
 PI Kim KS, Wisniewski HM, Wen GY, Chen CMJ, Sapienza VJ;  
 DR WPI: 90-348474/46.  
 PT Cerebrovascular amyloid protein-specific monoclonal antibody  
 PT SV17-6E10 - for immunosay of peptide whose levels are raised in  
 PT Down's syndrome or Alzheimer's disease patients  
 PS Example 4; page 11; 24pp; English.  
 CC This peptide is used in a "Double Ab Sandwich Immunoassay" to  
 CC detect beta-amyloid protein. SV17-6E10 MAb(capture Ab) is used  
 CC to coat microtitre plate wells. The plate is then washed (dist-  
 CC illed water), coated with PBS(IGB) and this (SCVAP2) protein is  
 CC added. The plate is washed and a 2nd Ab (detection Ab), MAb 4G8-  
 CC This double Ab sandwich ELISA test is a highly sensitive and  
 CC accurate detection system for the beta-amyloid protein.  
 CC See also R07752.  
 SQ Sequence 22 AA;

Query Match 100.0%; Score 16; DB 1; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 7.4e-12;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16  
 DB 1 DAEFRHDSGYEVHHQK 16

RESULT 5

ID P90381 standard; protein; 28 AA.  
 AC P90381;  
 DT 1-NOV-1989 (first entry)  
 DE Synthetic A4 amyloid peptide  
 KW Synthetic; A4 amyloid polypeptide; Alzheimer's disease;  
 KW immunoassays; antibodies.  
 OS Synthetic  
 PN W08906242-A.  
 PD 13-JUL-1989.  
 PF 11-OCT-1988; U03590.  
 PR 08-OCT-1987; US-105751.  
 PA (MCLE) McLean Hospital Corp; (UYRO) University of Rochester.  
 PI Majocha R, Marotta CA, Zain S;  
 DR WPI: 89-220551/30.  
 PT Antibodies to A4 amyloid polypeptide  
 PT - used in immunoassays and for imaging of A4 amyloid  
 PT in Alzheimer's diseased patients.  
 PS Claim 1; page 27; 30pp; English.  
 CC Synthetic A4 amyloid polypeptide (see also P90382, P90383).  
 CC Used as immunogen, (un)coupled or to produce antibodies. Used in  
 CC immunoassays and for imaging of A4 amyloid in Alzheimer's disease.  
 SQ Sequence 28 AA;

Query Match 100.0%; Score 16; DB 1; Length 28;



Best Local Similarity 100.0%; Pred. No. 9.2e-12;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16  
| | | | | | | | | | | | | | | |  
Db 1 DAEFRHDSGYEVHHQK 16

RESULT 6  
R54702  
ID R54702 standard; peptide; 28 AA.  
AC R54702;  
DT 15-DEC-1994 (first entry)  
DE Beta-amyloid fragment (1-28).  
KW Beta-amyloid protein; BAP; Alzheimer's disease; diagnosis.  
OS Homo sapiens.  
PN W03409364-A.  
PD 28-APR-1994.  
PF 13-OCT-1993; U09772.  
PR 13-OCT-1992; US-959251.  
PA (UYDU-) UNIV DUKE.  
PI Strittmatter WJ.  
DR WPI; 94-151484/18.  
PT Immobilised beta-amyloid protein or fragments - used in assays  
PT for obtaining prods for use in the diagnosis and treatment of  
PT disorders such as Alzheimer's disease.  
PS Claim 4; Page 28; 49pp; English.  
CC A construct comprising a beta-amyloid protein (BAP) or fragment (esp.  
CC the peptides given in R54702-03) immobilised on a solid support can be  
CC used to detect cpds. which bind to BAP. Binding of proteins in  
CC human cerebrospinal fluid proteins were shown to bind to beta-  
CC amyloid peptides 1-28 and 12-28. Hydropathic mimic peptide (12-28)  
CC was used as control.  
SQ Sequence 28 AA;

Query Match 100.0%; Score 16; DB 1; Length 28;  
Best Local Similarity 100.0%; Pred. No. 9.2e-12;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16  
| | | | | | | | | | | | | | | |  
Db 1 DAEFRHDSGYEVHHQK 16

RESULT 7  
R60368  
ID R60368 standard; peptide; 28 AA.  
AC R60368;  
DT 15-MAR-1995 (first entry)  
DE Beta-amyloid (1-28).  
KW Amyloid precursor protein; APP; Alzheimer's disease; beta-amyloid;  
KW anti-beta-amyloid antibody; diagnosis; immunogen; antigen; epitope.  
OS Homo sapiens.  
PN W09417197-A.  
PD 04-AUG-1994.  
PF 24-JAN-1994; J00089.  
PR 25-JAN-1993; JP-010132.  
PR 05-FEB-1993; JP-019035.  
PR 16-NOV-1993; JP-286985.  
PR 28-DEC-1993; JP-334773.  
PA (TAKE ) TAKEDA CHEM IND LTD.  
PI Kitada C, Odaka A, Suzuki N;  
DR WPI; 94-264110/32.  
PT Antibodies recognising specific parts of beta-amyloid - can be  
PT used for diagnosis of diseases implicating beta-amyloid, such as,  
PT Alzheimer's disease  
PS Claim 7; Page 84; 116pp; Japanese.  
CC Antibodies which recognise specific subfragments of the beta-amyloid  
CC protein are claimed. Specifically, the antibodies (which are pref.  
CC monoclonal) recognise residues 1-16 and/or 1-28 from the N-terminal  
CC portion of beta-amyloid or they recognise residues 25-35 or 35-43  
CC from the C-terminal portion. The antibodies are useful for assaying

CC beta-amyloid and its derivatives for diagnosis of Alzheimer's  
CC disease.  
SQ Sequence 28 AA;

Query Match 100.0%; Score 16; DB 1; Length 28;  
Best Local Similarity 100.0%; Pred. No. 9.2e-12;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16  
| | | | | | | | | | | | | | | |  
Db 1 DAEFRHDSGYEVHHQK 16

RESULT 8  
W01413  
ID W01413 standard; Protein; 28 AA.  
AC W01413;  
DT 20-JAN-1997 (first entry)  
DE Beta/A4-amyloid peptide; tissue plasminogen activator;  
KW Beta/A4-amyloid peptide; investigation; pathogenesis;  
KW Alzheimer's disease; stimulation; investigation; pathogenesis;  
KW hereditary cerebral haemorrhage with amyloidosis-Dutch type;  
KW control; cerebral amyloid angiopathy; cerebral; haemorrhage;  
KW hemorrhage.  
OS Homo sapiens.  
PN W09615799-A1.  
PD 30-MAY-1996.  
PF 22-NOV-1995; U15007.  
PR 22-NOV-1994; US-347144.  
PA (RUTF ) UNIV RUTGERS STATE NEW JERSEY.  
PI Anderson S;  
DR WPI; 96-288332/27.  
PT Use of agents which bind beta-amyloid peptide - for diagnosis,  
PT prevention and treatment of vascular damage caused by amyloid  
PT deposits, Part. in haemorrhaging and Alzheimer's disease  
PS Example 1; Fig 1; 52pp; English.  
CC To investigate the effects of beta-amyloid peptide (BAP) on  
CC tissue plasminogen activator (t-PA) 3 synthetic peptides were used.  
CC One peptide contained 42 amino acids and corresp. to the full  
CC length BAP (R95248). The other 2 peptides (R95249 and 50) contained  
CC the 28 N-terminal residues of the BAP found in Alzheimer's disease  
CC and hereditary cerebral haemorrhage with amyloidosis-Dutch type  
CC (HCHWA-D), respectively. In an assay to determine the effect of  
CC the peptides on t-PA activation, each peptide (R95248, 49 and 50)  
CC gave 1st order rate constant of activation (k<sub>app</sub>) values of  
CC 13.4, 13.9 and 14.8, respectively, compared to 1.7 and 7.8 for null  
CC and fibrinogen controls. The results demonstrate that the BAP are  
CC able to stimulate t-PA activity in vitro, which is significant in  
CC that it provides a means for investigating and controlling the  
CC pathogenesis of Alzheimer's disease, HCHWA-D and cerebral amyloid  
CC angiopathy related cerebral haemorrhage.  
SQ Sequence 28 AA;

Query Match 100.0%; Score 16; DB 1; Length 28;  
Best Local Similarity 100.0%; Pred. No. 9.2e-12;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQK 16  
| | | | | | | | | | | | | | | |  
Db 1 DAEFRHDSGYEVHHQK 16

RESULT 9  
W01414  
ID W01414 standard; Protein; 28 AA.  
AC W01414;  
DT 20-JAN-1997 (first entry)  
DE Beta/A4-amyloid peptide residues 1-28 Dutch.  
KW Beta/A4-amyloid peptide; tissue plasminogen activator; Dutch;  
KW Alzheimer's disease; stimulation; investigation; pathogenesis;  
KW hereditary cerebral haemorrhage with amyloidosis-Dutch type;

control; cerebral amyloid angiopathy; cerebral; haemorrhage;  
hemorrhage.  
Homo sapiens.  
Key Location/Qualifiers  
misc\_difference 22 /note= "wild type Glu substd. with Gln"  
W09615799-A1. PN  
30-MAY-1996. PN  
22-NOV-1995; U15007. PF  
22-NOV-1994; US-347144. PF  
(RUTE ) UNIV RUTGERS STATE NEW JERSEY. PR  
Anderson S. PR  
WPI; 96-268332/27. PR  
Use of agents which bind beta-amyloid peptide - for diagnosis, prevention and treatment of vascular damage caused by amyloid deposits, partic. in haemorrhaging and Alzheimer's disease Example 1; Fig 1; 52pp; English. PR  
To investigate the effects of beta-amyloid peptide (BAP) on tissue plasminogen activator (t-PA) 3 synthetic peptides were used. One peptide contained 42 amino acids and corresp. to the full length BAP (R95248). The other 2 peptides (R95249 and 50) contained the 28 N-terminal residues of the BAP found in Alzheimer's disease and hereditary cerebral haemorrhage with amyloidosis-Dutch type (HCHWA-D), respectively. In an assay to determine the effect of the peptides on t-PA activation, each peptide (R95248, 49 and 50) gave 1st order rate constant of activation (k(app)) values of 13.4, 13.9 and 14.5, respectively, compared to 1.7 and 7.8 for null and fibrinogen controls. The results demonstrate that the BAP are able to stimulate t-PA activity in vitro, which is significant in that it provides a means for investigating and controlling the pathogenesis of Alzheimer's disease, HCHWA-D and cerebral amyloid angiopathy related cerebral haemorrhage.  
Sequence 28 AA;  
Query Match 100.0%; Score 16; DB 1; Length 28;  
Best Local Similarity 100.0%; Pred. No. 9.2e-12;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DAEFRHDSGYEVHHQK 16  
| | | | | | | | | | | | | | | | | |  
DB 1 DAEFRHDSGYEVHHQK 16  
| | | | | | | | | | | | | | | | | |  
RESULT 10  
R64170  
ID R64170 standard; peptide; 28 AA.  
AC R64170;  
DT 03-AUG-1995 (first entry)  
DE A4-O(1-28) a partial beta amyloid peptide.  
DE beta amyloid protein; mutant; variant; detection; amyloid deposition;  
KW diagnosis; amyloidosis associated disease; Alzheimer's disease;  
KW Down's syndrome; A4-O(1-28).  
OS Synthetic.  
PN W09428412-A.  
PD 08-DEC-1994. U05809.  
PF 27-MAY-1994; US-069010.  
PR 28-MAY-1993; US-069010.  
PA (MIRI-) MIRIAM HOSPITAL.  
PA Majocha RE, Marotta CA;  
PI WPI; 95-023013/03.  
DR Amyloid binding composition comprising labelled amyloid protein and carrier - useful for in vivo imaging of amyloid deposits, for diagnosing Alzheimer's disease and Down's Syndrome.  
PS Example 3; Page 23; 58pp; English.  
CC AD (Alzheimer's disease) brain and a Down Syndrome brain. Three of the CC R64172, the A4-B(1-28) polypeptide is deriv. from vascular amyloid of the CC R64172, the A4-B(1-28) polypeptide is deriv. from vascular amyloid of the CC 28 amino acids are different from the A4-O(1-28) peptide shown in R64170. CC A4-O has strong aggregation properties, and binds to itself strongly. It CC is used to obtain and select beta amyloid proteins that can be used for CC in vivo imaging of amyloid deposits and hence diagnosis of an CC amyloidosis-associated disease, such as AD or Down's syndrome. R64165 CC shows the generic sequence of the amyloid protein for generation of CC variants.  
Sequence 28 AA;  
Query Match 100.0%; Score 16; DB 1; Length 28;  
Best Local Similarity 100.0%; Pred. No. 9.2e-12;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DAEFRHDSGYEVHHQK 16  
| | | | | | | | | | | | | | | | | |  
DB 1 DAEFRHDSGYEVHHQK 16  
| | | | | | | | | | | | | | | | | |  
RESULT 12  
W81467  
ID W81467 standard; peptide; 28 AA.  
AC W81467;  
DT 28-JAN-1999 (first entry)  
DE Synthetic amyloid beta (Abeta) peptide 2 (residues 1-28).  
DE Amyloid beta; Abeta; deoxygenated solvent; evaporative deposition;  
KW research; neurotoxicity; free-radical; glutamine synthetase.  
OS Synthetic.  
PN US5840838-A.  
PD 24-NOV-1998. 609090.  
PF 29-FEB-1996; US-609090.  
PR 29-FEB-1996; US-609090.  
PA (KENT ) UNIV KENTUCKY RES FOUND.  
PI Alexenoy M, Butterfield DA, Carney JM, Hensley K;  
DR WPI; 99-034120/03  
PT Process for treating synthetic amyloid beta peptides - by organic solvent treatment, useful for studying neurotoxicity  
PS Claim 5; Columns 9-10; 14pp; English.

CC Sequences W81466 to W81476 represent synthetic amyloid beta (Abeta)  
 CC peptides. The invention provides a process for treating a synthetic  
 CC Abeta peptide that comprises dissolving the peptide in a deoxygenated  
 CC solvent selected from trifluoroethanol, hexafluorocyclohexane, dimethyl-  
 CC sulphoxide, morpholinopropanesulphonic acid, dimethylformamide and  
 CC acetonitrile to a concentration of 0.01-10 mg/ml, incubating the solution  
 CC at 20-65 deg. C for 0.5-4 hour, and removing the solvent by 'evaporative  
 CC deposition' in 5-10 minutes. Synthetic amyloid beta peptides are useful  
 CC as research tools for studying neurotoxicity resulting from Abeta peptide  
 CC enhanced free-radical production. The treatment increases the activity  
 CC of the synthetic Abeta peptides in tests to determine free-radical  
 CC generating capacity and glutamine synthetase inactivation.  
 SQ Sequence 28 AA;

Query Match 100.0%; Score 16; DB 1; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-12;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16  
 |||||  
 Db 1 DAEFRHDSGYEVHHQK 16

RESULT 13

ID W81468 standard; peptide; 30 AA.  
 AC W81468:  
 DT 28-JAN-1999 (first entry)  
 DE Synthetic amyloid beta (Abeta) peptide 3 (residues 1-30).  
 KW Amyloid beta; Abeta; deoxygenated solvent; evaporative deposition;  
 KW research; neurotoxicity; free-radical; glutamine synthetase.  
 OS Synthetic.  
 PN US5840838-A.  
 PD 24-NOV-1998.  
 PF 29-FEB-1996; 609090.  
 PR 29-FEB-1996; US-609090.  
 PA (KENT ) UNIV KENTUCKY RES FOUND.  
 PI Aksenov M, Butterfield DA, Carney JM, Hensley K;  
 DR WPI: 99-034120/03.  
 PT Process for treating synthetic amyloid beta peptides - by organic  
 PT solvent treatment, useful for studying neurotoxicity  
 PS Claim 5; Columns 9-10; 14pp; English.  
 CC Sequences W81466 to W81476 represent synthetic amyloid beta (Abeta)  
 CC peptides. The invention provides a process for treating a synthetic  
 CC Abeta peptide that comprises dissolving the peptide in a deoxygenated  
 CC solvent selected from trifluoroethanol, hexafluorocyclohexane, dimethyl  
 CC sulphoxide, morpholinopropanesulphonic acid, dimethylformamide and  
 CC acetonitrile to a concentration of 0.01-10 mg/ml, incubating the solution  
 CC at 20-65 deg. C for 0.5-4 hour, and removing the solvent by 'evaporative  
 CC deposition' in 5-10 minutes. Synthetic amyloid beta peptides are useful  
 CC as research tools for studying neurotoxicity resulting from Abeta peptide  
 CC enhanced free-radical production. The treatment increases the activity  
 CC of the synthetic Abeta peptides in tests to determine free-radical  
 CC generating capacity and glutamine synthetase inactivation.  
 SQ Sequence 30 AA;

Query Match 100.0%; Score 16; DB 1; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 9.8e-12;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16  
 |||||  
 Db 1 DAEFRHDSGYEVHHQK 16

RESULT 14

ID W81469 standard; peptide; 33 AA.  
 AC W81469:  
 DT 28-JAN-1999 (first entry)  
 DE Synthetic amyloid beta (Abeta) peptide 4 (residues 1-33).  
 KW Amyloid beta; Abeta; deoxygenated solvent; evaporative deposition;  
 KW research; neurotoxicity; free-radical; glutamine synthetase.  
 OS Synthetic.  
 PN US5840838-A.  
 PD 24-NOV-1998.  
 PF 29-FEB-1996; 609090.  
 PR 29-FEB-1996; US-609090.  
 PA (KENT ) UNIV KENTUCKY RES FOUND.  
 PI Aksenov M, Butterfield DA, Carney JM, Hensley K;  
 DR WPI: 99-034120/03.  
 PT Process for treating synthetic amyloid beta peptides - by organic  
 PT solvent treatment, useful for studying neurotoxicity  
 PS Claim 5; Columns 9-10; 14pp; English.  
 CC Sequences W81466 to W81476 represent synthetic amyloid beta (Abeta)  
 CC peptides. The invention provides a process for treating a synthetic  
 CC Abeta peptide that comprises dissolving the peptide in a deoxygenated  
 CC solvent selected from trifluoroethanol, hexafluorocyclohexane, dimethyl  
 CC sulphoxide, morpholinopropanesulphonic acid, dimethylformamide and  
 CC acetonitrile to a concentration of 0.01-10 mg/ml, incubating the solution  
 CC at 20-65 deg. C for 0.5-4 hour, and removing the solvent by 'evaporative  
 CC deposition' in 5-10 minutes. Synthetic amyloid beta peptides are useful  
 CC as research tools for studying neurotoxicity resulting from Abeta peptide  
 CC enhanced free-radical production. The treatment increases the activity  
 CC of the synthetic Abeta peptides in tests to determine free-radical

KW Beta-cleavage site: beta amyloid precursor protein; APP; beta-secretase;  
 KW alpha-secretase; proteolytic cleavage; inhibitor; Alzheimer's disease.  
 OS Synthetic.  
 PN WO9640885-A2.  
 PD 19-DEC-1996.  
 PF 07-JUN-1996; U09985.  
 PR 07-JUN-1995; US-485152.  
 PR 07-JUN-1995; US-480498.  
 PA (ATHE-) ARHENA NEUROSCIENCES INC.  
 PI Anderson JP, Chrysler SMS, Jacobson-croak KL, Keim PS;  
 FI Mcconlogue LC, Sinha S, Tan H;  
 DR WPI: 97-052304/05.  
 PT Beta-secretase which specifically cleaves beta-amyloid precursor  
 PT protein - useful to screen for inhibitors useful in treatment of  
 PT Alzheimer's disease  
 PS Disclosure; Page 44; 92pp; English.  
 CC W08359-W08362 represent substrates for the enzyme of the invention. The  
 CC enzyme of the invention is beta-secretase, and specifically cleaves  
 CC beta-amyloid precursor protein (beta-APP). Normal processing of beta-APP  
 CC is thought to occur via cleavage between residues 16 and 17 of the  
 CC beta-amyloid peptide region by an alpha-secretase. Pathogenic processing  
 CC is thought to occur by beta-secretase cleavage of beta-APP.  
 CC Beta-secretase activity can be detected and measured using a method of  
 CC the invention, which detects at least one of the beta-secretase cleavage  
 CC products formed on cleavage. The method can be used to determine whether  
 CC a test substance inhibits proteolytic cleavage, by beta-secretase, of  
 CC beta-APP. Compounds effective to at least partially inhibit  
 CC beta-secretase activity can be used to inhibit cleavage of beta-APP in  
 CC cells or mammalian hosts. Isolation and purification of beta-secretase  
 CC will permit chemical modelling of a critical event in the pathology of  
 CC Alzheimer's disease.  
 SQ Sequence 33 AA;

Query Match 100.0%; Score 16; DB 1; Length 33;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-11;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16  
 |||||  
 Db 18 DAEFRHDSGYEVHHQK 33

RESULT 15

ID W81469 standard; peptide; 33 AA.  
 AC W81469:  
 DT 28-JAN-1999 (first entry)  
 DE Synthetic amyloid beta (Abeta) peptide 4 (residues 1-33).  
 KW Amyloid beta; Abeta; deoxygenated solvent; evaporative deposition;  
 KW research; neurotoxicity; free-radical; glutamine synthetase.  
 OS Synthetic.  
 PN US5840838-A.  
 PD 24-NOV-1998.  
 PF 29-FEB-1996; 609090.  
 PR 29-FEB-1996; US-609090.  
 PA (KENT ) UNIV KENTUCKY RES FOUND.  
 PI Aksenov M, Butterfield DA, Carney JM, Hensley K;  
 DR WPI: 99-034120/03.  
 PT Process for treating synthetic amyloid beta peptides - by organic  
 PT solvent treatment, useful for studying neurotoxicity  
 PS Claim 5; Columns 9-10; 14pp; English.  
 CC Sequences W81466 to W81476 represent synthetic amyloid beta (Abeta)  
 CC peptides. The invention provides a process for treating a synthetic  
 CC Abeta peptide that comprises dissolving the peptide in a deoxygenated  
 CC solvent selected from trifluoroethanol, hexafluorocyclohexane, dimethyl  
 CC sulphoxide, morpholinopropanesulphonic acid, dimethylformamide and  
 CC acetonitrile to a concentration of 0.01-10 mg/ml, incubating the solution  
 CC at 20-65 deg. C for 0.5-4 hour, and removing the solvent by 'evaporative  
 CC deposition' in 5-10 minutes. Synthetic amyloid beta peptides are useful  
 CC as research tools for studying neurotoxicity resulting from Abeta peptide  
 CC enhanced free-radical production. The treatment increases the activity  
 CC of the synthetic Abeta peptides in tests to determine free-radical

CC generating capacity and glutamine synthetase inactivation.  
SQ Sequence 33 AA;

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Query Match      100.0%; Score 16; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 1,1e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	1	DAEFRHDSGYEVHHQK	16
Db	1	DAEFRHDSGYEVHHQK	16

Search completed: September 13, 2000, 02:25:00  
Job time: 173 sec